



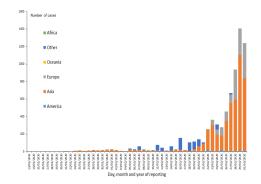
Mathematical models for epidemics like Covid-19

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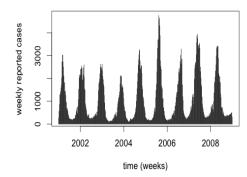
Reality: Ongoing Covid-19 outbreak, outside of China



Reported cases outside China up to mid March, 2020 **Possible scientific questions**: How many will get infected, when is peak, effects of prevention, data collection, ...



Reality: Endemic diseases: Rotavirus in Germany



Rotavirus in Germany

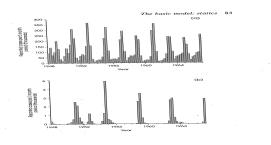
Possible scientific questions: Average age of infection, critical vaccination coverage, seasonality, under-reporting, ...

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Reality: Endemicity or extinction of measles (pre-vac)

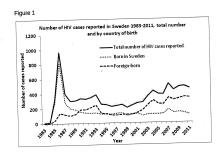


Top: 1948-1968 UK: Endemic

Bottom: 1948-1968 Iceland: outbreaks, extinction, reintroduction **Possible scientific questions**: Critical community size, time to extinction, ...



Reality: endemicity in sub-communities of HIV in Sweden



Possible scientific questions: Endemic level, sub-communities and networks, targeted prevention, new data streams (virus sequences), ...

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A model for the spread of an infectious disease

Today: simplest model (more advanced/realistic models exist!)

Assumptions:

- No prior immunity
- All individuals are similar (susceptibility and infectivity) and mix uniformly
- An individual who recovers becomes immune (**SIR**: Susceptible Infectious Recovered/immune)
- No behavioural changes during course of epidemic!



An epidemic model, cont'd

Model (Reed-Frost, 1929):

- Discrete time (e.g. week by week)
- *n* = population size (assumed fixed but large)
- Start: n-1 susceptible , 1 infectious , 0 recovered
- An individual who gets infected one week, infects each susceptible individual with probability *p* (independently) the next week, and then recovers (and remains immune)
- Goes on until no new infected, then epidemic stops

The most important quantity (parameter):

 R_0 = average number of new infections caused by a typical infected during early phase of an outbreak ("basic reproduction number") **Question**: What is R_0 if p = 0.0015 and n = 1000?



An epidemic model, cont'd

Model (Reed-Frost, 1929):

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The most important quantity (parameter):

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Answer:
$$R_0 = (n-1)p \approx np = 1000 * 0.0015 = 1.5$$
.



The final epidemic size

Question: How many will get infected (possible values: 1, ..., n = 1000)? How does incidence/prevalence vary over time?

First: Final epidemic size (not time evolution)

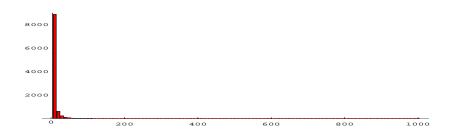
On the next two slides I have simulated the epidemic model 10 000 times for a population of size n = 1000.

Histograms of final size x-axis: number of infected y-axis: frequency of simulations

First figure for $R_0 = 0.8$ and second figure for $R_0 = 1.5$

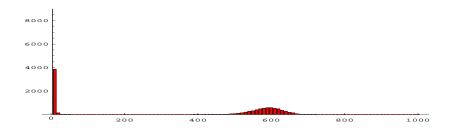


Histogram: final epidemic size: $R_0 = 0.8$ (Only small outbreaks!)





Histogram: final epidemic size: $R_0 = 1.5$ (Small and major outbreaks)





Mathematical formula for final epidemic size

So either very few get infected, or else a positive fraction τ (if $R_0 > 1$). Minor/major outbreak

It is actually possible to derive an equation for the final size τ . Remember: $n\tau$ = number infected, and $p = R_0/n$ = transmission probability



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$$1 - \tau = \text{proportion not infected}$$

$$\approx \text{probability not to get infected}$$

$$= \text{probability to avoid infection from all } n\tau \text{ infected}$$

$$= (1 - p)^{n\tau}$$

$$= \left(1 - \frac{R_0}{n}\right)^{n\tau}$$

$$\approx e^{-R_0\tau} \quad (\text{since } (1 - x/n)^n \approx e^{-x}, \text{ for large } n)$$



Mathematical formula, cont'd

So final epidemic size τ solves equation

$$1-\tau = e^{-R_0\tau}$$

Solution depends on R_0 but is not explicit. Easily solved numerically: $R_0 = 1.5 \Longrightarrow \tau = 58\%$

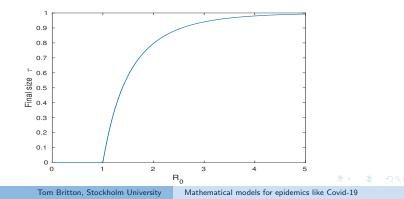


Mathematical formula, cont'd

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Our assumptions

Important: If $R_0 \leq 1 \implies$ no major outbreak!

Model/results are based on three assumptions:

1. No immunity (natural or by vaccination). True for Corona but not for seasonal influenza. If half the community are immune then final epidemic size changes dramatically!

2. A homogeneous community. Not true for Corona or any disease. Which heterogenenties are relevant depends on means of spreading (a lot of research in this direction). Often effect is that 10%-20% fewer get infected

3. No changing behaviour during epidemic. Preventive measures during outbreak may give very different outcome



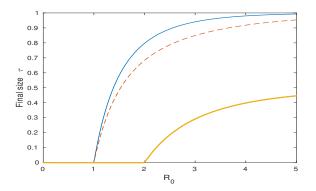
Final epidemic size, different scenarios

Below: Final epidemic size: under model, with heterogeneity, and with 50% initial immunity



Final epidemic size, different scenarios

Below: Final epidemic size: under model, with heterogeneity, and with 50% initial immunity





Characterization of R_0 and prevention

 R_0 can be factorized:

 $R_0 = p * c * \ell$, where

- p = transmission probability for a "contact"
- c = number of c "contacts" per day
- $\ell = {\sf duration}$ of infectious period

All **prevention** aims at decreasing R_0 by decreasing

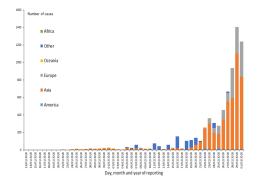
- p: face mask, hand washing, condom, ...
- c: quarantine, avoid: public transport, public events, ...
- $\ell:$ quicker diagnosis, isolation, \ldots

If the combined effect of preventive measures reduces R_0 by factor a, then "effective" reproduction number $R_E = (1-a)R_0$

 \implies No outbreak if $R_E \leq 1$, i.e. if $a \geq 1 - 1/R_0!$



How to estimate R_0 for a new emerging disease?



What is R_0 ?

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How to estimate R_0 for a disease?

Unfortunately not possible by only observing incidence curve

Growth rate r of curve depends on two things: R_0 , but also generation time G (typical time between getting infected and infecting others, highly affected by incubation time)

Big R_0 increases r, and small G increases r (formulae exist)

Many combinations of R_0 and G give rise to observed growth rate r

But if you also observe generation time G for some cases (e.g. from contact tracing), then it is possible to estimate R_0 !



What happens through time?

So far: final epidemic size

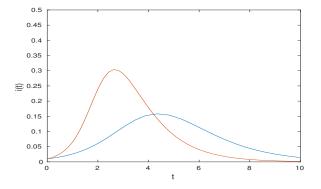
Now: What happens with outbreak over time?

Next page we plot fraction infectious over time, i(t), for a related but deterministic model. For $R_0 = 3$ but also assuming preventive measures which reduce reproduction number to $R_E = 2$

From above we know that final epidemic sizes approximately equal 92% and 78% respectively. Not a huge difference but ...



Fraction infectives i(t) over time, for $R_0 = 3$ and $R_E = 2$



The peak drops close to 50% and is delayed 70%! Both effects are very important for healthcare system!!



Prevention and vaccine immunity

From before: If overall effect of preventive measures reduce infectious contacts by factor p then reproduction number equals

$$R_E = R_0 * (1-p)$$

So minimal preventive effect (such that $\textit{R}_{\textit{E}} \leq 1):~\textit{p}_{\textit{Min}} = 1 - 1/\textit{R}_{0}$

If additionally a (uniformly distributed) fraction \hat{i} are immune from vaccination, then

$$R_E^{(Vac)} = R_0*(1-p)*(1-\hat{i})$$
 and $p_{Min}^{(Vac)} = 1-1/(R_0*(1-\hat{i}))$



Disease-induced immunity

Based on Britton et al (2020) (*Science* + *MedRxiv*) If instead a fraction \hat{i} are immune from disease spreading, then socially active and highly susceptible individuals are over-represented among immune.

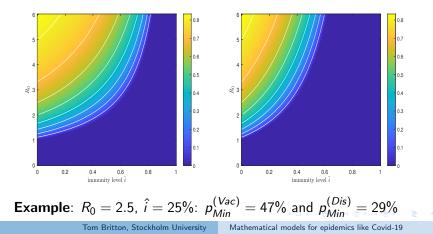
 \Longrightarrow immunity is more efficiently distributed

$$\Longrightarrow {\cal R}_E^{(Dis)} < {\cal R}_E^{(Vac)} = {\cal R}_0 * (1-p) * (1-\hat{i}) \$$
 $\Longrightarrow {\cal p}_{(Min)}^{(Dis)} < {\cal p}_{Min}^{(Vac)} = 1 - 1/({\cal R}_0 * (1-\hat{i})) \$



Heatmap of minimal preventive measures p_{Min}

Left: Vaccine-induced immunity and/or homogeneous model Right: Disease-induced immunity + heterogeneous model





Herd immunity

Herd immunity: $R_E < 1$ without preventive measures (i.e. when $\rho = 0$)

Herd immunity from vaccination: $i_{H}^{(Vac)} = 1 - 1/R_0$

If vaccine has efficacy E (for example 90%) then critical vaccination coverage v_c given by

$$v_c = \frac{1}{E} \left(1 - \frac{1}{R_0} \right)$$

If $R_0 = 2.5$ and 90% vaccine efficacy, then $v_c = 67\%$

Disease induced Herd immunity is smaller $i_{H}^{(Dis)} < 1 - 1/R_0$

. . .



Global challenges in Infectious disease modelling

Pandemics: Prediction, evaluating effects of preventive measures (including vaccine programs), ...

Endemic diseases (malaria, measles, TB, Polio, ...): effects of different preventive measures, what fraction necessary to vaccinate,

HIV and other STI's: risk-groups, targeted preventive measures and treatment, ...

Diseases among domestic animals: stop outbreaks without culling too many animals

Antibiotic resistance: How reduce resistance levels without stopping the *important* use of antibiotics