

Epidemics, Networks, Interventions

Things I Learned About Very Recently

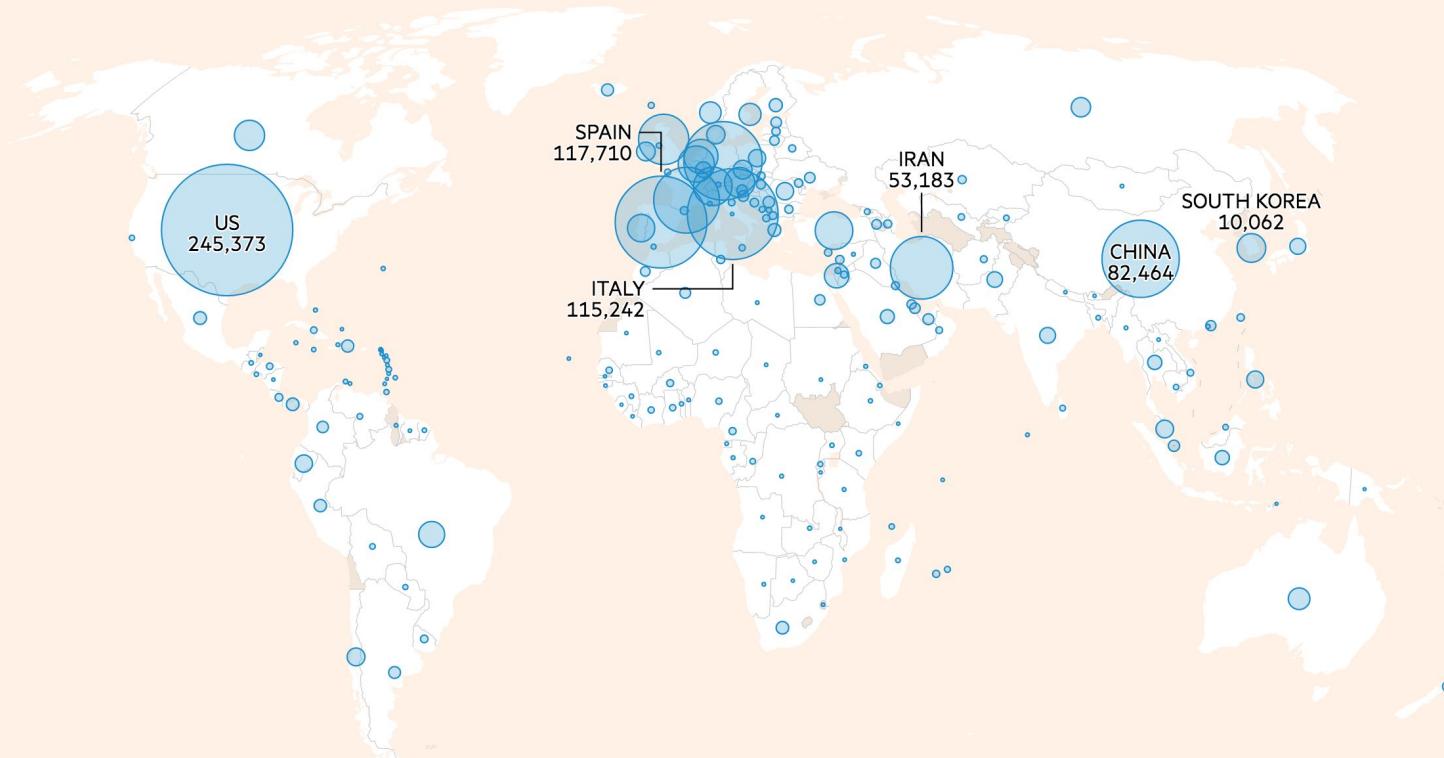
Fabian Dablander, PhD Candidate

Department of Psychological Methods
University of Amsterdam

As of 11:41am Apr 3 BST

Confirmed cases
1,031,283

Deaths
54,206



Graphic: Steven Bernard and Cale Tilford

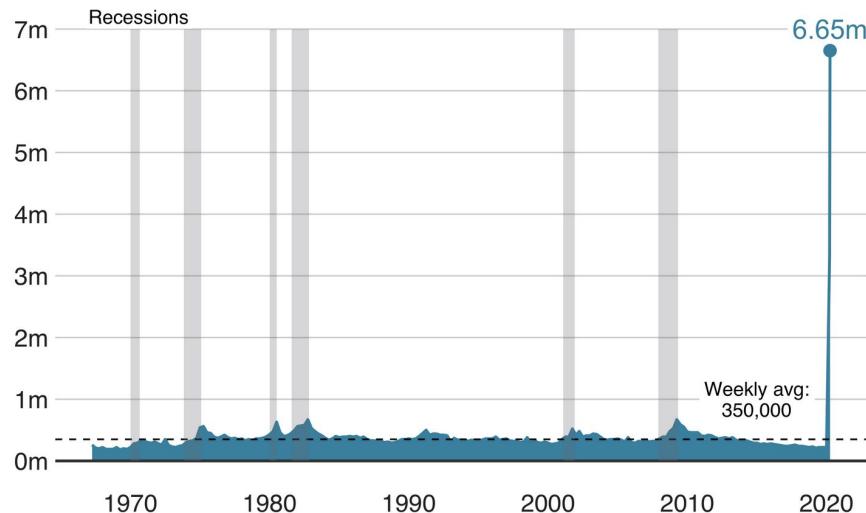
Source: Johns Hopkins University, CSSE; Worldometers

© FT



Source: Bloomberg, 01 April 2020, 09:00 GMT

BBC



<https://www.bbc.com/news/business-51706225>

Source: US Bureau of Labor Statistics

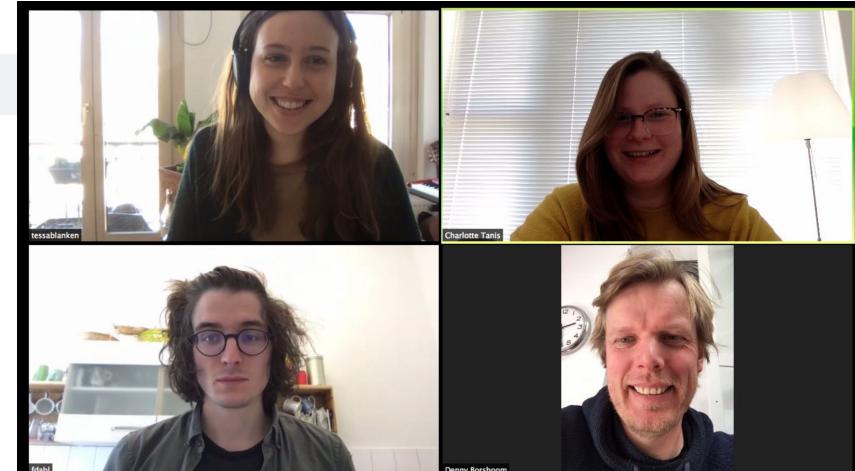
BBC

Mission Statement

Without data, society cannot see. And if society cannot see, it cannot act wisely. Our mission is to make our skills as data scientists available to help society in its battle against the Coronavirus by improving its observations of the world. We do this by providing advice and assistance in the analysis of data, as well as initiating novel research projects designed to fully exploit tools of modern dat science.

To get an idea for what we can do for you, take a look at the [Projects](#) page.

Do you have a data task that you think we can help with? Then head over to the [Data Consultancy Desk](#) to let us know.



<https://dataversuscorona.com/>

Outline

- 1) Basic Epidemiological Models
 - a) SIR and SIRS
 - b) SEIRS and SEIRS with Testing
 - c) Interventions
- 2) Epidemics on Networks
 - a) Spatial Structure
 - b) Interventions
- 3) How do the grown-ups model these things?
 - a) Modeling Interventions
 - b) Assessing Interventions

Basic Epidemiological Models

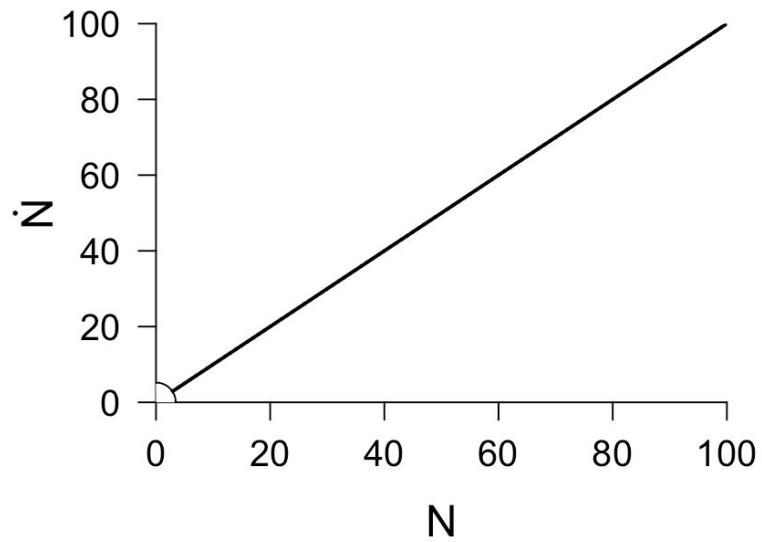
Preliminaries

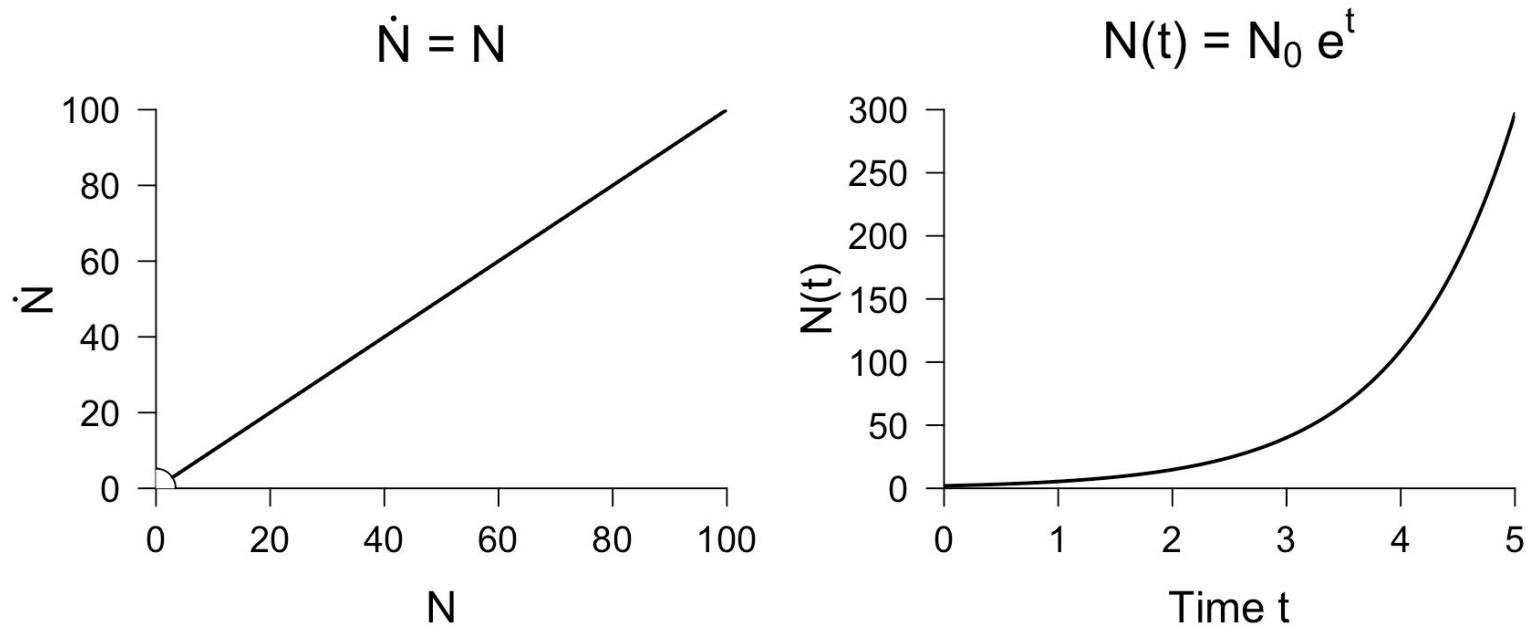
- Suppose N is the size of a population
- How does this population change over time?

$$\frac{dN}{dt} = \dot{N} = f(N)$$

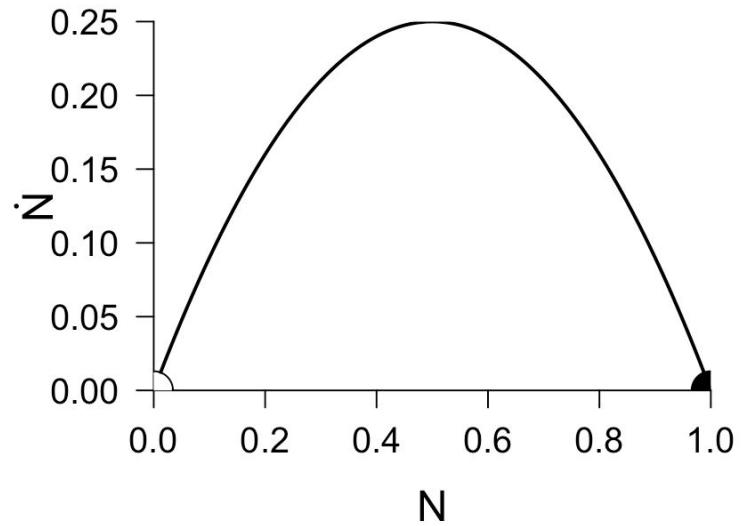
- Let's look at $\dot{N} = N$ and $\dot{N} = N(1 - N)$

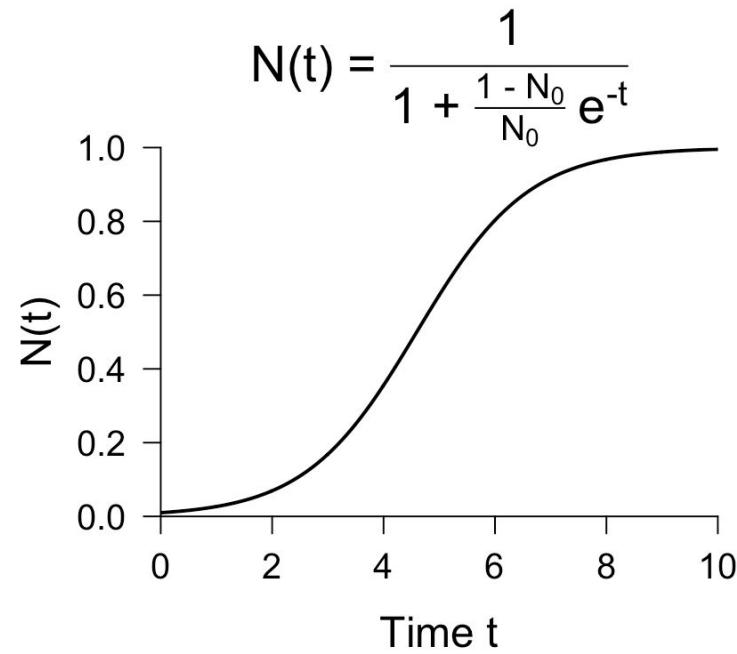
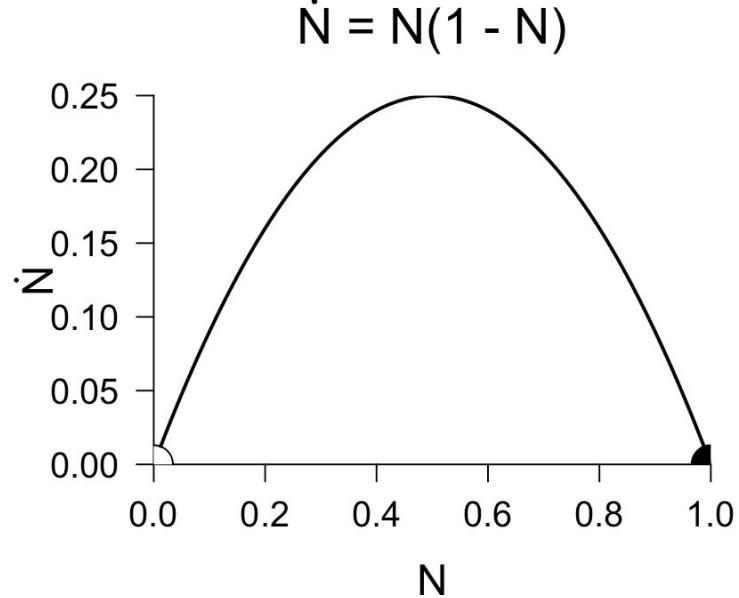
$$\dot{N} = N$$

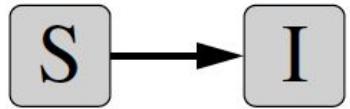




$$\dot{N} = N(1 - N)$$







Model

$$\dot{S} = -\beta IS$$

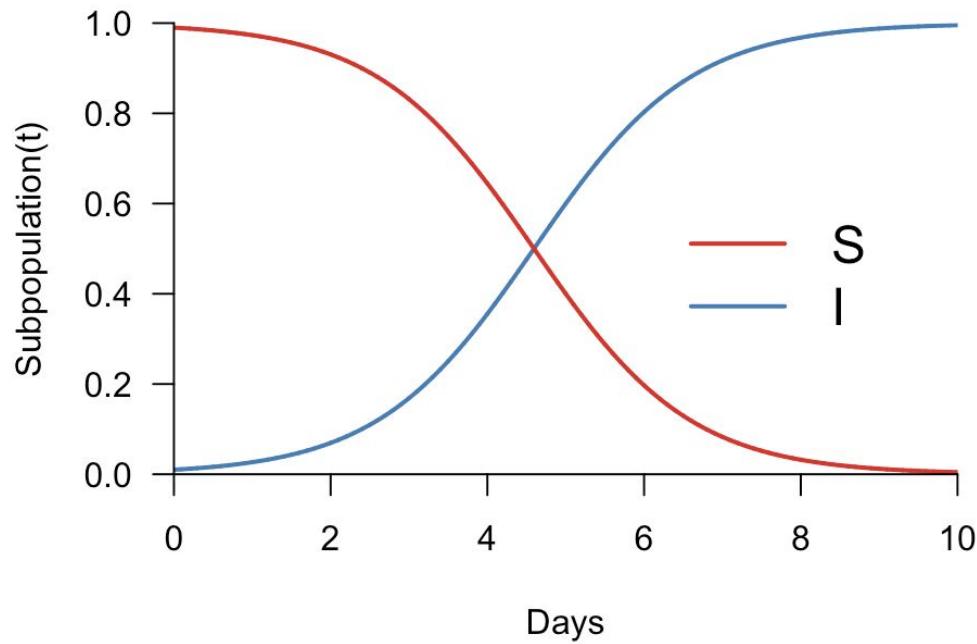
$$\dot{I} = \beta IS$$

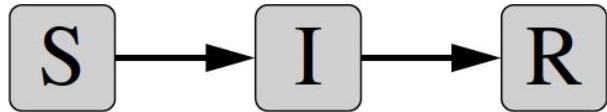
$$\begin{aligned}\dot{S} + \dot{I} &= 0 \\ S(t) + I(t) &= 1\end{aligned}$$

β ... is the contact rate

(each individual has β contacts per unit time with a randomly chosen other)

Inevitable Epidemic





Model

$$\dot{S} = -\beta IS$$

$$\dot{S} + \dot{I} + \dot{R} = 0$$

$$S(t) + I(t) + R(t) = 1$$

$$\dot{I} = \beta IS - \gamma I$$

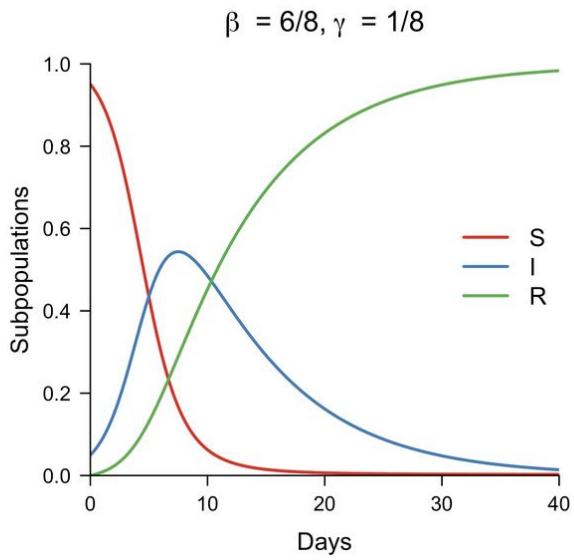
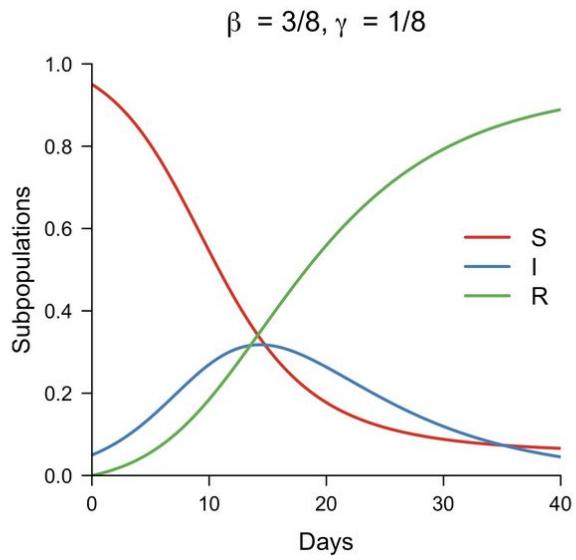
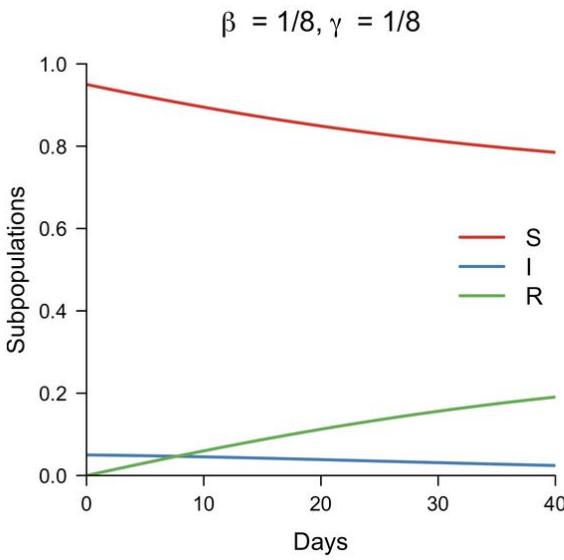
$$\dot{R} = \gamma I$$

β ... is the contact rate

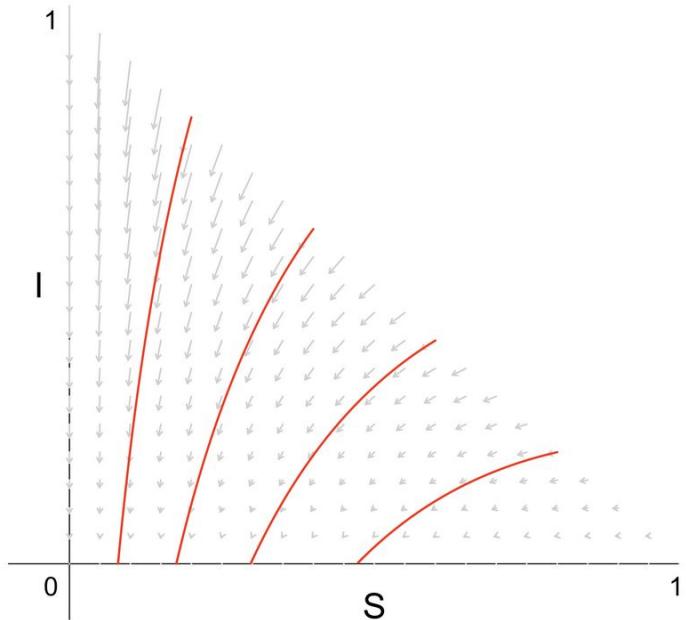
(each individual has β contacts per unit time with a randomly chosen other)

γ ... is the recovery rate

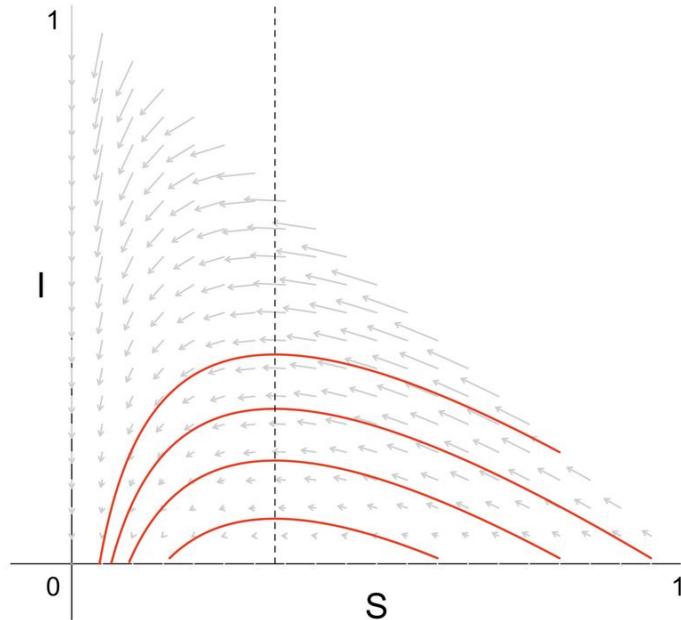
($\gamma = 1/D$ where D is the time it takes an individual to recover)



$$\beta = 1/8, \gamma = 1/8$$



$$\beta = 3/8, \gamma = 1/8$$





Basic Reproduction Number: R_0

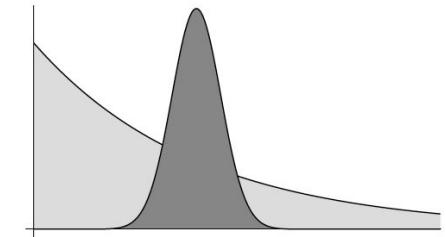
- Average number of additional people an infected person infects before recovering
 - Assumes that everybody is susceptible (we are at the start of an epidemic)
 - $R_0 = \beta / \gamma$
- Averages might be a poor summary of the distribution
 - Fat tails, super-spreaders, requires different interventions



Basic Reproduction Number: R_0

- The probability of being infected until time τ and then recovering is

$$p(\tau) = \gamma e^{-\gamma\tau}$$

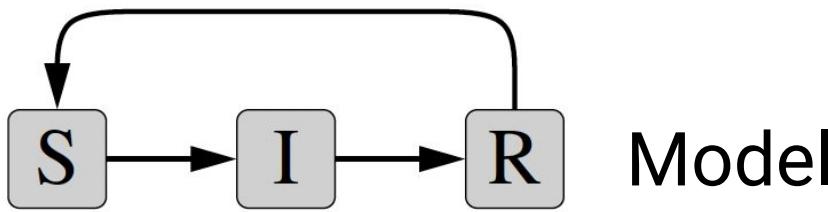


- On average, one individual infects $\tau\beta$ others during time τ

$$R_0 = \beta\tau \int_0^{\infty} \gamma e^{-\gamma\tau} d\tau = \beta\gamma \int_0^{\infty} \tau e^{-\gamma\tau} d\tau = \beta/\gamma$$

The Complexity of R_0

- Variation in R_0
 - 3 key influences: duration of infectiousness, likelihood of infection at contact, contact rate
 - 20 different R_0 values have been reported for measles (ranging from 3.7 - 203.3)
 - “Limited evidence supports the applicability of R_0 outside the region where the value was calculated” (p. 2)
- R_0 is technically not influenced by vaccination campaigns
 - It assumes a completely susceptible population; R_t is the right measure
- R_0 is very difficult to estimate
 - Nearly always retrospectively estimated
 - When estimated using mathematical models, highly dependent on assumptions



Model

$$\dot{S} = -\beta IS + \mu R$$

$$\dot{I} = \beta IS - \gamma I$$

$$\dot{R} = \gamma I - \mu R$$

β ... is the contact rate

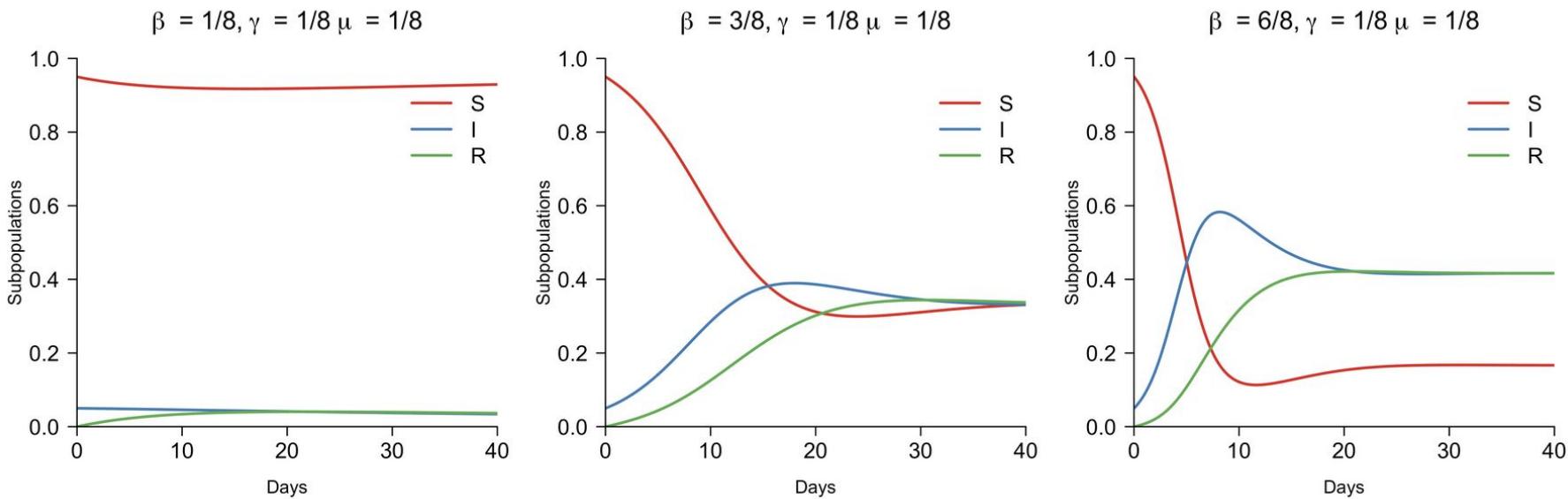
(each individual has β contacts per unit time with a randomly chosen other)

γ ... is the recovery rate

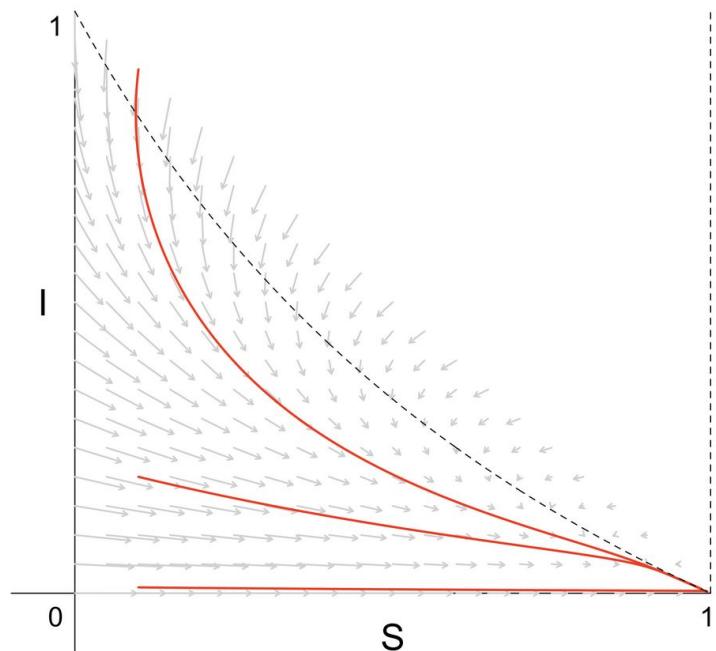
($\gamma = 1/D$ where D is the time it takes an individual to recover)

μ ... is the reinfection rate

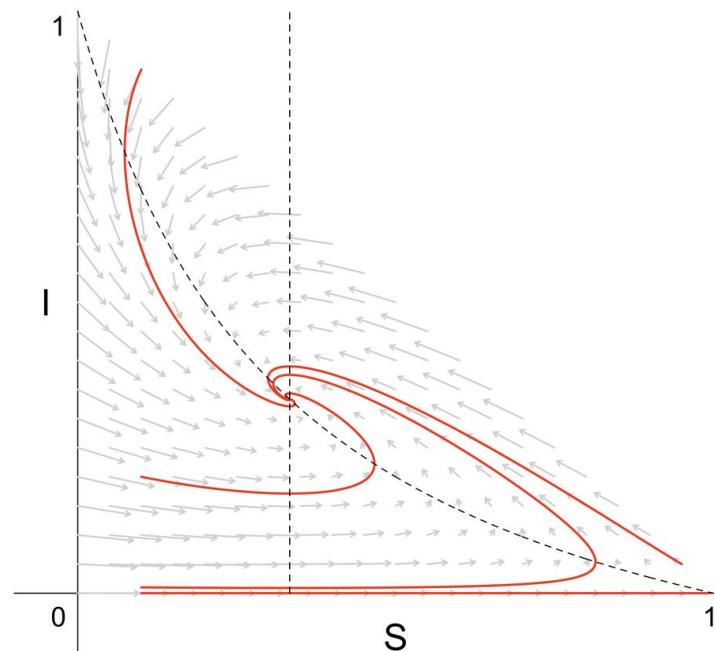
($\mu = 1/D$ where D is the time it takes an individual to lose immunity)

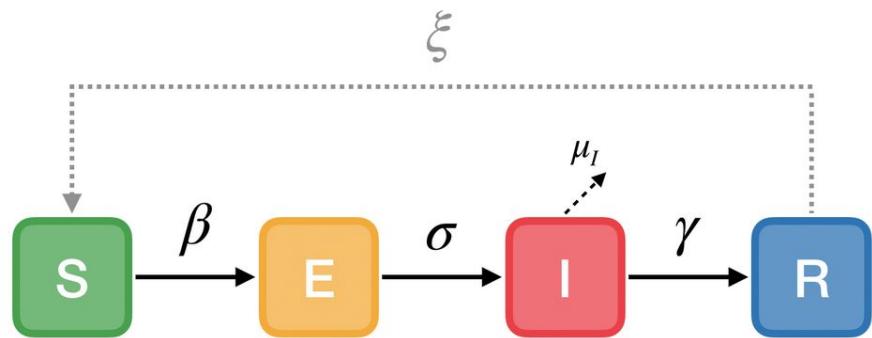


$$\beta = 1/8, \gamma = 1/8, \mu = 1/8$$



$$\beta = 3/8, \gamma = 1/8, \mu = 1/8$$





$$\dot{S} = \frac{-\beta SI}{N} + \xi R$$

$$\dot{E} = \frac{\beta SI}{N} - \sigma E$$

$$\dot{I} = \sigma E - \gamma I - \mu_I I$$

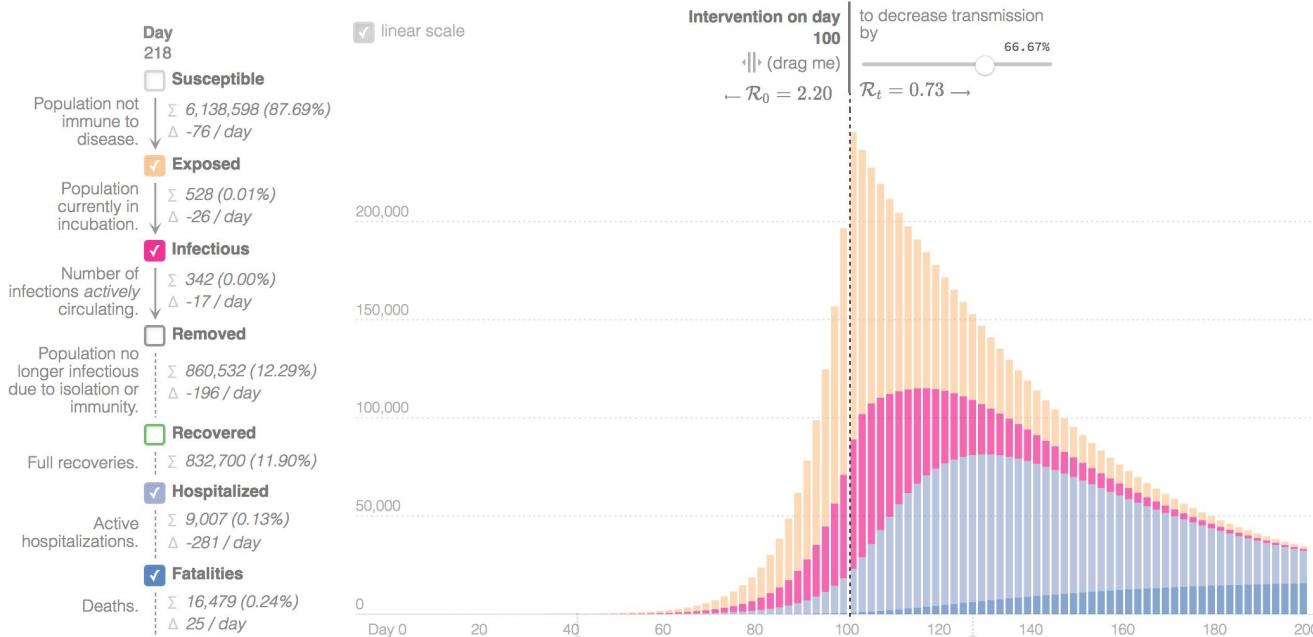
$$\dot{R} = \gamma I - \xi R$$

$$\dot{F} = \mu_I I$$

$$N = S + E + I + R$$

Interventions

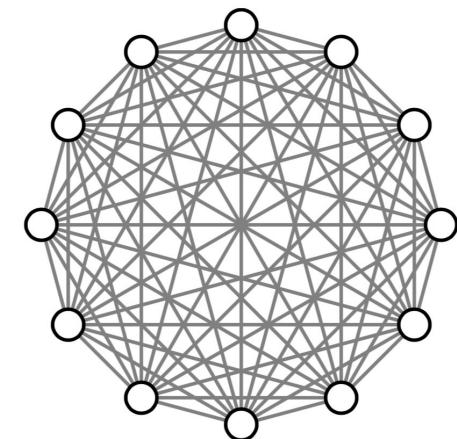
Epidemic Calculator



<https://gabgoh.github.io/COVID/index.html>

Limitations

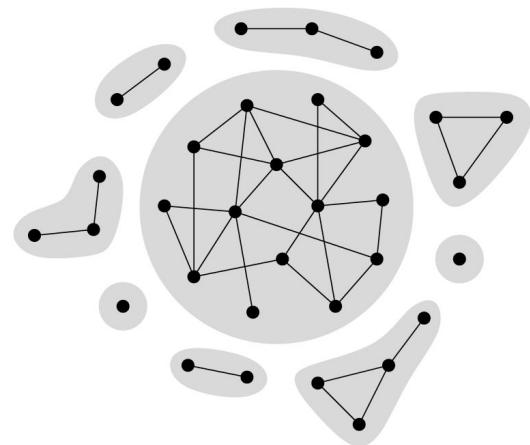
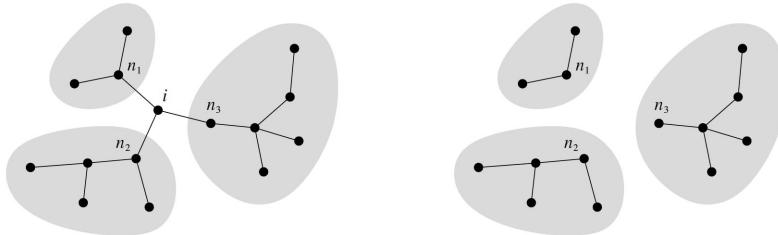
- Interventions change R_0 by magic, leading to no mechanistic insight
- All these models assume uniform mixing
- Every person is equally likely to have contact with every other person
- One way to incorporate spatial structure is with networks



Epidemics on Networks

Adding Network Structure

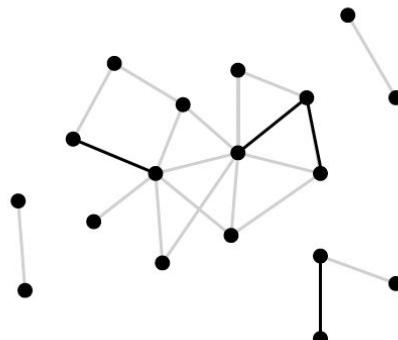
- Relax the assumption of a fully connected graph
- Nodes need to be connected for disease to transmit
 - Epidemic depends on network structure and position of initially infected people



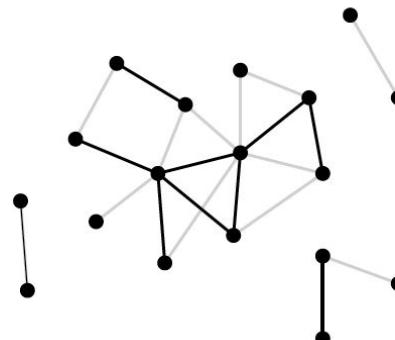
Size of the Outbreak

- Use bond percolation to calculate the expected size of the outbreak
 - A fraction of ϕ edges is occupied at random
 - Disease starts at a randomly chosen node

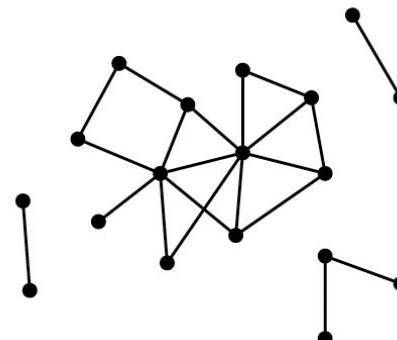
$$\phi = 1 - e^{-\beta\tau}$$



(a) $\phi = 0.2$



(b) $\phi = 0.5$



(c) $\phi = 1$

Dynamics on Networks

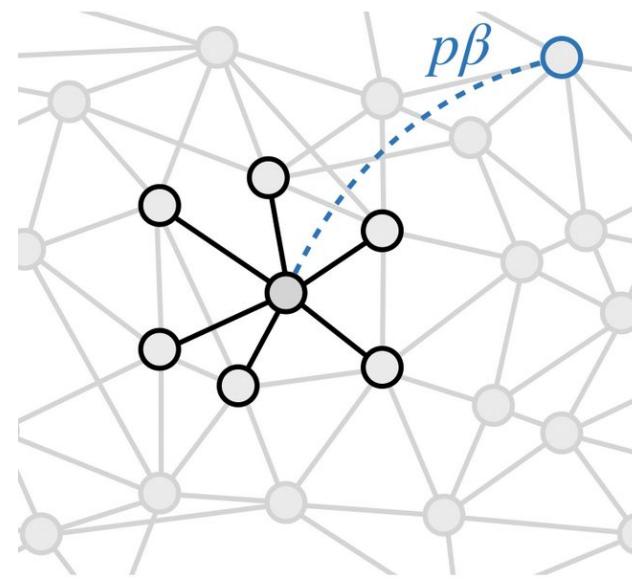
$$\Pr(X_i = S \rightarrow E) = \left[p \frac{\beta I}{N} + (1 - p) \frac{\beta \sum_{j \in C_G(i)} \delta_{X_j=I}}{|C_G(i)|} \right] \delta_{X_i=S}$$

$$\Pr(X_i = E \rightarrow I) = \sigma \delta_{X_i=E}$$

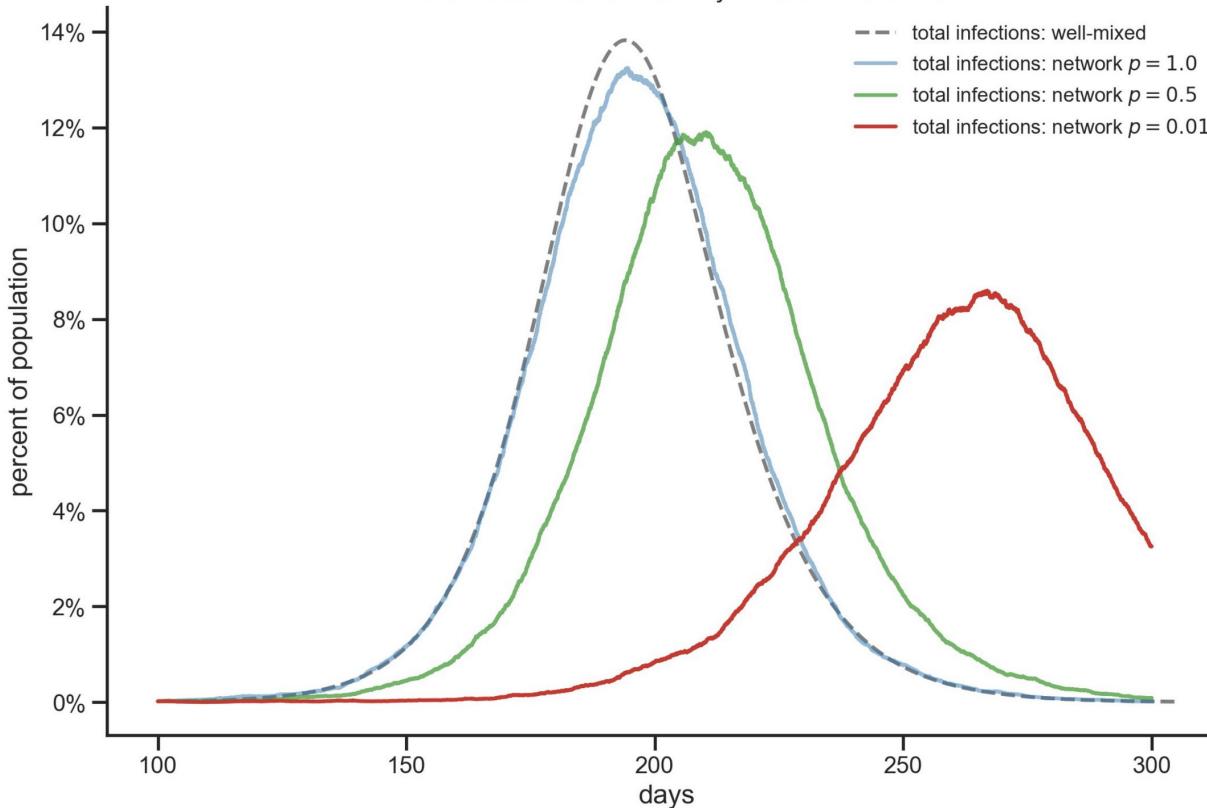
$$\Pr(X_i = I \rightarrow R) = \gamma \delta_{X_i=I}$$

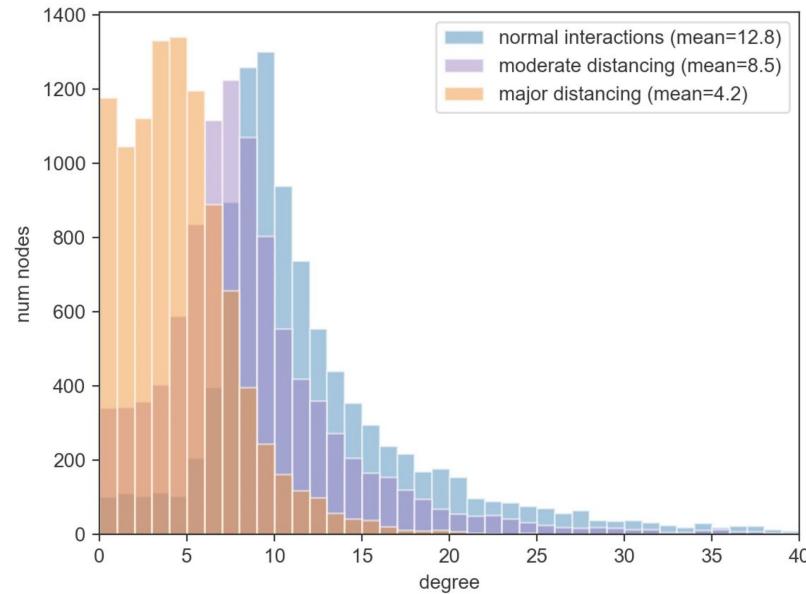
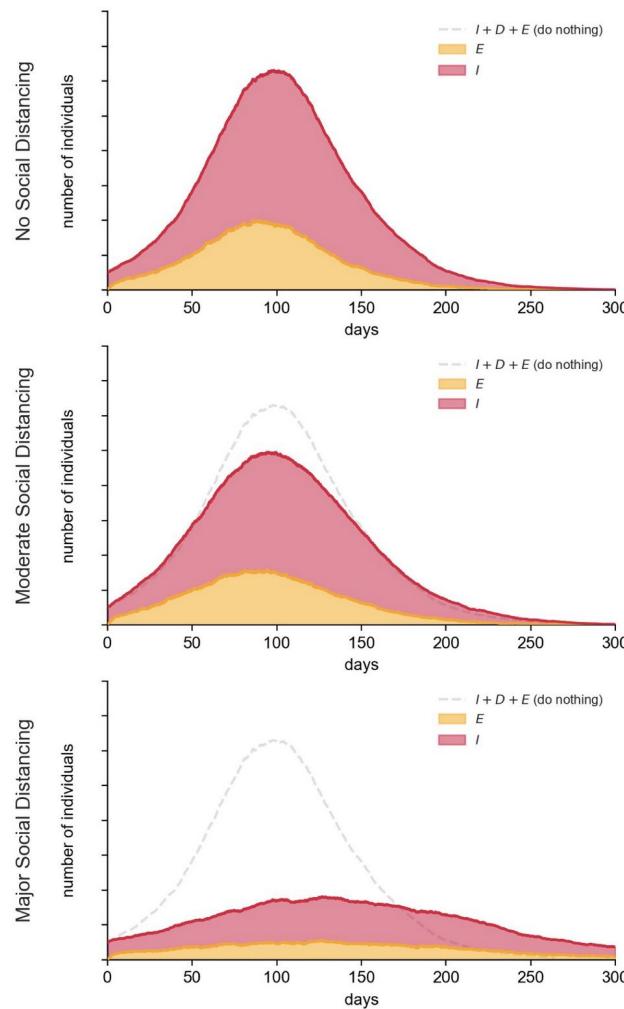
$$\Pr(X_i = I \rightarrow F) = \mu_I \delta_{X_i=I}$$

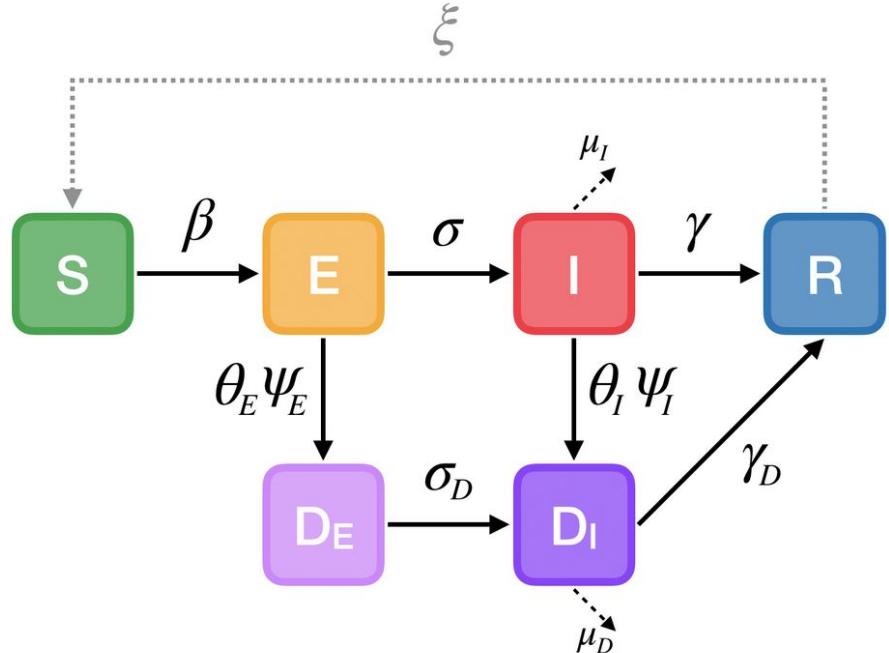
$$\Pr(X_i = R \rightarrow S) = \xi \delta_{X_i=R}$$



The effect of network locality on total infections







$$\dot{S} = -\frac{\beta SI}{N} - q \frac{\beta_D SD_I}{N} + \xi R$$

$$\dot{E} = \frac{\beta SI}{N} + q \frac{\beta_D SD_I}{N} - \sigma E - \theta_E \psi_E E$$

$$\dot{I} = \sigma E - \gamma I - \mu_I I - \theta_I \psi_I I$$

$$\dot{D}_E = \theta_E \psi_E E - \sigma_D D_E$$

$$\dot{D}_I = \theta_I \psi_I I + \sigma_D D_E - \gamma_D D_I - \mu_D D_I$$

$$\dot{R} = \gamma I + \gamma_D D_I - \xi R$$

$$\dot{F} = \mu_I I + \mu_D D_I$$

$$N = S + E + I + D_E + D_I + R$$

Incorporating Interventions

$$\Pr(X_i = S \rightarrow E) = \left[p \left(\frac{\beta I + q\beta_D D_I}{N} \right) + (1-p) \left(\frac{\beta \left[\sum_{j \in C_G(i)} \delta_{X_j=I} \right] + \beta_D \left[\sum_{k \in C_Q(i)} \delta_{X_k=D_I} \right]}{|C_G(i)|} \right) \right] \delta_{X_i=S}$$

$$\Pr(X_i = E \rightarrow I) = \sigma \delta_{X_i=E}$$

$$\Pr(X_i = I \rightarrow R) = \gamma \delta_{X_i=I}$$

$$\Pr(X_i = I \rightarrow F) = \mu_I \delta_{X_i=I}$$

$$\Pr(X_i = E \rightarrow D_E) = \left(\theta_E + \phi_E \left[\sum_{j \in C_G(i)} \delta_{X_k=D_E} + \delta_{X_k=D_I} \right] \right) \psi_E \delta_{X_i=E}$$

$$\Pr(X_i = I \rightarrow D_I) = \left(\theta_I + \phi_I \left[\sum_{j \in C_G(i)} \delta_{X_k=D_E} + \delta_{X_k=D_I} \right] \right) \psi_I \delta_{X_i=I}$$

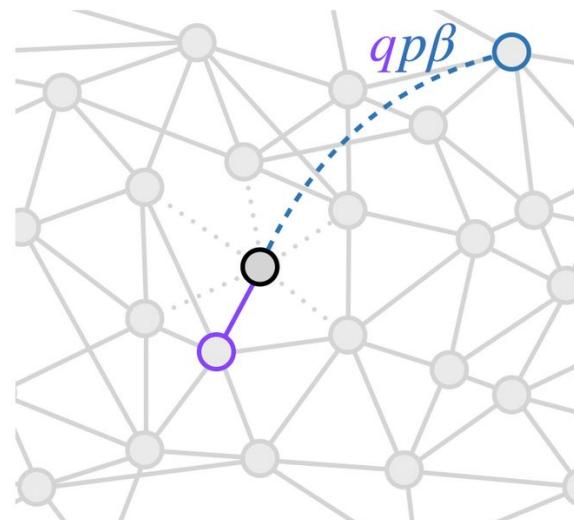
$$\Pr(X_i = D_E \rightarrow D_I) = \sigma_D \delta_{X_i=D_E}$$

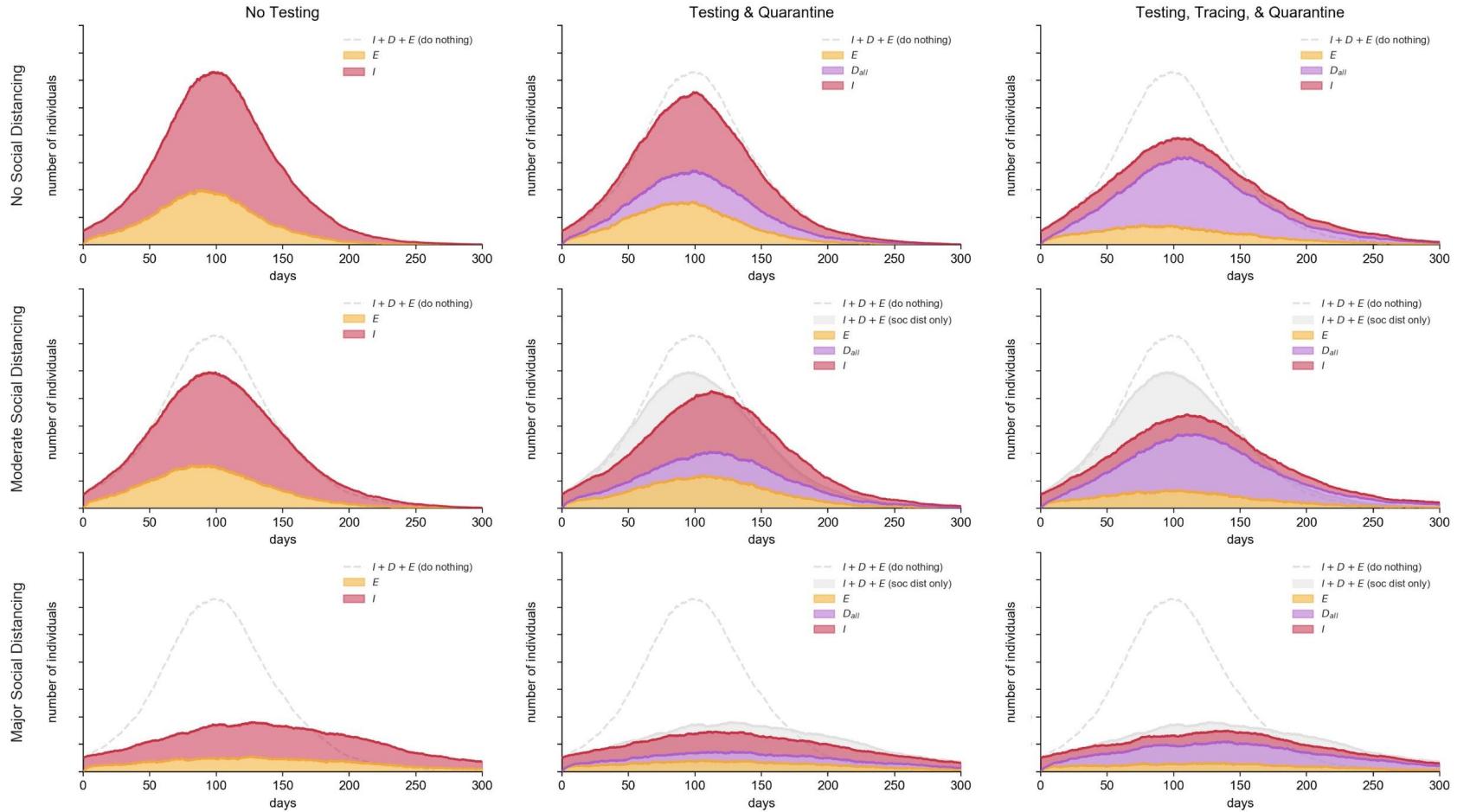
$$\Pr(X_i = D_I \rightarrow R) = \gamma_D \delta_{X_i=D_I}$$

$$\Pr(X_i = D_I \rightarrow F) = \mu_D \delta_{X_i=D_I}$$

$$\Pr(X_i = R \rightarrow S) = \xi \delta_{X_i=R}$$

$$\Pr(X_i = \text{any} \rightarrow S) = \nu \delta_{X_i \neq F}$$





<https://bit.ly/3bFDshk>

Modeling in the Real-world

Modeling in the Real-world

Modeling Interventions

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

16th March

Neil M Ferguson, Daniel Laydon, Gemma Nedjati-Gilani, Natsuko Imai, Kylie Ainslie, Marc Baguelin, et al.

- Two Strategies: Mitigation and Suppression
 - Mitigation: Slowing but not necessarily stopping epidemic growth
 - Suppression: Reversing epidemic growth (i.e., $R_0 < 1$)
- Authors used an individual-based transmission model developed for influenza
 - Individuals reside in areas defined by high-resolution population density data
 - Contacts are made within households, schools, at work, etc.
 - Age and household size defined by census data
 - Schools defined by data on schools (average class-sizes, staff-student ratios)
 - Workplace size and commuting distance between them was also calibrated
 - Individuals start at locations and then move around
 - $\frac{1}{3}$ of transmission occur in households, $\frac{1}{3}$ in schools & workplace, $\frac{1}{3}$ in community (match social mixing surveys)

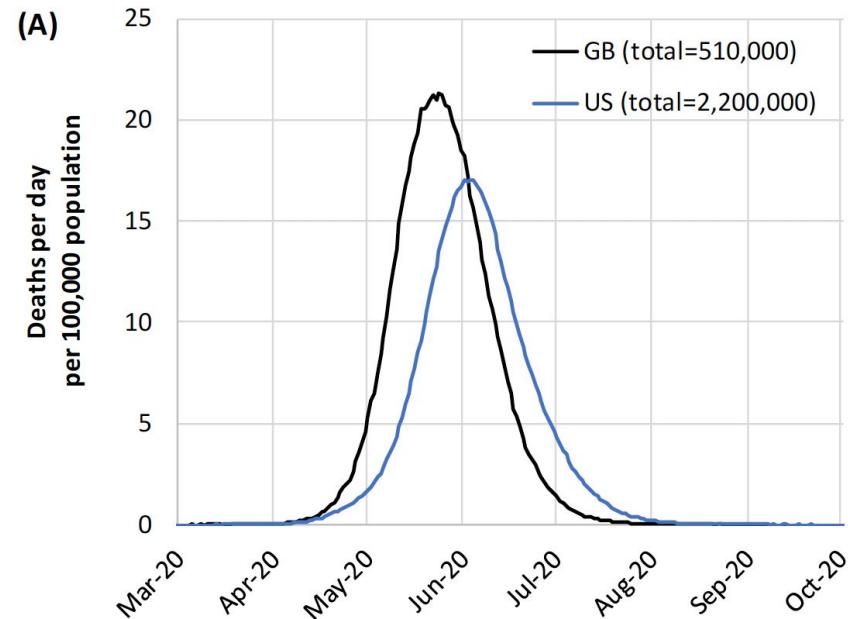
Imperial College Report: Modeling Interventions

- Parameters (among others)
 - Incubation period 5.1 days
 - 6.5 days mean duration of infectiousness (50% more infectious than asymptomatic)
 - $R_0 = 2.4 [2.0, 2.6]$
 - Infection seeded early January to reach cumulative number of deaths (14th March)
 - $\frac{2}{3}$ assumed to be sufficiently symptomatic to self-isolate within 1 day of symptom onset
 - 5 days mean duration from infection to hospitalization
- Bed demand
 - 8 days if no critical care
 - 16 if critical care (10 days ICU)

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%

Type of Interventions

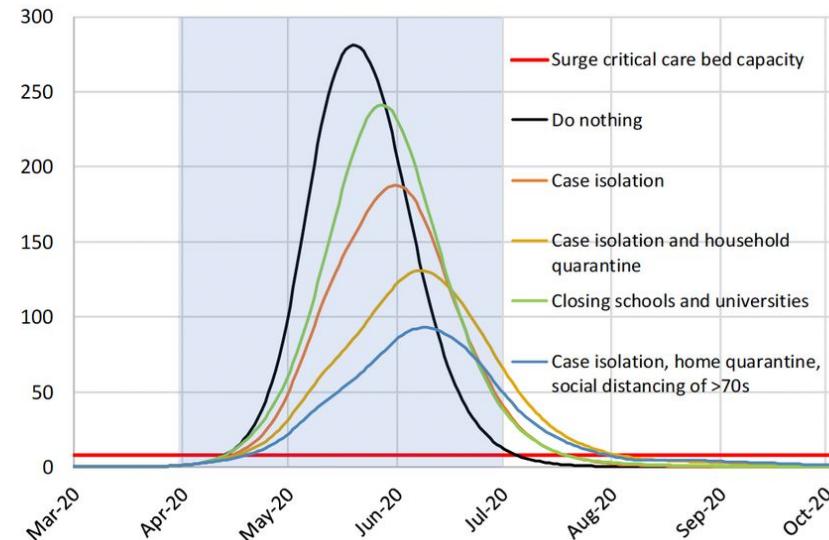
Label	Policy	Description
CI	Case isolation in the home	Symptomatic cases stay at home for 7 days, reducing non-household contacts by 75% for this period. Household contacts remain unchanged. Assume 70% of household comply with the policy.
HQ	Voluntary quarantine home	Following identification of a symptomatic case in the household, all household members remain at home for 14 days. Household contact rates double during this quarantine period, contacts in the community reduce by 75%. Assume 50% of household comply with the policy.
SDO	Social distancing of those over 70 years of age	Reduce contacts by 50% in workplaces, increase household contacts by 25% and reduce other contacts by 75%. Assume 75% compliance with policy.
SD	Social distancing of entire population	All households reduce contact outside household, school or workplace by 75%. School contact rates unchanged, workplace contact rates reduced by 25%. Household contact rates assumed to increase by 25%.
PC	Closure of schools and universities	Closure of all schools, 25% of universities remain open. Household contact rates for student families increase by 50% during closure. Contacts in the community increase by 25% during closure.



Type of Interventions

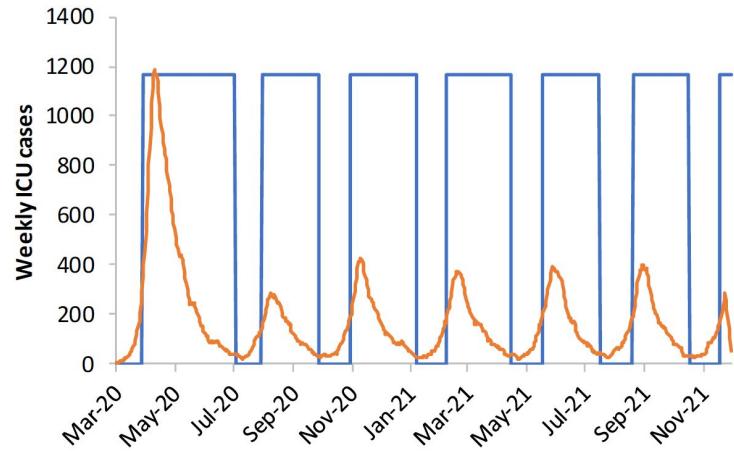
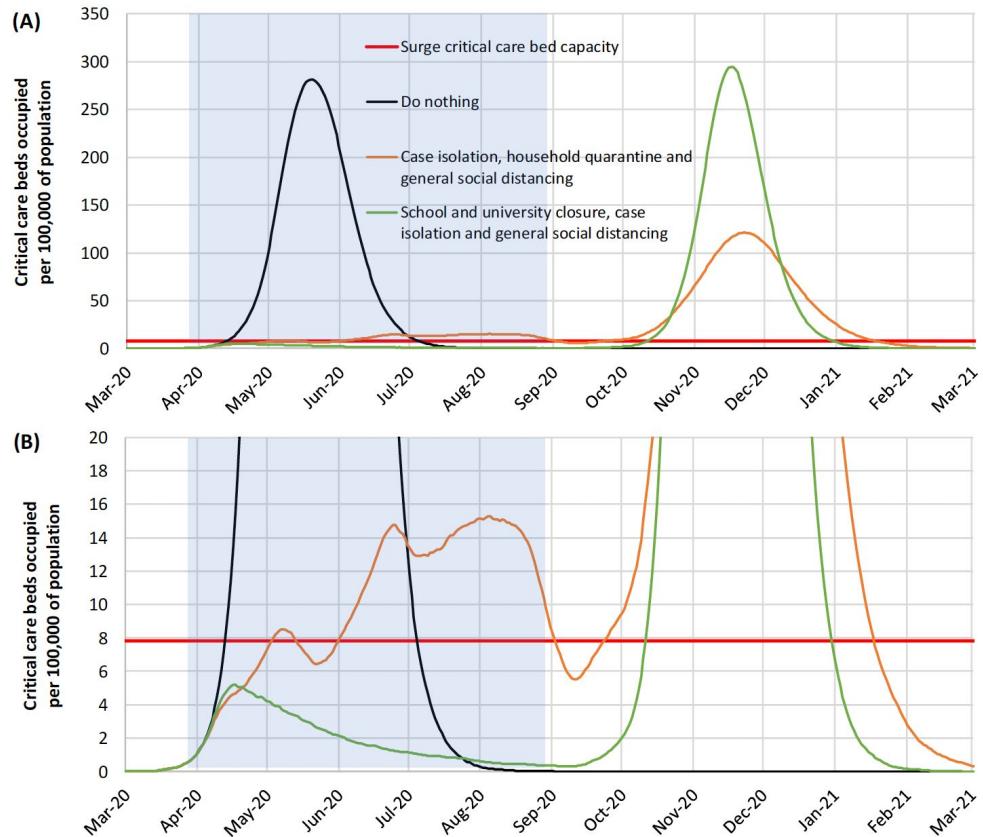
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Mitigation Strategies



Deaths (Best case): 250,000 GB and 1.1-1.2 Million US

Modeling Interventions



Modeling Interventions: Conclusions

- Mitigation is not feasible (healthcare system overloaded many times over)
- Need population-wide social distancing + other interventions (home case isolation, school and university closure) to suppress R_0 below 1
- These measures need to be in place for a long time (could be 18 months or more) to avoid rebound
 - Adaptive population-wide social distancing is an idea, but in place still $\frac{2}{3}$ of the time

Critique

Italy and Spain's daily death tolls are plateauing, but in the UK and US every day brings more new deaths than the last

Daily deaths with coronavirus (7-day rolling average), by number of days since 3 daily deaths first recorded
Stars represent national lockdowns ★



FT graphic: John Burn-Murdoch / @burnmurdoch
Source: FT analysis of European Centre for Disease Prevention and Control; Worldometers; FT research. Data updated April 02, 19:00 GMT

FT

<https://www.ft.com/coronavirus-latest>

Review of Ferguson et al "Impact of non-pharmaceutical interventions..."

Chen Shen[†], Nassim Nicholas Taleb*, Yaneer Bar-Yam[†]

[†]New England Complex Systems Institute, *School of Engineering, New York University

First version, March 17, 2020. Corresponding author: yaneer@necsi.edu

Neil Ferguson and an Imperial College team perform detailed simulations of outbreak response [1]. This is an important work because they model social/government response, not just contagion. They show suppression (lockdown so that $R_0 < 1$) is essential because mitigation ($R_0 > 1$, "flattening the curve") necessarily results in massive overload of hospitals and many dead. This is an important conclusion that should inform policy makers.

However, they make structural mistakes in analyzing outbreak response. They ignore standard Contact Tracing [2] allowing isolation of infected prior to symptoms. They also ignore door-to-door monitoring to identify cases with symptoms [3]. Their conclusions that there will be resurgent outbreaks are wrong. After a few weeks of lockdown almost all infectious people are identified and their contacts are isolated prior to symptoms and cannot infect others [4]. The outbreak can be stopped completely with no resurgence as in China, where new cases were down to zero yesterday, after excluding imported international travelers that are quarantined.

Their assumptions are equivalent to ergodicity, as they consider new infections to be a function of infected fraction and immunity, and not influenced by where in the trajectory of the outbreak they are, distinguishing going up from going down.

They also don't specify whether achieving less than one case (extinction of the virus) is possible in their model. The actual minimal number for resurgence is larger than 1 because (1) a significant percentage of infected individuals do not infect others, indeed only 5% of close contacts of infected individuals traced in China subsequently tested positive [2], and (2) small outbreaks can be stopped by contact tracing, which is enhanced by the availability of testing [5]. The availability of testing is also not included in their analysis. These interventions imply the exponential growth they report after relaxing restrictions would require a significant number of initial cases.

Since lockdowns result in exponentially decreasing numbers of cases, a comparatively short amount of time can be sufficient to achieve pathogen extinction, after which relaxing restrictions can be done without resurgence. Since the exponential decay is highly sensitive to the interventions made by both government and social action, simulating their effects is less helpful than the advice to "go all out" and refine the effort over time with improved tracing, testing, and other protocols.

Finally, the use of geographic boundaries and travel restrictions allows for effective and comparatively low cost imposition and relaxation of interventions. Such a multiscale approach accelerates response efforts, reduces social impacts,

allows for relaxing restrictions in areas earlier that are less affected, enables uninfected areas to assist in response in the areas that are infected, and is a much more practical and effective way to stop otherwise devastating outbreaks [6]. If actions had been taken earlier, successful local lockdowns, as performed in China in Hubei province, would have been possible instead of national lockdowns.

A few other issues are of importance: They ignore the possibility of superspread events in gatherings by not including the fat tail distribution of contagion in their model. This leads them to deny the importance of banning them, which has been shown to be incorrect, including in South Korea [7]. Cutting the fat tail of the infection distribution is critical to reducing R_0 [8].

The model they use appears to be in the general class of SIR differential equations used in epidemiology and is therefore not well suited for incorporating real world conditions at fine or large scale. These include (1) significant interactive local dynamics and travel restrictions that cannot be seen from aggregate quantities or averages across geographic locations, (2) non-normal distributions of the number of infections per person (superspread events) as well as the infection period, and (3) dynamic or stochastic values of parameters that arise from variations in sampling of distributions as well as the impact of changing social response efforts. Despite including details of the contagion and response options, their model is several degrees of abstraction away from what is warranted by the situation.

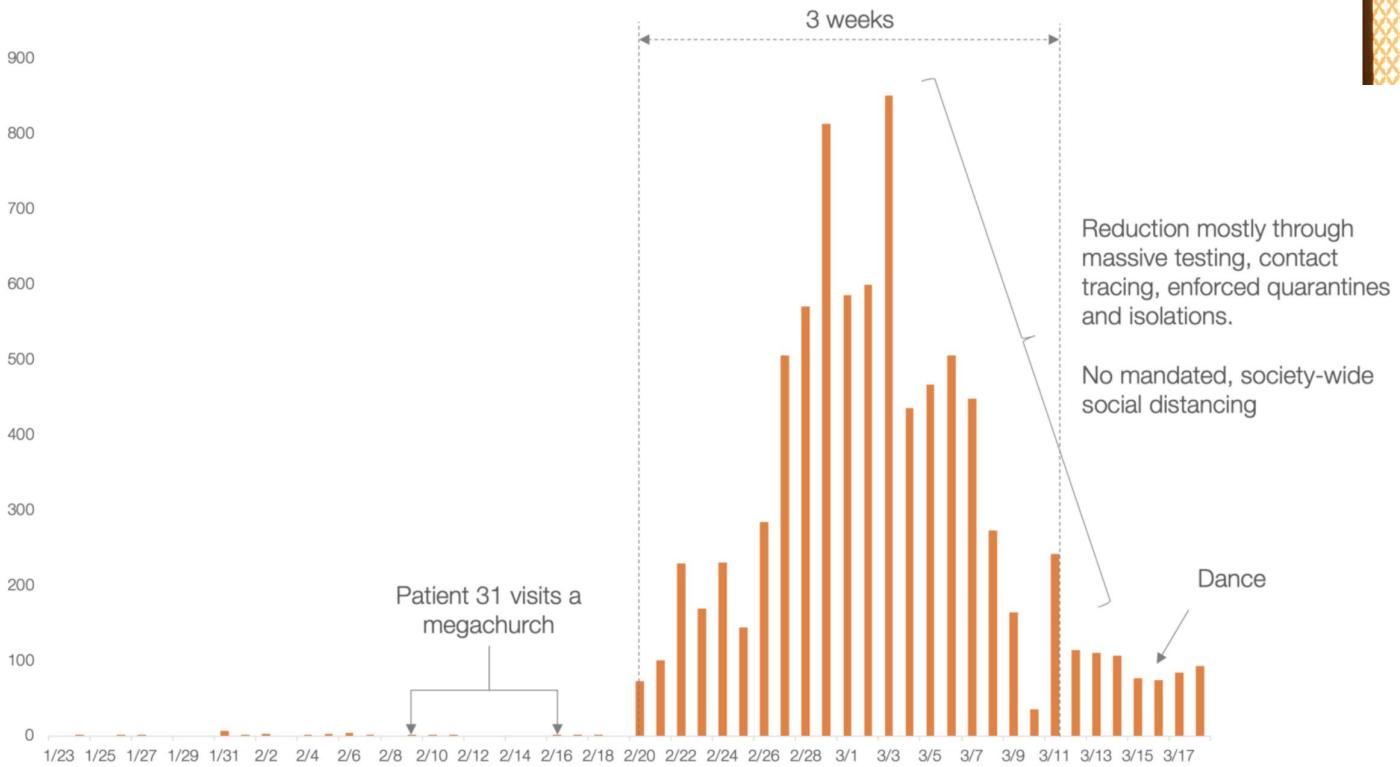
While the efforts to model social response are important, leaving out critical aspects of the response yields incorrect answers. Focusing on details but using incorrect assumptions makes for bad policy advice. Where lives are at stake, it is essential for science to adhere to higher standards.

REFERENCES

- [1] Ferguson et al., Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand. <https://www.imperial.ac.uk/mrc-institute-of-global-health-and-wellbeing/research/imperial-college-COVID19-NPI-modelling-16-03-2020.pdf>
- [2] Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19) <https://www.who.int/docs/default-source/coronavirus/who-china-joint-mission-on-covid-19-report.pdf?sfvrsn=1>
- [3] China Goes to Door to Door in Wuhan. Seeking Infections <https://www.courthousenews.com/china-goes-door-door-in-wuhan-seeking-infections/>
- [4] <https://www.cnn.com/2020/03/23/asia/coronavirus-drive-through-station-china/index.html>
- [5] Daniel Cooney, Vincent Wong, and Yaneer Bar-Yam. Beyond contact tracing: how increased early detection can lead to Ebola response. *PLoS Currents Outbreaks* (March 2020) [7]
- [6] Chen Shen and Yaneer Bar-Yam. First thoughts on superspread events, NECI (February 28, 2020). <https://necsi.edu/first-thoughts-on-superspread-events>



Chart 12.b: New Daily Cases in South Korea



Source: Tomas Pueyo analysis from primary data from Johns Hopkins uploaded to Github by Ryan Lau:

https://github.com/CSSEGISandData/COVID-19/blob/master/csse_covid_19_data/csse_covid_19_time_series/time_series_19-covid-Confirmed.csv

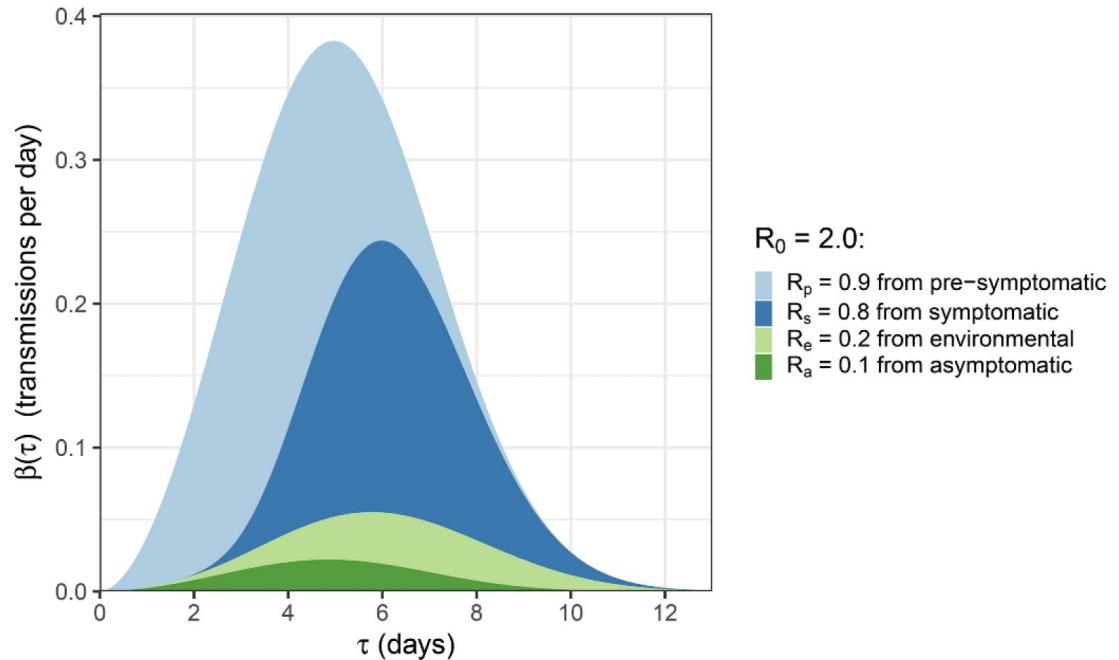
Ferguson et al. (2020) on South Korea

"The measures used to achieve suppression might also evolve over time. As case numbers fall, it becomes more feasible to adopt intensive testing, contact tracing and quarantine measures akin to the strategies being employed in South Korea today. Technology – such as mobile phone apps that track an individual's interactions with other people in society – might allow such a policy to be more effective and scalable if the associated privacy concerns can be overcome. However, if intensive NPI packages aimed at suppression are not maintained, our analysis suggests that transmission will rapidly rebound, potentially producing an epidemic comparable in scale to what would have been seen had no interventions been adopted."

- Ferguson et al. (2020, p. 15)

Contact Tracing

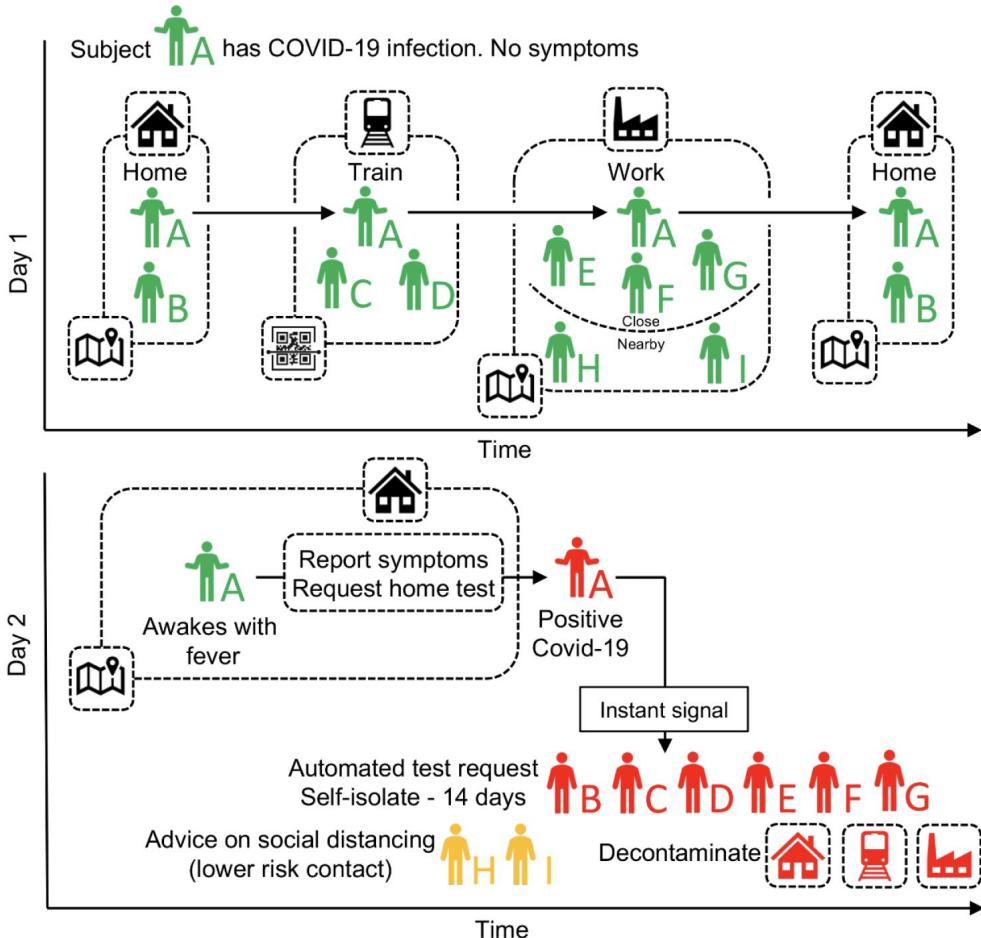
- Ferretti et al. ([2020](#))
- Transmission can be
 - Pre-symptomatic
 - Symptomatic
 - Environmental
 - Asymptomatic

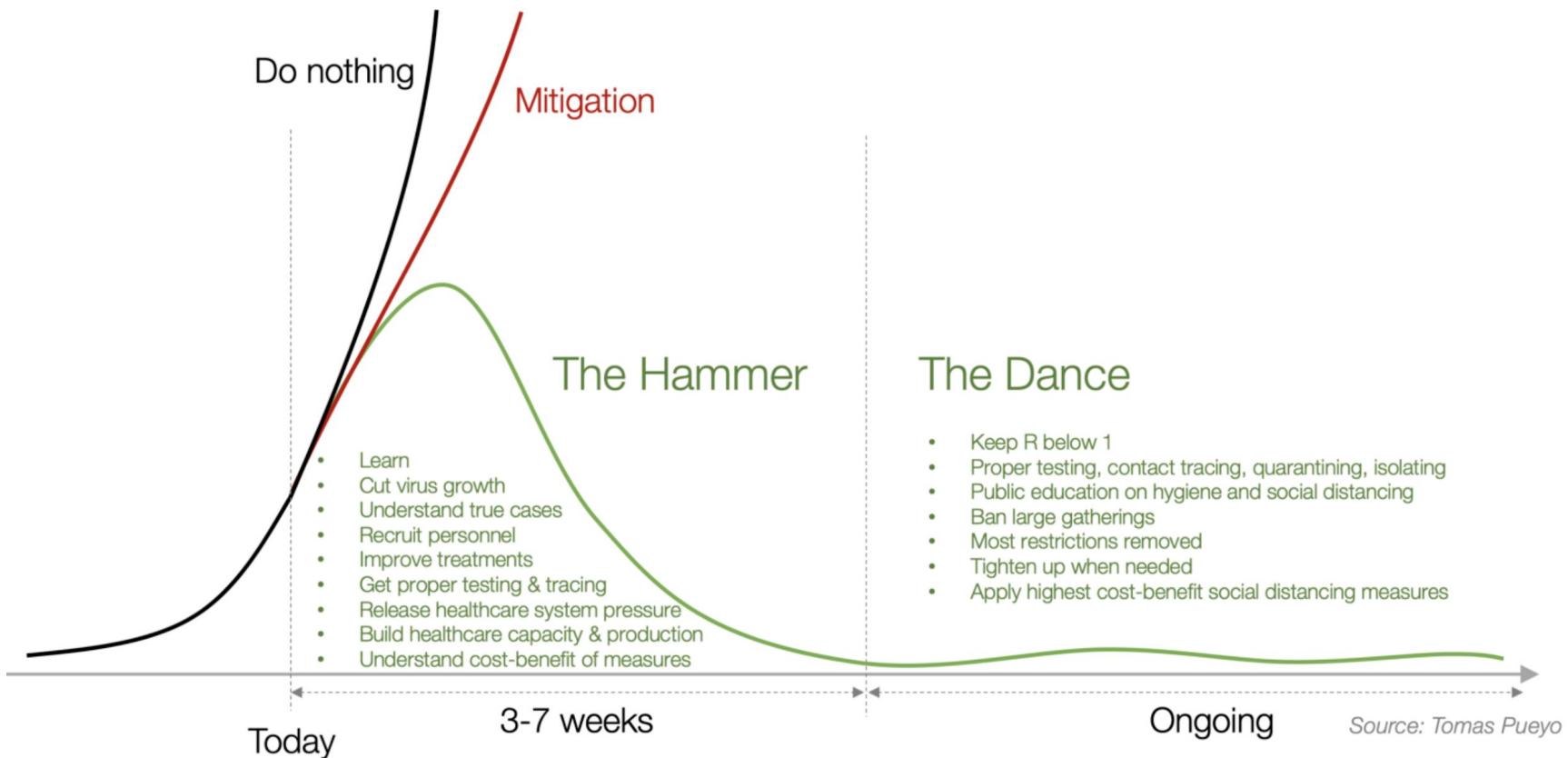


$$\beta(\tau) = \underbrace{P_a x_a \beta_s(\tau)}_{\text{asymptomatic}} + \underbrace{(1 - P_a)(1 - s(\tau))\beta_s(\tau)}_{\text{pre-symptomatic}} + \underbrace{(1 - P_a)s(\tau)\beta_s(\tau)}_{\text{symptomatic}} + \underbrace{\int_{l=0}^{\tau} \beta_s(\tau - l) E(l) dl}_{\text{environmental}}$$

Contact Tracing

- Ferretti et al. ([2020](#))
- Transmission can be
 - Pre-symptomatic
 - Symptomatic
 - Environmental
 - Asymptomatic





Modeling in the Real-world

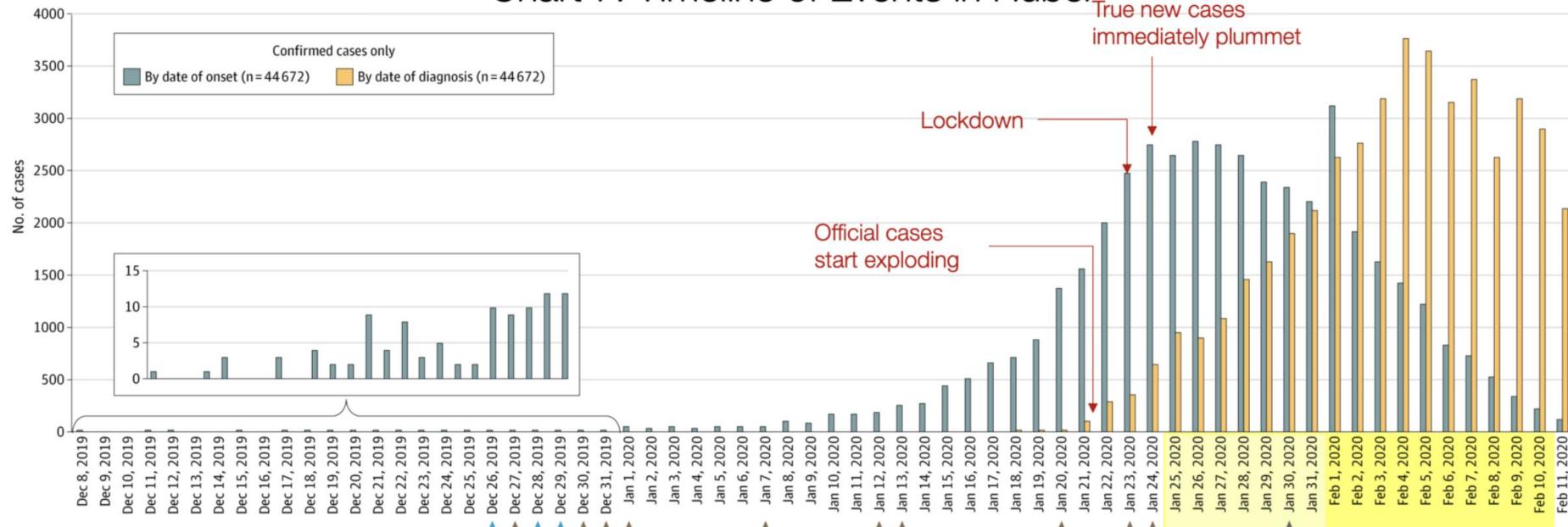
Assessing the Effect of Interventions

Estimating the number of infections and the impact of non-pharmaceutical interventions on COVID-19 in 11 European countries

Seth Flaxman*, Swapnil Mishra*, Axel Gandy*, H Juliette T Unwin, Helen Coupland, Thomas A Mellan, Harrison et al.

- Interventions influence the basic reproductive number R_t
- Difficulties in estimating R_t :
 - High proportion of infections not detected
 - Different proportions of infections being detected over time due to changes in testing policies
 - Most countries measure only severely ill patients or high-risk groups

Chart 7: Timeline of Events in Hubei



Wu & McGoogan ([2020](#)) in Pueyo ([2020a](#))

Estimating Number of Infections: Hack

- Case data is unreliable
- Alternative way: back-calculate infections from observed deaths (Pueyo, [2020a](#))
- Germany has 85,025 reported cases and 1,111 reported deaths ([Wikipedia](#), 3rd of April, 09:51)

```
guesstimate_cases <- function(deaths, infect_to_death = 17.8,
                                doubling_time = 6.2, fatality_rate = 0.014) {

  # Number of infections at time today - infect_to_death
  previous_infections <- deaths * (1 / fatality_rate)

  # How much the number of infections have increased since then
  multiplication_factor <- 2^(infect_to_death / doubling_time)

  # Current infections
  previous_infections * multiplication_factor

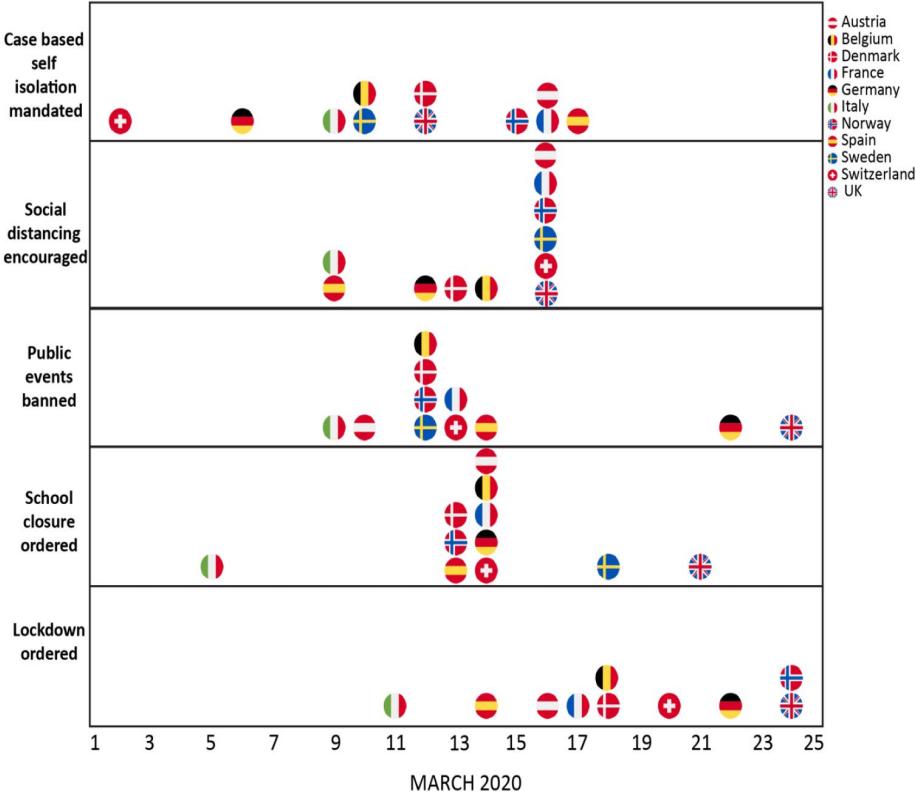
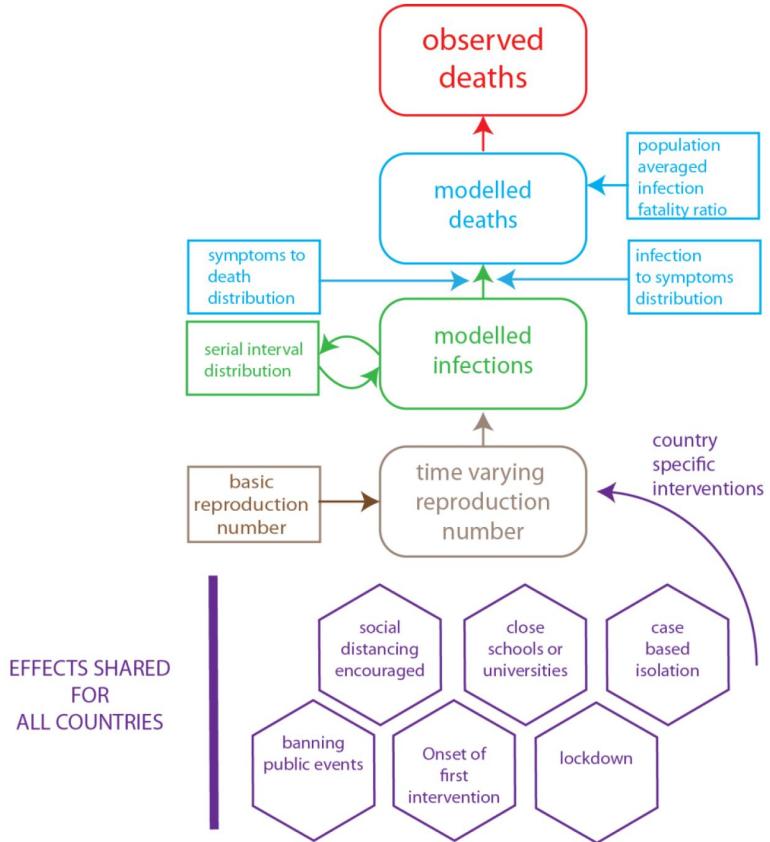
}

guesstimate_cases(1111)
```

[1] 580541.7

Verity et al. ([2020](#))

Imperial College Model



Flaxman et al. (2020)

Imperial College Death Model

$$D_{tm} \sim \text{Negative-Binomial} \left(d_{t,m}, d_{t,m} + \frac{d_{t,m}^2}{\psi} \right)$$

$$\psi \sim \text{Half-Normal}(0, 5)$$

$$\pi_m \sim \text{ifr}_m \cdot (\text{Gamma}(5.1, 0.86) + \text{Gamma}(18.8, 0.45))$$

$$d_{t,m} = \sum_{\tau=0}^{t-1} c_{\tau,m} \cdot \pi_{t-\tau,m}$$

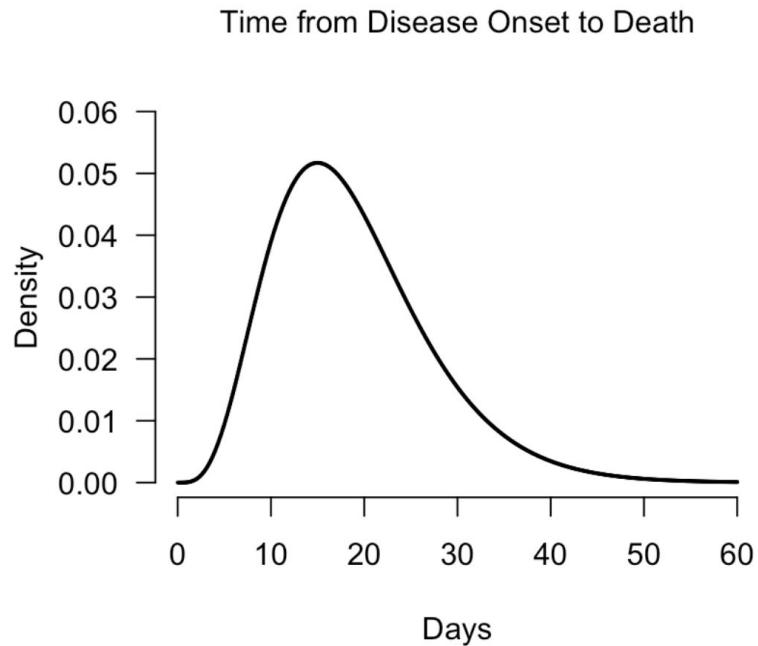
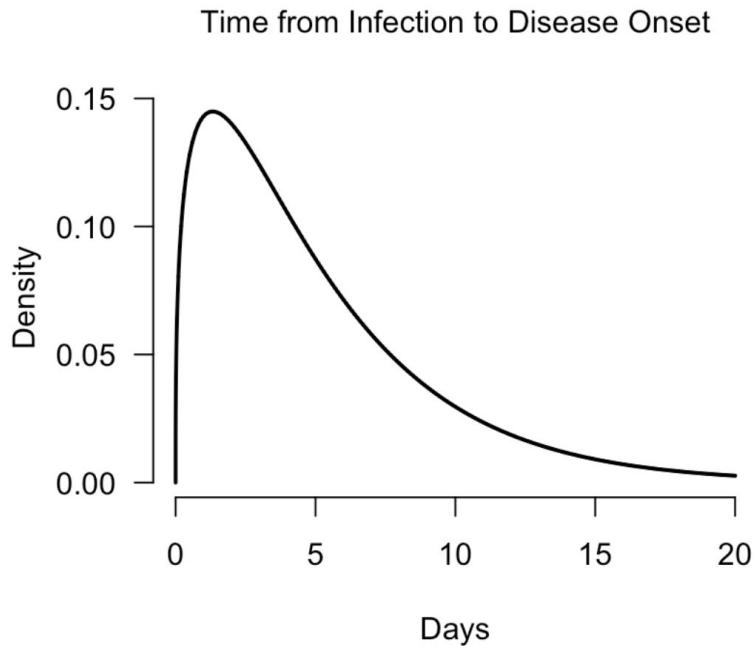
D_{tm} ... deaths for day t and country m

π_m ... time from infection to death

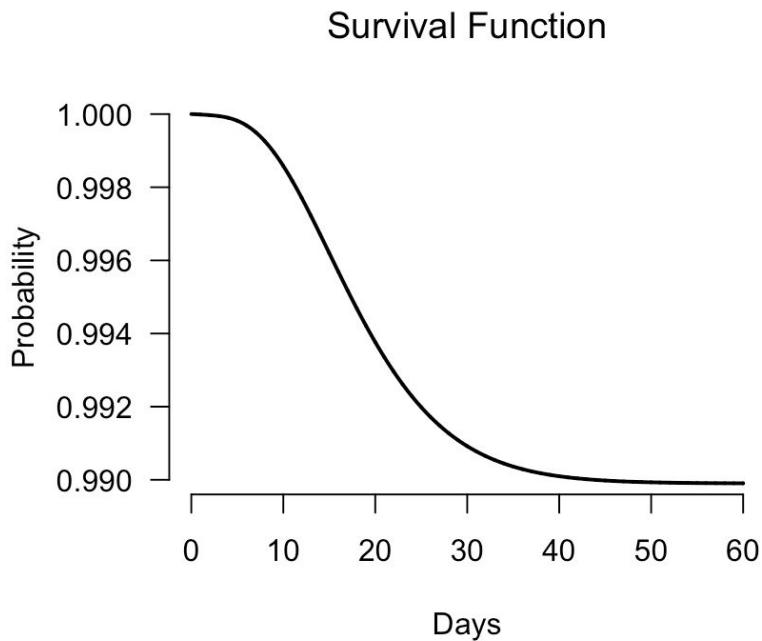
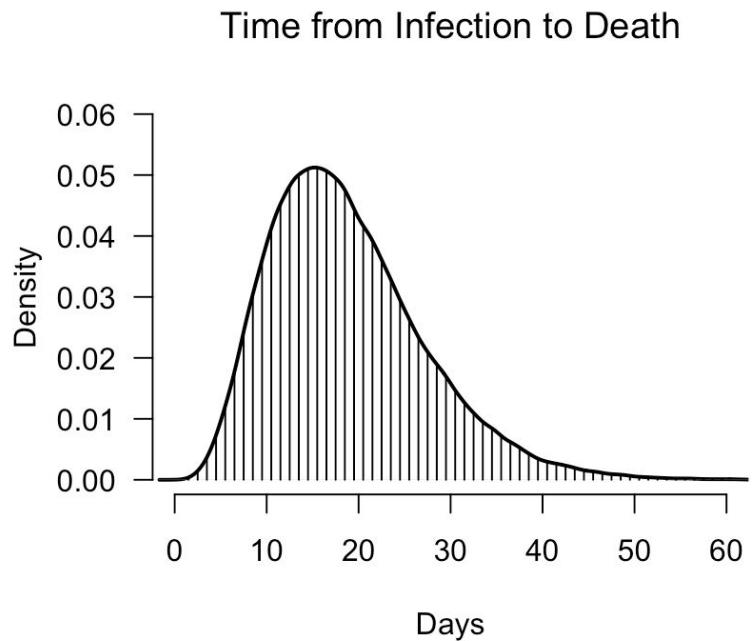
ifr_m ... infection-fatality ratio per country

$c_{\tau m}$... number of new infections

Imperial College Death Model



Imperial College Death Model



Imperial College Infection Model

$g \sim \text{Gamma}(6.5, 0.62)$

$$c_{t,m} = R_{t,m} \sum_{\tau=0}^{t-1} c_{\tau,m} \cdot g_{t-\tau}$$

$$R_{t,m} = R_{0,m} \exp \left(- \sum_{k=1}^6 \alpha_k \cdot I_{k,t,m} \right)$$

$\alpha_k \sim \text{Gamma}(0.50, 1)$

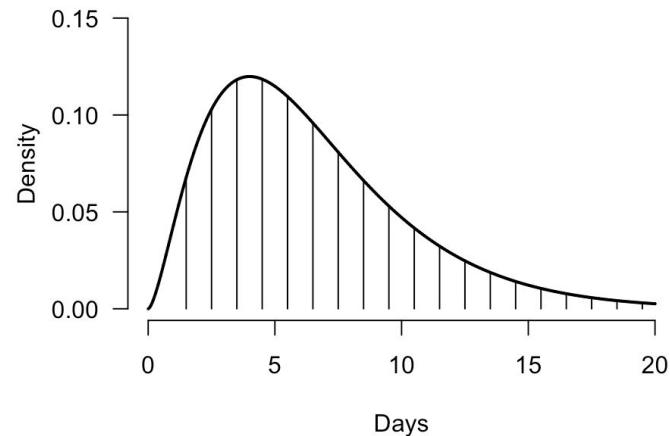
$R_{0,m} \sim \text{Normal}(2.4, |\kappa|)$

$\kappa \sim \text{Normal}(0, 0.50)$

$c_{1,m}, \dots, c_{6,m} \sim \text{Exponential}(\tau)$

$\tau \sim \text{Exponential}(0.03)$

Serial Interval Distribution



g ... serial interval distribution
(time between when a person gets infected and subsequently infects others)

c_{tm} ... number of new infections

R_{tm} ... Reproduction number

I_{ktm} ... Indicator variable for Intervention

α_k ... coefficient for intervention k

Imperial College Modeling Results

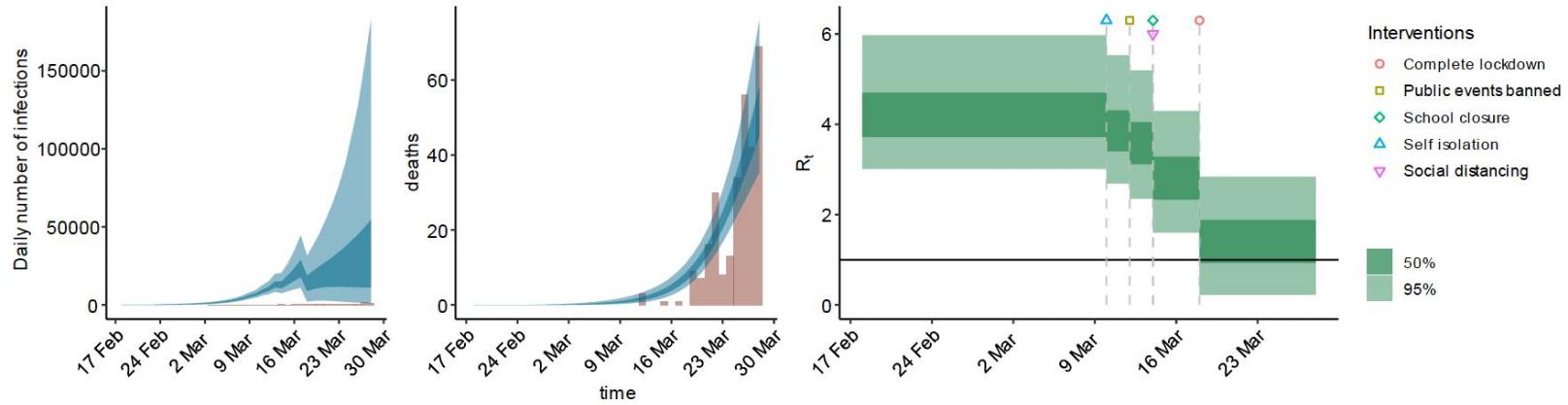
Table 1: Posterior model estimates of percentage of total population infected as of 28th March 2020.

Country	% of total population infected (mean [95% credible interval])	Reported Cases ¹
Austria	1.1% [0.36%-3.1%]	~ 15,000
Belgium	3.7% [1.3%-9.7%]	~ 832,000
Denmark	1.1% [0.40%-3.1%]	~ 59,000
France	3.0% [1.1%-7.4%]	~ 85,000
Germany	0.72% [0.28%-1.8%]	~ 115,000
Italy	9.8% [3.2%-26%]	~ 5.9 Million
Norway	0.41% [0.09%-1.2%]	~ 112,000
Spain	15% [3.7%-41%]	~ 7 Million
Sweden	3.1% [0.85%-8.4%]	~ 34,000
Switzerland	3.2% [1.3%-7.6%]	
United Kingdom	2.7% [1.2%-5.4%]	

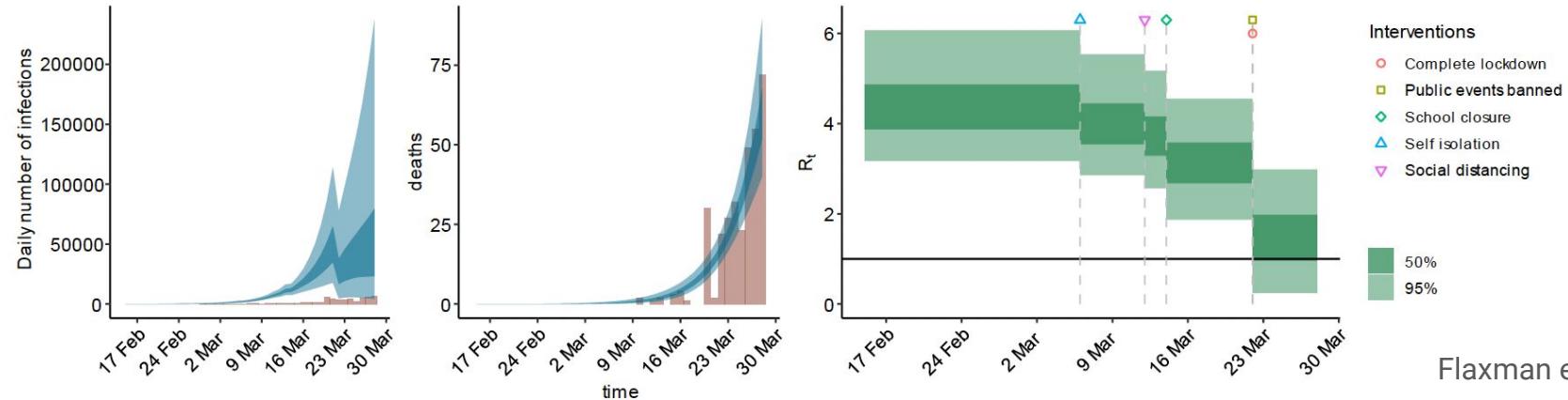
¹Wikipedia, 3rd of April, 09:51

Flaxman et al. (2020)

(B) Belgium



(E) Germany



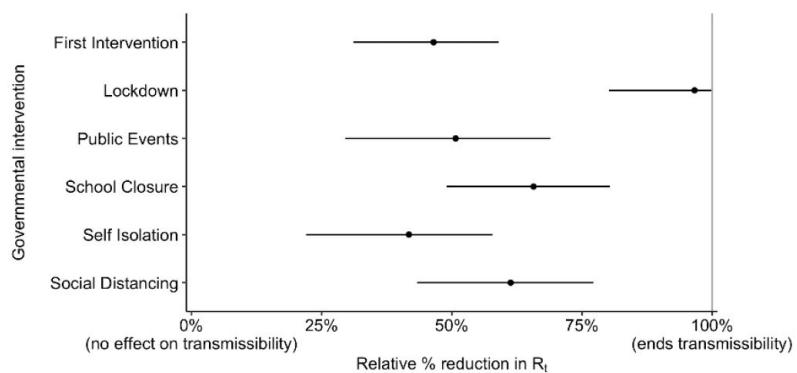
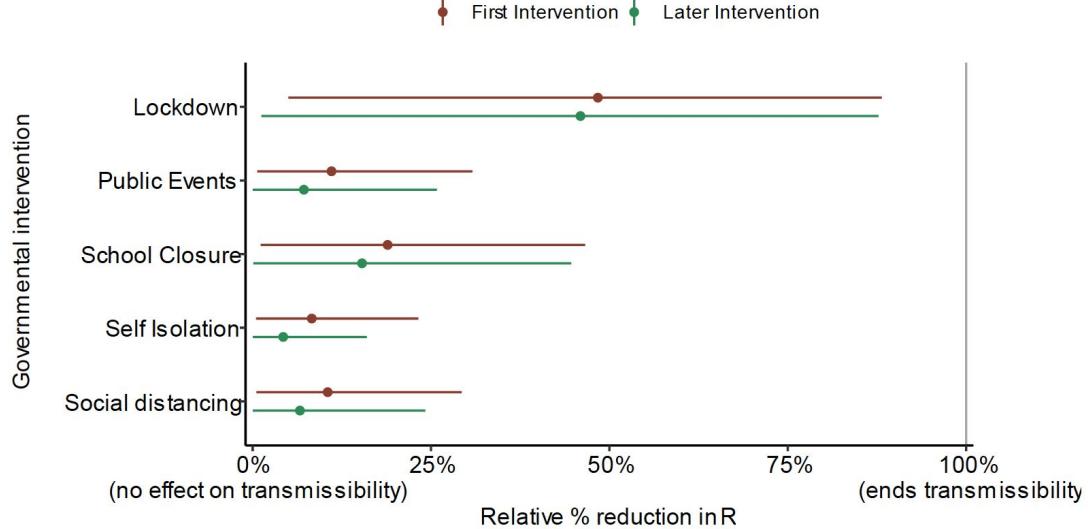


Figure 15: Effects of different interventions when used as the only covariate in the model.

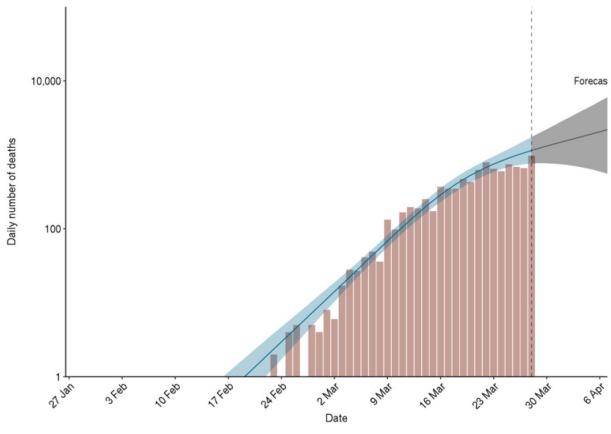


Figure 10: 7-day-ahead forecast for Italy.

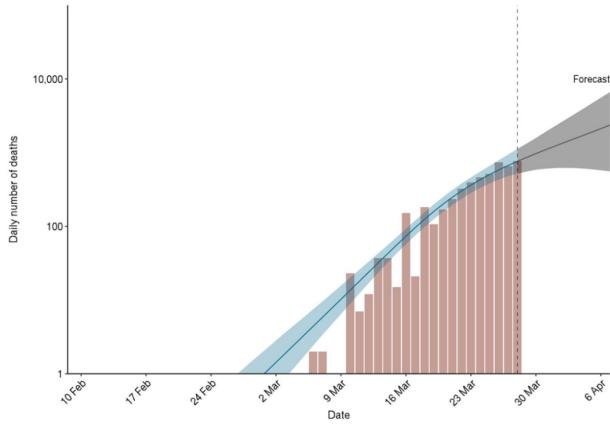
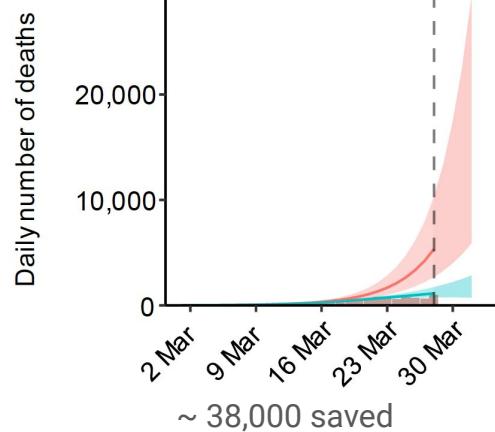
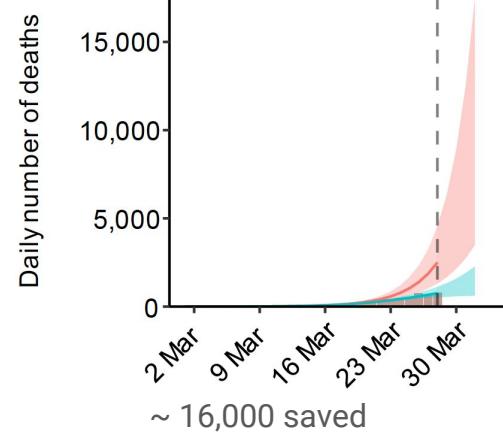


Figure 11: 7-day-ahead forecast for Spain.



(a) Italy



(b) Spain

Assessing Interventions: Conclusions

- Interventions have drastically reduced R_t and saved lives
 - Too little data to estimate effect of intervention per country
 - Difficult to disentangle individual intervention effects due to correlation in time
- Substantially more infections than currently reported
 - Yet still only about 4.9% [1.1% - 11%] of people have been infected
 - Too few to get herd immunity (which is ~ 50 - 75% for an $R_0 = 2-4$)
 - Interventions reduce rate of herd immunity drastically
 - Virus will be able to spread quickly after they are lifted
 - Estimates of the attack rate need to be validated using newly developed antibody tests
- Seriously cool modeling, all code [publicly available](#)

Covid-19's death toll appears higher than official figures suggest

Measuring the total number of deaths tells a grimmer tale

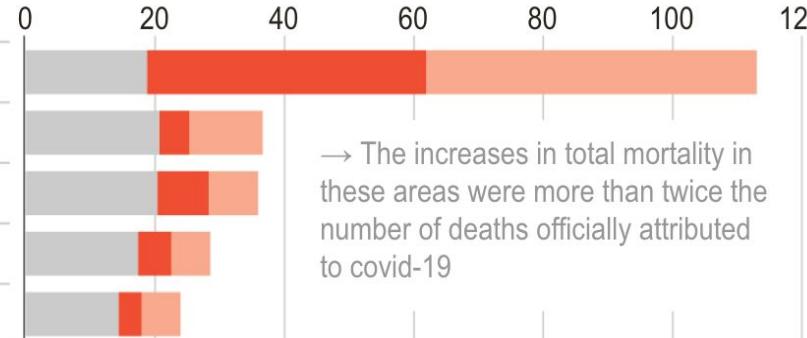
Deaths per 100,000 people per week, selected regions

Region's normal death rate

Confirmed covid-19 deaths

Excess deaths not attributed to covid-19

	Population	Time period
Bergamo, Italy	1,115,000	Mar 1st-Mar 31st
Castile & León, Spain	2,419,000	Mar 17th-Mar 24th
Castile-La Mancha, Spain	2,033,000	Mar 15th-Mar 24th
Haut-Rhin, France	761,000	Mar 1st-Mar 20th
Madrid, Spain	6,425,000	Mar 10th-Mar 16th

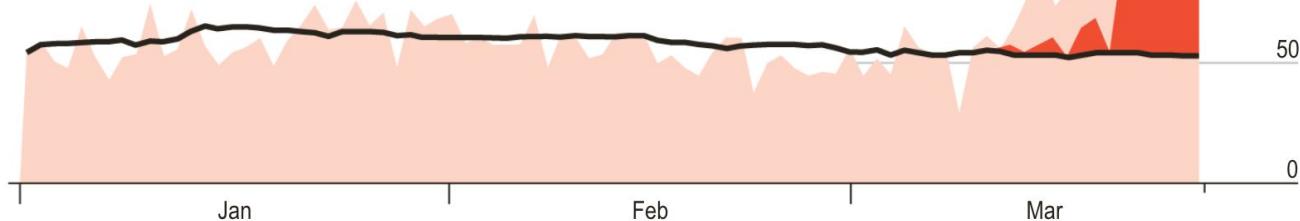


Spain, confirmed covid-19 deaths per 100,000 people per week*

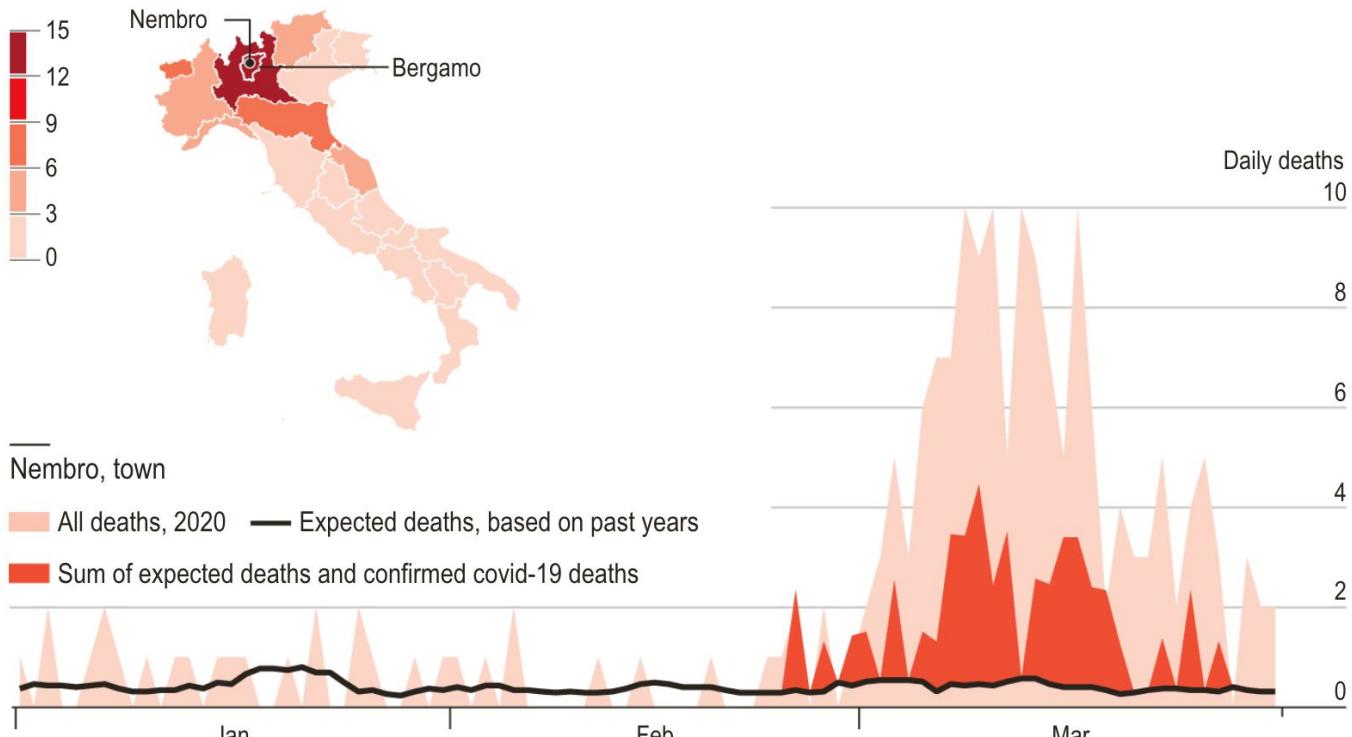


Castile-La Mancha, region

All deaths, 2020 Expected deaths, based on past years
Sum of expected deaths and confirmed covid-19 deaths



Italy, confirmed covid-19 deaths per 100,000 people per week*



Thank you for your attention!