

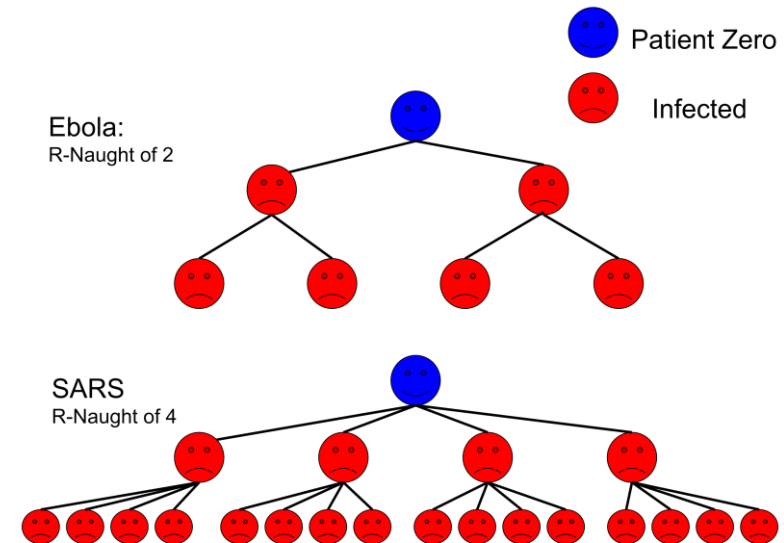
The background of the slide features three large, overlapping circles in a medium blue color, set against a dark gray background. The circles are arranged horizontally, with the middle circle overlapping the other two. A white horizontal band runs across the center of the image, containing the title text.

Forecasting the Basic Reproduction Number (R_0) for COVID-19

Dom Heger (2020)

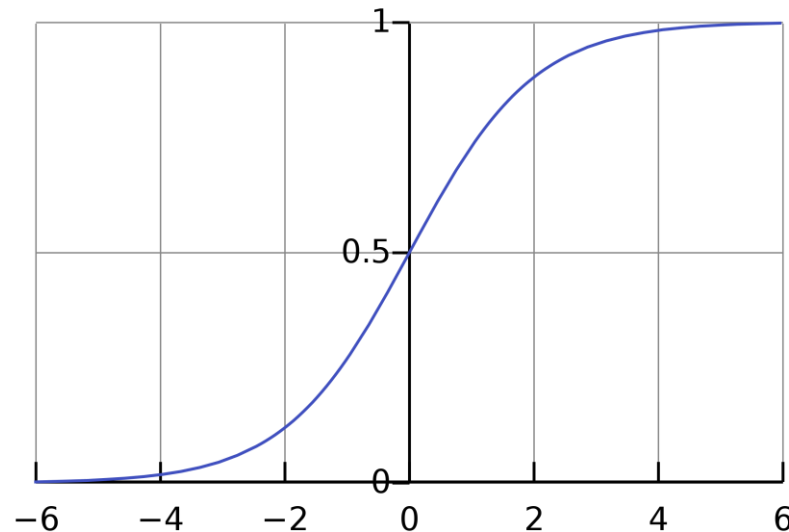
Basic Reproduction Number (R_0)

- The basic reproduction number (R_0) of an infection describes the expected number of cases directly generated by 1 case (person) in a population where all individuals are susceptible to infection.
- The definition describes the state where no other individuals are infected or immunized (naturally or through vaccination).
- It is very difficult to approximate R_0 for Covid-19 as only a few months worth of data is available, and some of the data is probably not even any good.



Our Approach – Stretched Sigmoid Function

- Our approach basically follows a sigmoid logistic curve with an interval $[-7 .. 7]$. To generate a path for R_0 , we evenly divide the closed interval $[-7 .. 7]$ by the number of days we assume it will take to get from $R_{0,t-1}$ to $R_{0,target}$ and insert the results into the formula as x .
- Rather than merely guessing the number of days, we take the average daily rate of the progress towards $R_{0,target}$ over the last several days (via a log function).



Traditional Sigmoid Function

Mathematical Details (1/2)

We forecast each day's new confirmed cases according to the formula:

$$c_t = contagious_{t-1} \times R_{0,t} / days_{contagious} \times (1 - immune_{t-1})$$

where

- $c_t \Rightarrow$ new confirmed cases @ time t
- $C_t \Rightarrow$ cumulative confirmed cases @ time t
- $contagious_t \Rightarrow C_t - C_{t-days_{contagious}}$
- $days_{contagious} \Rightarrow$ number of days each case is assumed to be contagious = 12, by default
- $immune \Rightarrow$ fraction of the population that is immune = $prevalence / (1 - unreported)$
- $prevalance \Rightarrow$ cumulative confirmed cases as a fraction of the total population = $C_t / population$
- $unreported \Rightarrow$ fraction of all cases that are not reported
- $R_{0,t} \Rightarrow$ depicts the average number of people infected from 1 other person ≥ 0

Mathematical Details (2/2)

We assume that the path of R_0 (basic reproduction number) follows a sigmoid curve from the most recent R_0 to some target.

$$R_{0,t} = f(x) \Rightarrow \frac{R_{0,target} - R_{0,t-1}}{1 + e^{(-k \times (x - offset))}}$$

where

- $R_{0,target} \Rightarrow$ assumed target basic reproduction number
- $e \Rightarrow$ base of the natural logarithm ≈ 2.71828
- $offset \Rightarrow x$ value of the sigmoid's midpoint, default 0
- $k \Rightarrow$ logistic growth rate or steepness of the curve, default 1
- $x \Rightarrow$ real number in the closed interval -7 to 7

$$r_{\Delta} \Rightarrow \overline{\% \Delta(R_{0,target} - R_{0,t})}$$

and calculate the number of days to get from $R_{0,t-1}$ to $R_{0,target}$:

$$days \Rightarrow \log_{1+r_{\Delta}}(2) = \ln(2) / \ln(1 + r_{\Delta}), \text{ rounded}$$

This assumes that the recent daily percent progress holds true in the near future. Our approach differs from other research being conducted as our work has shown that adjusting the sigmoid's logistic growth rate (k) from its default value of 1 provides the best possible results, based on the data available for our study.