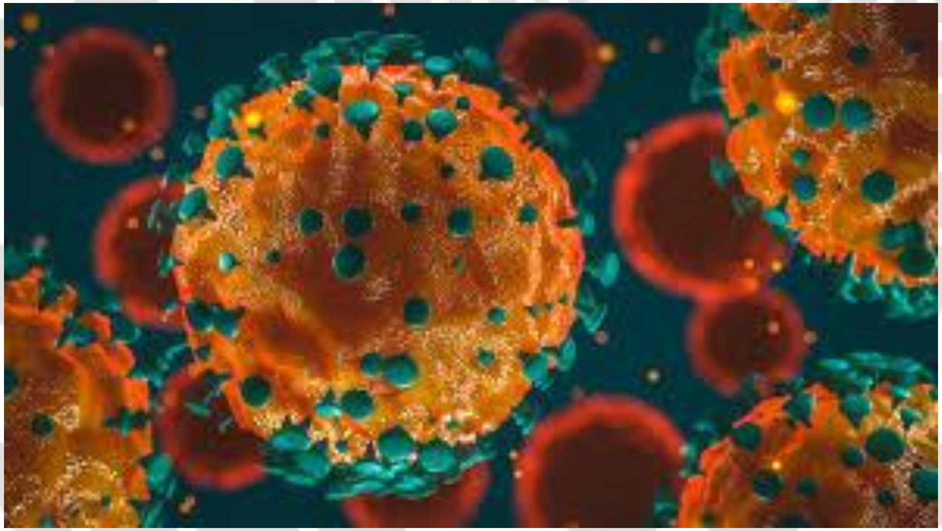
The maths of COVID-19



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Shaun Hendy
@hendysh

Te Pūnaha Matatini

- A national research centre in **complex systems and networks** established in 2015. Today it has >70 investigators and about 100 students involved.

- Broad expertise in natural sciences, maths, physics, and data science, working with domain experts on social, economic, and ecological systems

- We have also worked on disease e.g.
  - *M. bovis* (using NAIT data)
  - Seasonal flu (using genomics and telco data)
  - Havelock North gastroenteritis (using Westpac data)

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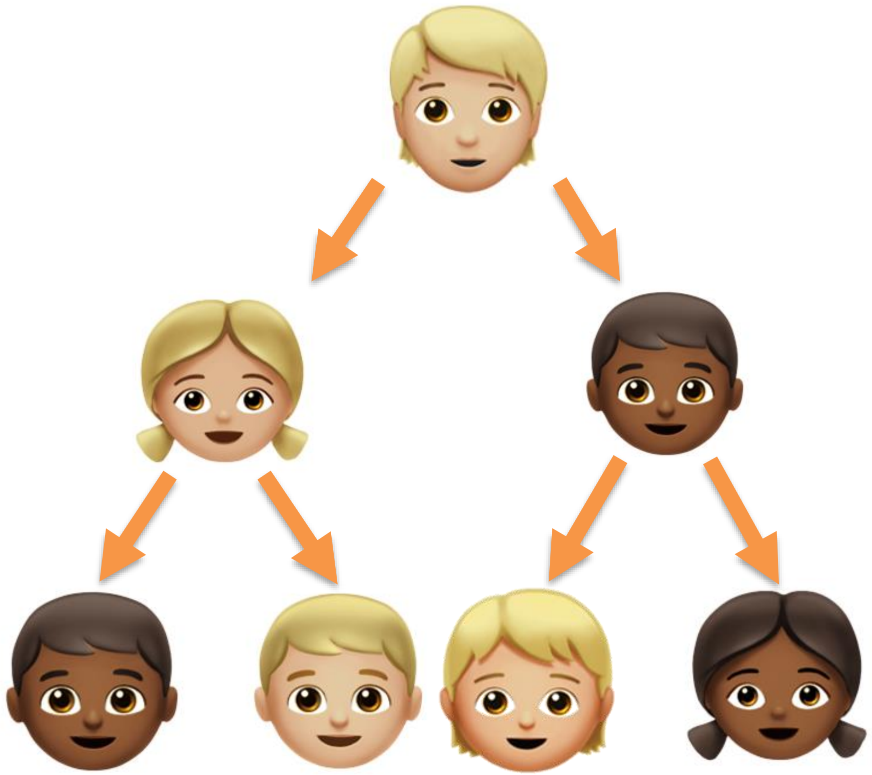
A disease simulation

RULES

- Everyone starts seated
- One volunteer is chosen to be the **index case**
- The index case stands up and ‘infects’ **two** others by pointing
- These two also stand up, having been ‘infected’
- Each of these two then infect two more, and so on, until everyone is standing up
- How many steps does it take to infect the whole room?



The reproduction number

- In the simulation, the number of people each person went on to infect was **two**
- This number, called R_0 or the *reproduction number* of the virus, depends on the disease

Disease	R_0
Measles	12 to 18
SARS-CoV-2	2.5 (up to 6)
SARS-CoV-1	2.4
Seasonal flu	1.2 to 1.4

A simple model (SIR)

In this model R_0 depends on:

- how many days people are infectious for (T)
- how many close contacts are exposed each day (c)

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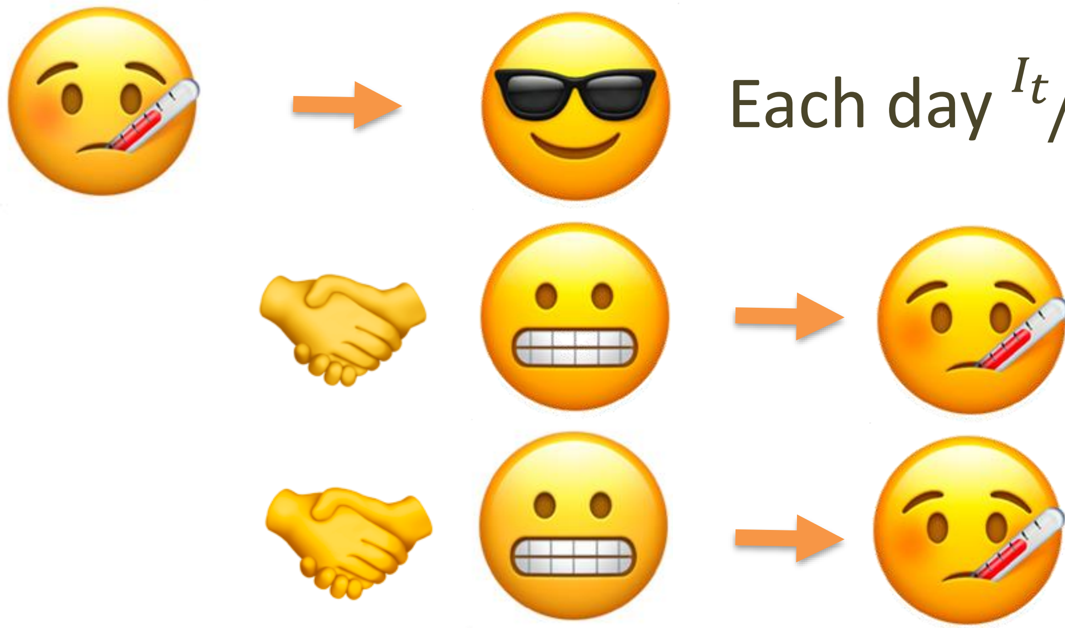
A simple model

At the start of day t, there are I_t infected people

I_t



Each day I_t/T people recover

There are cI_t possible new infections

i.e. the *reproduction number* is:

$$R_0 = cT$$

Each day I_t grows by

$$cI_t - I_t/T = (R_0 - 1)\,I_t/T$$

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A simple model

Each day (Δt) : $I_{t+1} \rightarrow I_t + (R_0 - 1)I_t \, {}^{\Delta t}/_{T}$

If $R_0 > 1$ the number of infected people will grow

If $R_0 < 1$ the number of infected people will decrease

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A simple model

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DIFFERENTIAL EQUATION ALERT:

$$\frac{dI}{dt} = \frac{I_{t+1} - I_t}{\Delta t} = (R_0 - 1)\, {}^{I}/_{T} \qquad I = I_0 e^{(R_0-1)\, {}^{t}/_{T}}$$

Exponential growth!

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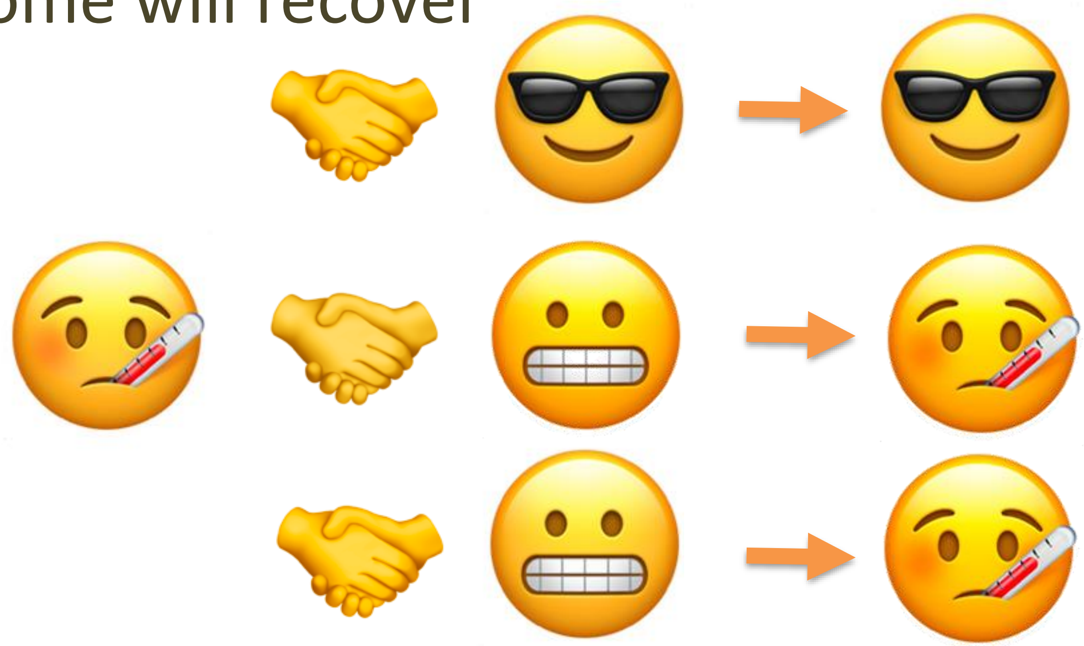
It's not that simple …

But after a while, not every contact will be susceptible, as some will recover



Recovered people are **immune**

The number of ***susceptible*** contacts exposed/day is only $c \times \left({}^{S_t}/_{N}\right)$

The ***reproduction number*** on day t is:

$$R_t = c \times \left({}^{S_t}/_{N}\right) \times T = R_0 \times \left({}^{S_t}/_{N}\right)$$

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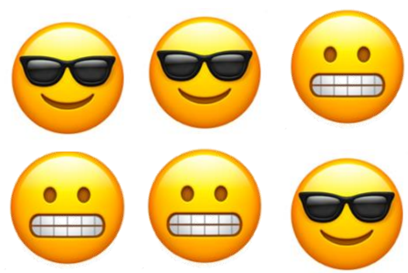
It's not quite that simple …

The ***reproduction number*** in this model *is:*

$$R_t = c\,{}^{S_t}/_{N}\,T = R_0\,{}^{S_t}/_{N}$$

When everyone is susceptible, $S_t = N$, *so* $R_t = R_0$



But as people recover the fraction of people who are susceptible ${}^{S_t}/_{N}$ decreases so R_t decreases

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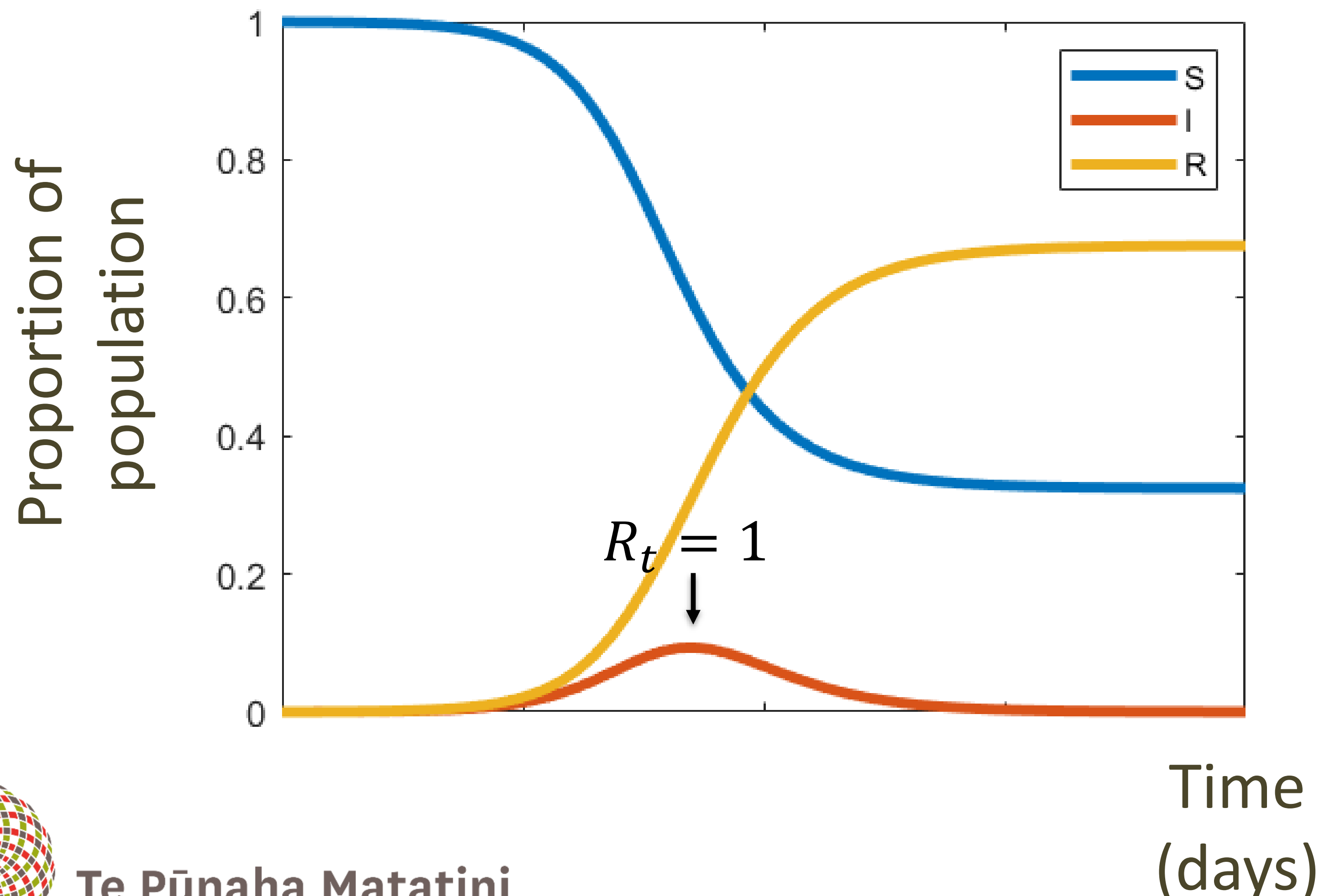
Example



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Controlling the epidemic

Once $R_t < 1$ the number of infected people starts to decrease and the epidemic will eventually fizzle out

How can we reduce R_t?

$$R_t = c \times \left(S_t/_N\right) \times T$$

Social distancing

Vaccinate

Trace and isolate

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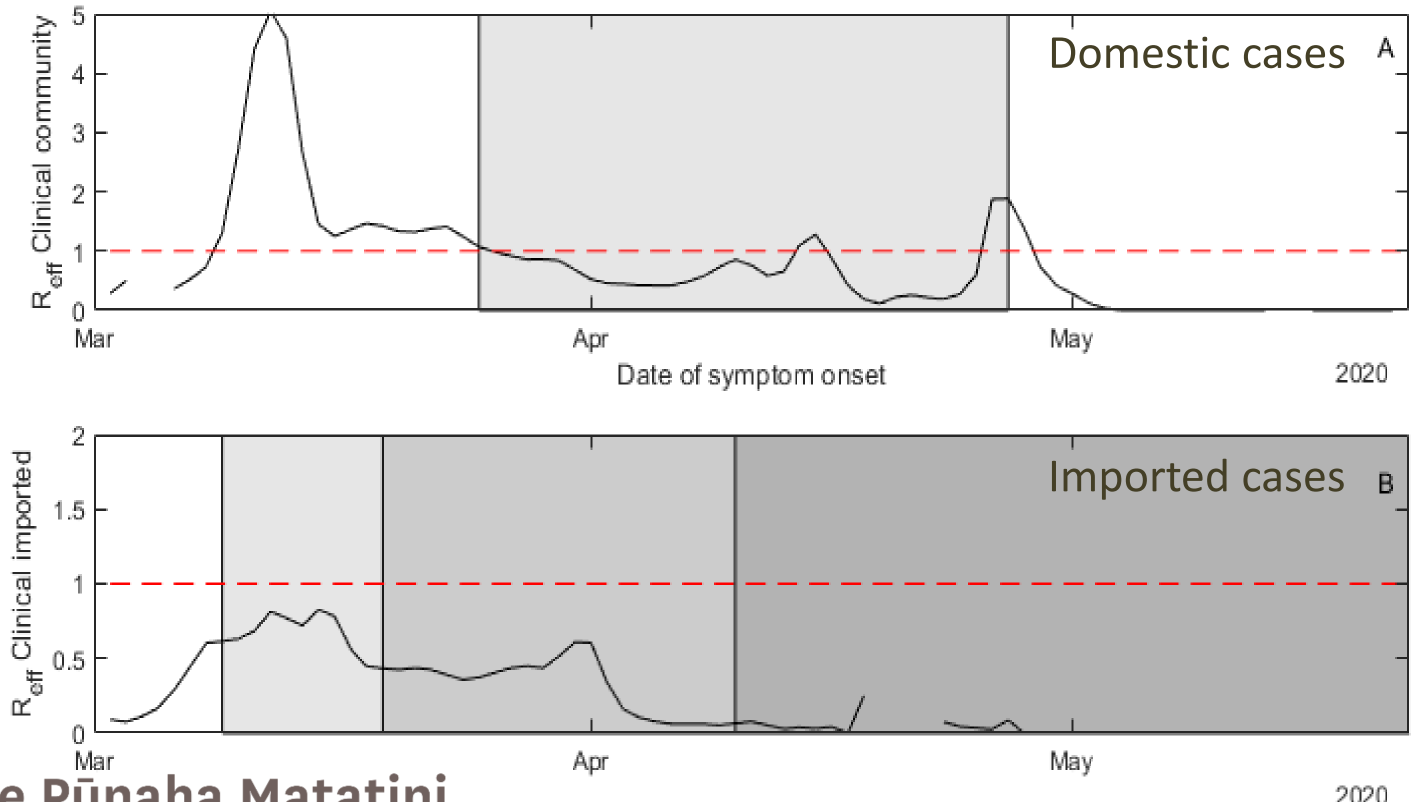
COVID-19 in New Zealand

Last year, we used the Alert Level system to bring $R_t < 1$

Reproduction number R_t



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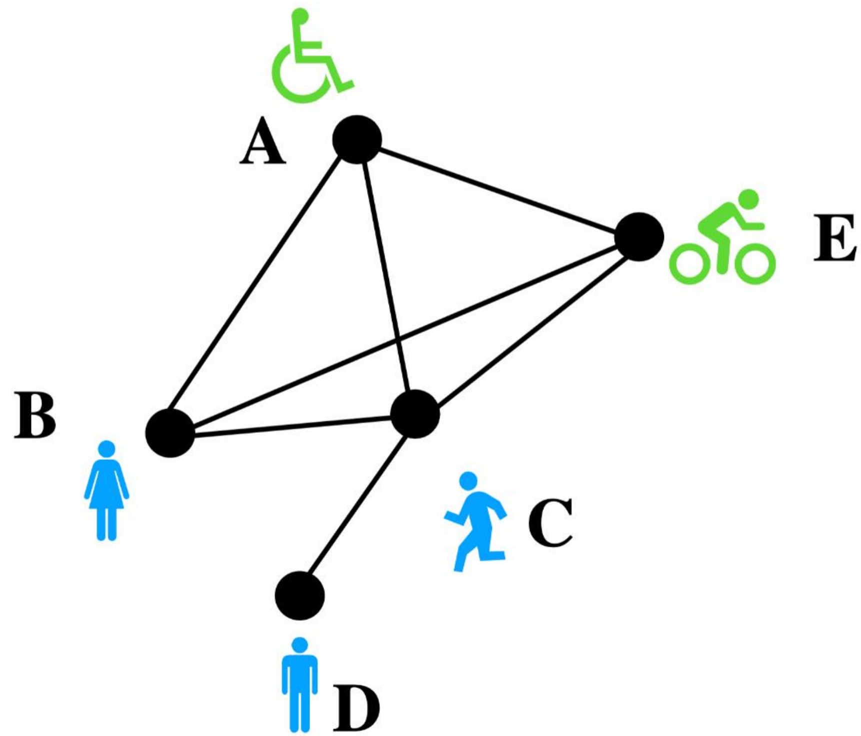
It’s not that simple …

The model so far assumes **everyone** is **equally likely** to infect others and everyone is equally like to be infected

But that is only an approximation to what really happens



People differ in how **infectious** they are and in who they come into **contact** with

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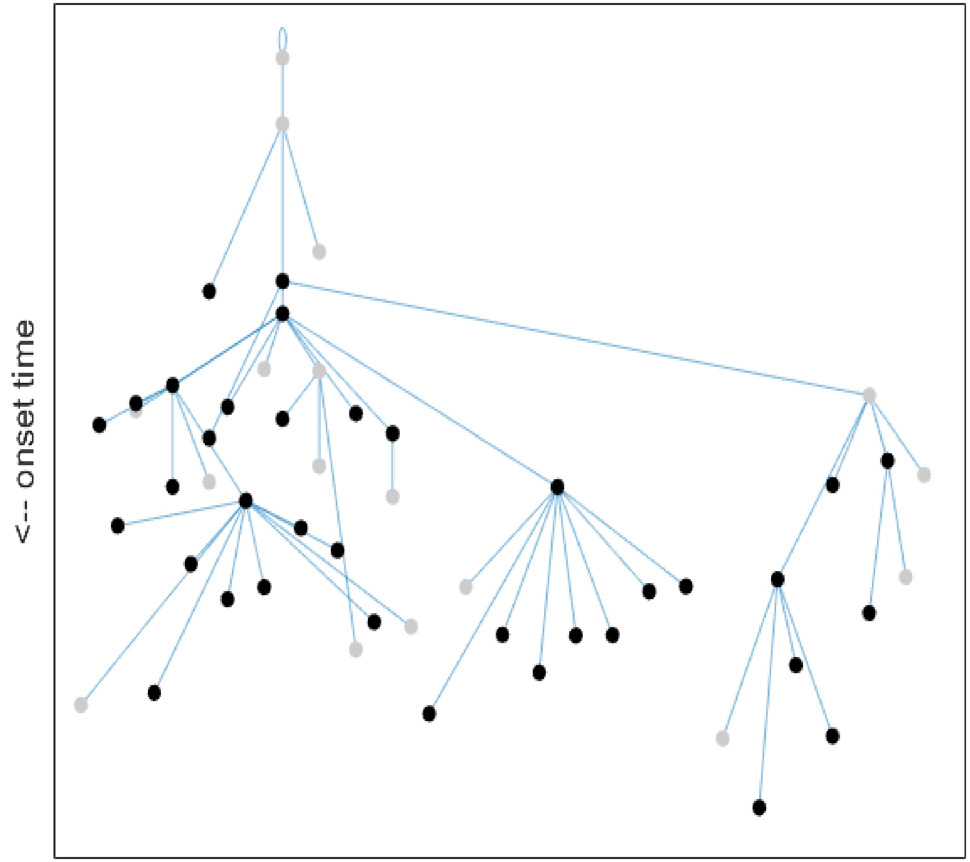
Superspreading

COVID-19 infections are mostly passed on via **superspreading**

i.e. only 20% cases are responsible for 80% of the spread

This means that most chains of infection fizzle while just a few take off



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A. James, M. Plank, S. Hendy, R. Binny, A. Lustig, and N. Steyn "Model-free estimation of COVID-19 transmission dynamics from a complete outbreak", PLoS One 16(3): e0238800 (2021).

A second disease simulation

RULES

- The index case stands up and draws a card
- If they draw a heart, they ‘infect’ **eight** others by pointing
- These eight also stand up, having been ‘infected’
- If they don’t draw a heart, they don’t infect anyone

♥ Superspreader!

♠ ♣ ♦

The reproduction number R_0 is still ***two*** *on average* but the simulation can play out quite differently by chance

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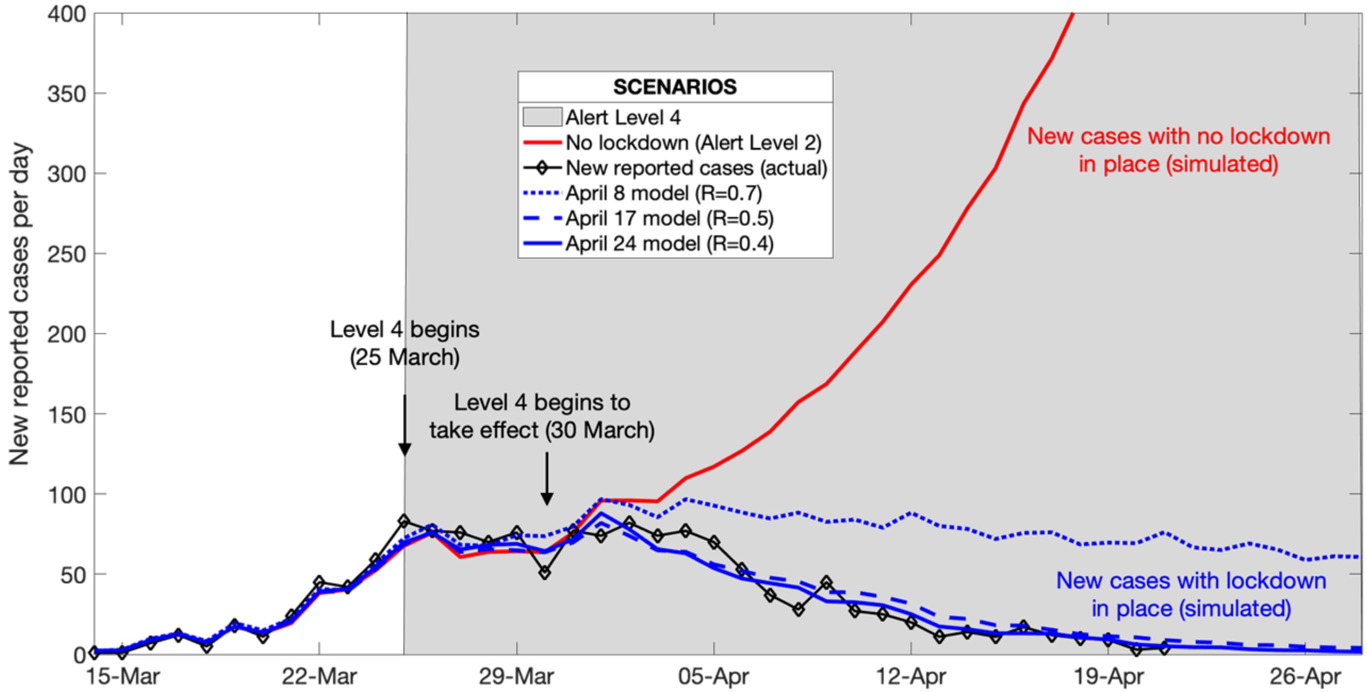

We run 1000s of simulations to find the most likely outcome. This worked well in March and April, when we had 100s of transmission chains ...

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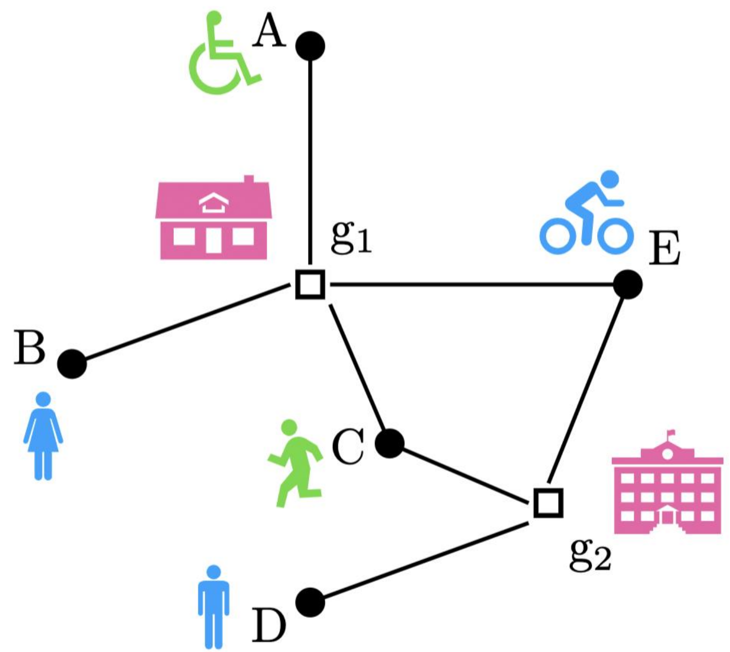
It’s still not that simple …

But when we only have a few chains of infection, the details of our **contact network** become very important

We connect with each other via

- Our homes
- Our schools
- Our workplaces
- Our friends



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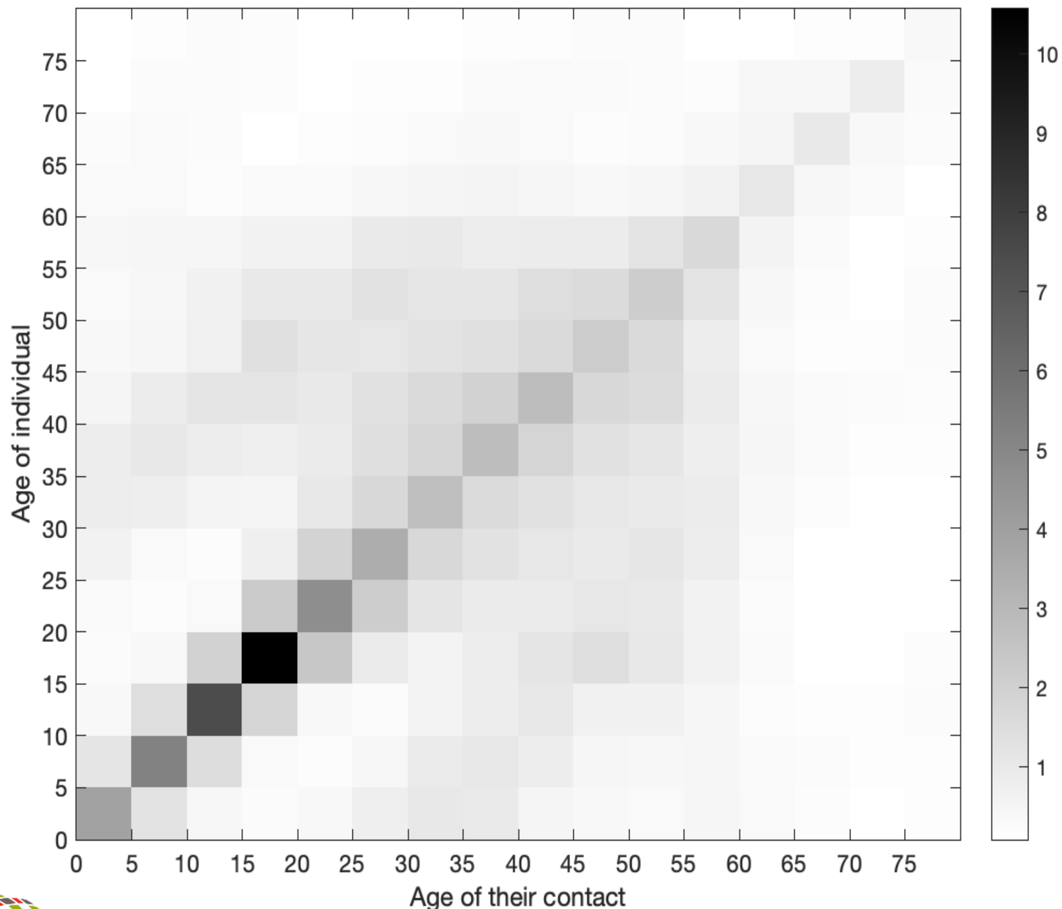
Contacts by age



Young adults and teenagers (aged 15-20) tend to have the most contacts

Older people (65+) have the fewest

Young people will tend to spread the virus more

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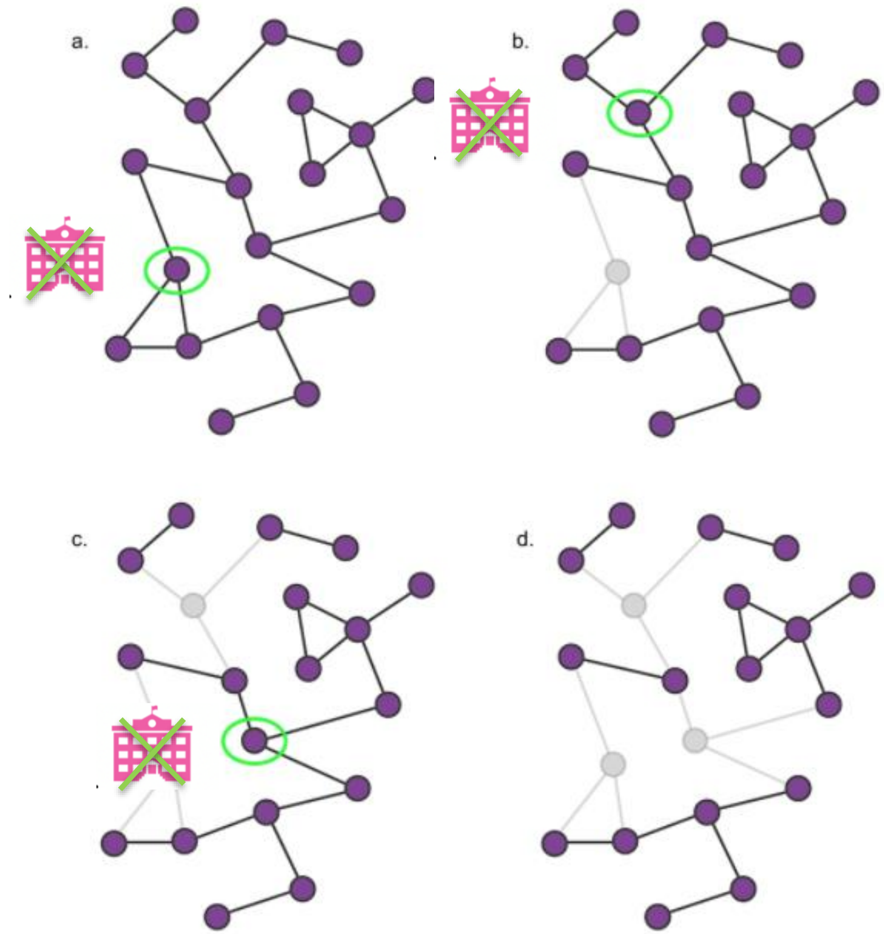
Prem K, Cook AR, Jit M (2017). PLOS Computational Biology 13(9): e1005697.

Phase transitions

Our Alert Level system didn't just reduce contacts overall, it broke our social network into bubbles

This process is described by **percolation theory**, which can be studied as a **phase transition**



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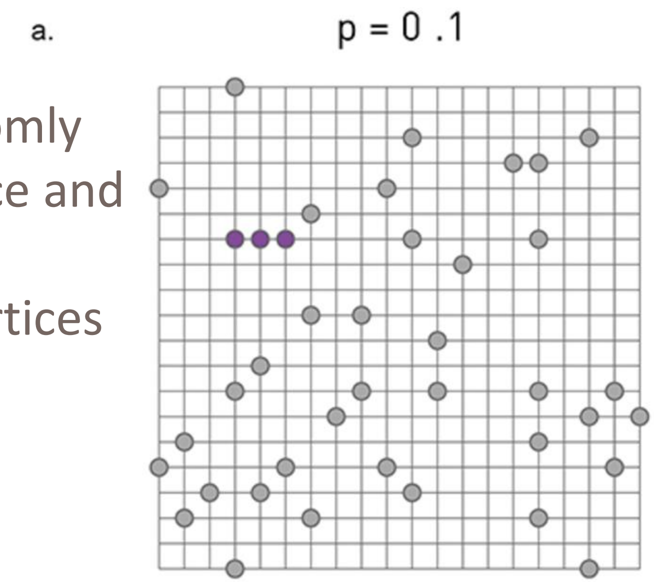
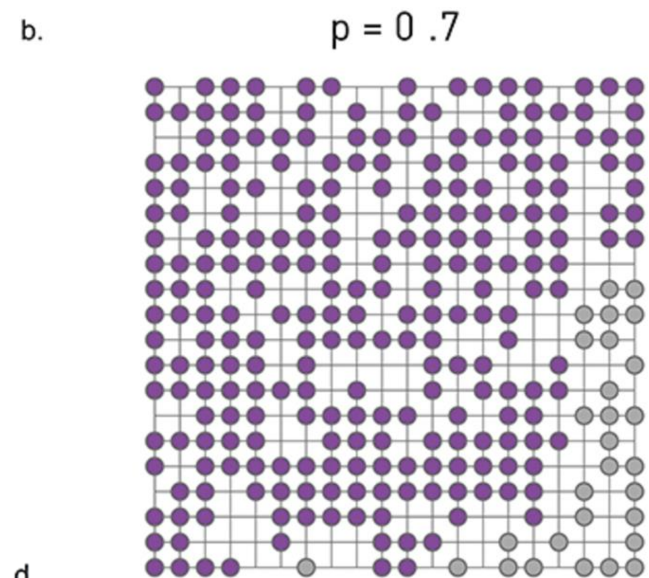
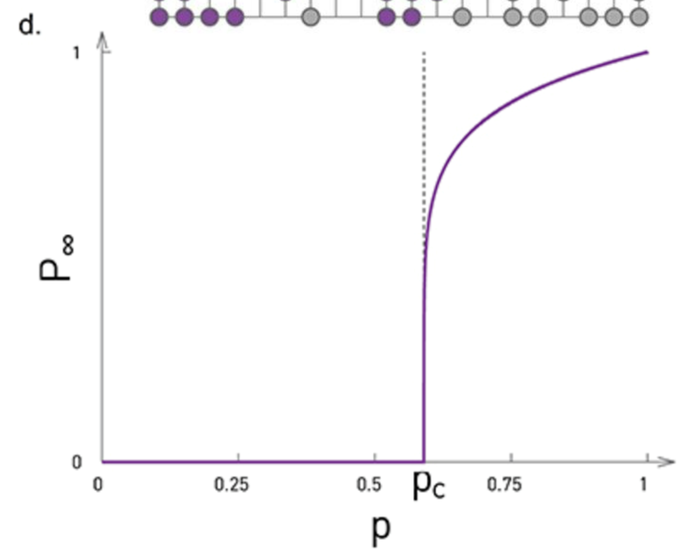
Percolation theory





Place discs randomly on a square lattice and monitor p, the proportion of vertices covered.



p_c is the **critical proportion** at which the largest cluster spans the lattice.

p_∞ is the probability a given disc belongs to the largest cluster.

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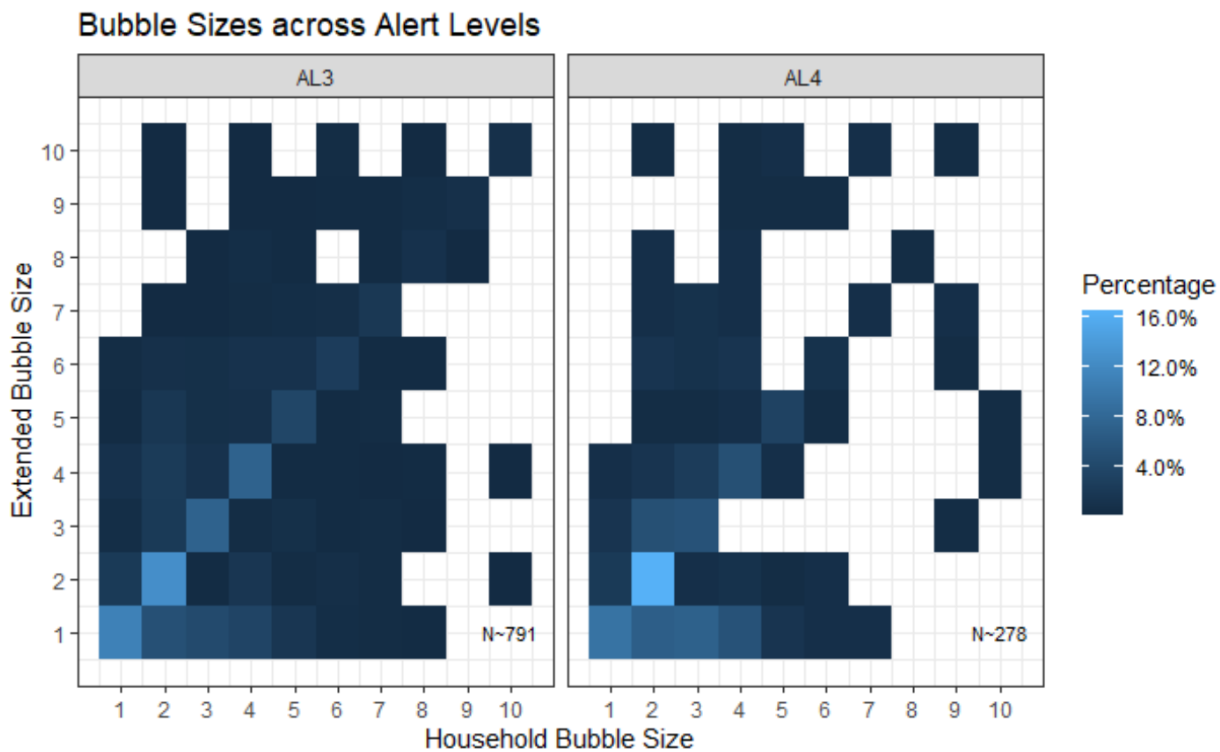
Barabasi, *Network Science, http://barabasi.com/networksciencebook/*

Percolation theory

Moving from Alert Level 4 to 3 shifted us across a **percolation threshold** in our social network, splitting us into bubbles



The largest connected social network grows from < 100,000 people to > 1 million people

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James Gilmour, Emily Harvey, Dion O'Neale, Steven Turnbull
"Network Consequences of Spread"

Vaccinations

How many people V do we need to vaccinate to stop the epidemic?

$$1 > R_t = c\, {}^{S}/_{N}\, T = R_0\, {}^{S}/_{N}$$

$$\Rightarrow {}^{S}/_{N} < {}^{1}/_{R_0} \qquad\qquad (V + S = N)$$

$$\Rightarrow {}^{V}/_{N} > 1 - {}^{1}/_{R_0}$$

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- For wild-type COVID-19, R_0=2.5 so ${}^{V}/_{N} >$ 60%
- For B.1.617.2 (delta), R_0=5.5 so ${}^{V}/_{N} >$ 82%

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Vaccinations

- That calculation assumes that the vaccine was 100% effective in reducing *transmission*

- Data suggests 3-doses is about 50% effective in reducing transmission for ~3-6 months for Omicron:

$$\Rightarrow {}^{V}\!/_{N} > {}^{\left(1-{}^{1}\!/_{R_0}\right)}\!/_{e} = 160\%$$

- The current vaccine won't stop the pandemic (!), but does reduce occurrence of severe disease

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Thanks to …

Mike Plank

Rachelle Binney

(Top, left to right) **Emily Harvey**, Oliver Maclaren, Ilze Zeidins, Andrew Sporle (Bottom, left to right) Shaun Hendy, Kate Hannah, Siouxsie Wiles, **Dion O'Neale**

Audrey Lustig

Nick Steyn

Alex James

Plus Melissa McLeod, Tahu Kukutai, Matt Parry, Joep de Ligt, Jemma Geoghegan

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Glossary

- **Index case:** the first case to be infected in a cluster
- **Reproduction number, $\boldsymbol{R_0}$:** the *average* number of secondary cases infected by single case at the start of an epidemic
- **Reproduction number, $\boldsymbol{R_t}$**: the reproduction number t days into an epidemic
- $\boldsymbol{T}$: the average number of days a person is infectious
- $\boldsymbol{c}$: the number of contacts per day that are exposed
- $\boldsymbol{N}$: the number of people in a population
- $\boldsymbol{S_t}$: the number of susceptible people on day t in a population
- $\boldsymbol{I_t}$: the number of infected people on day t in a population
- $\boldsymbol{V}$: the number of vaccinated people in a population
- $\Delta \boldsymbol{t}$: 1 day
- **Superspreading event**: an event where many more people than $\boldsymbol{R_0}$ become infected

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