

Reproduction numbers and superspreading – how to measure disease transmission

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INI talk
July 2020



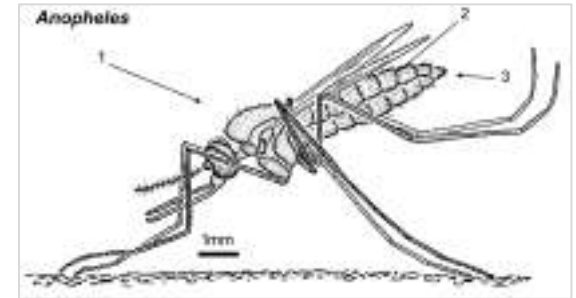
centre for
mathematical
modelling of
infectious
diseases

cmmid.github.io/ncov

LONDON
SCHOOL of
HYGIENE
& TROPICAL
MEDICINE



Village with 1,000 people and one person infected with malaria

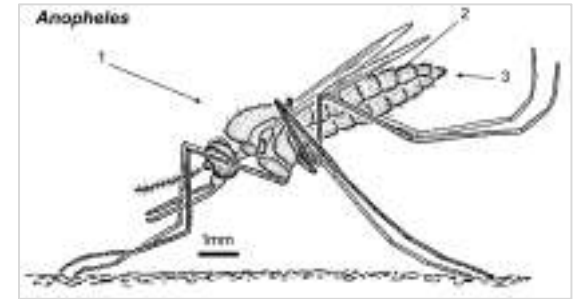


Ross R, *Prevention of Malaria*, 1911

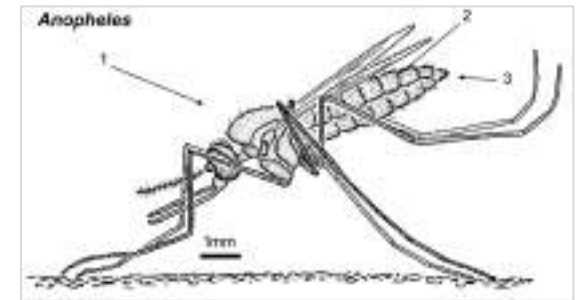
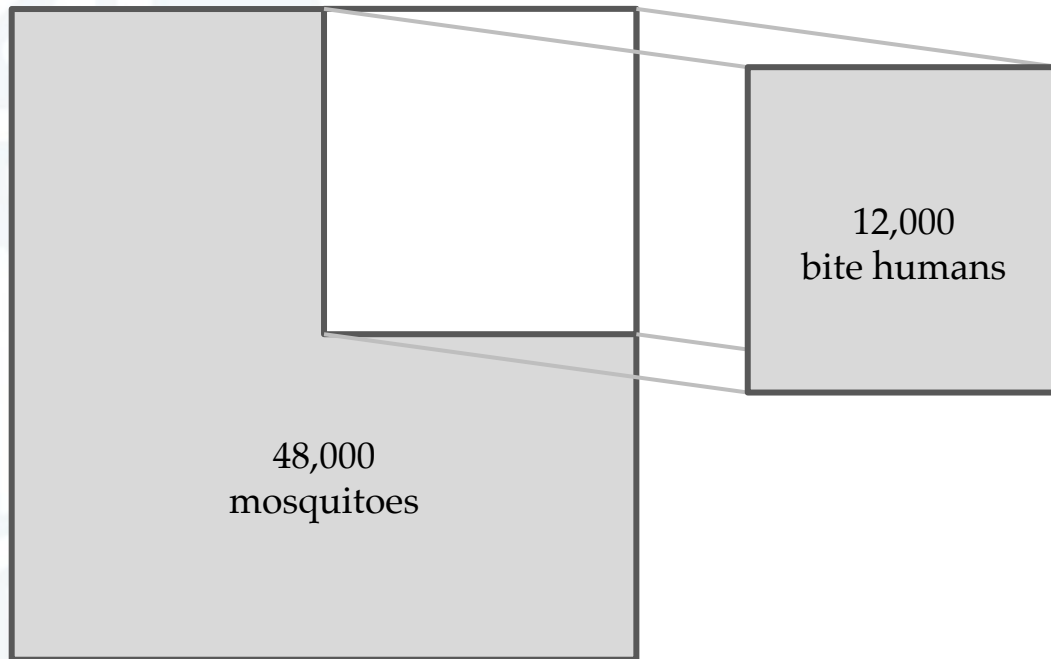
Acarologiste via WikiCommons

Village with 1,000 people and one person infected with malaria

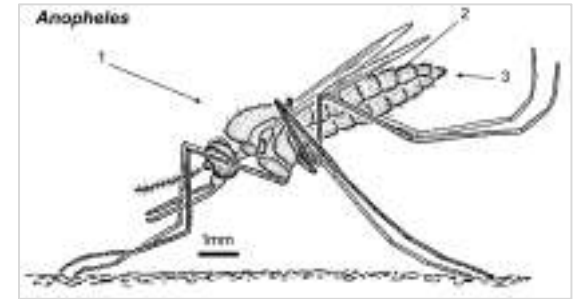
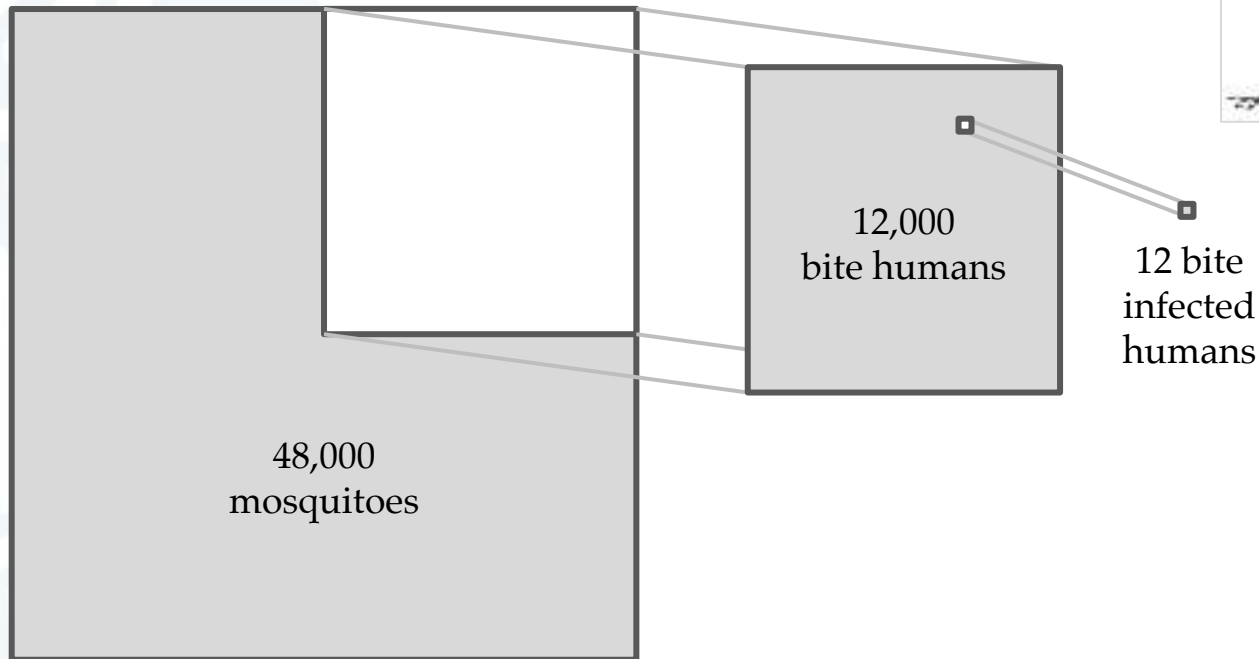
48,000
mosquitoes



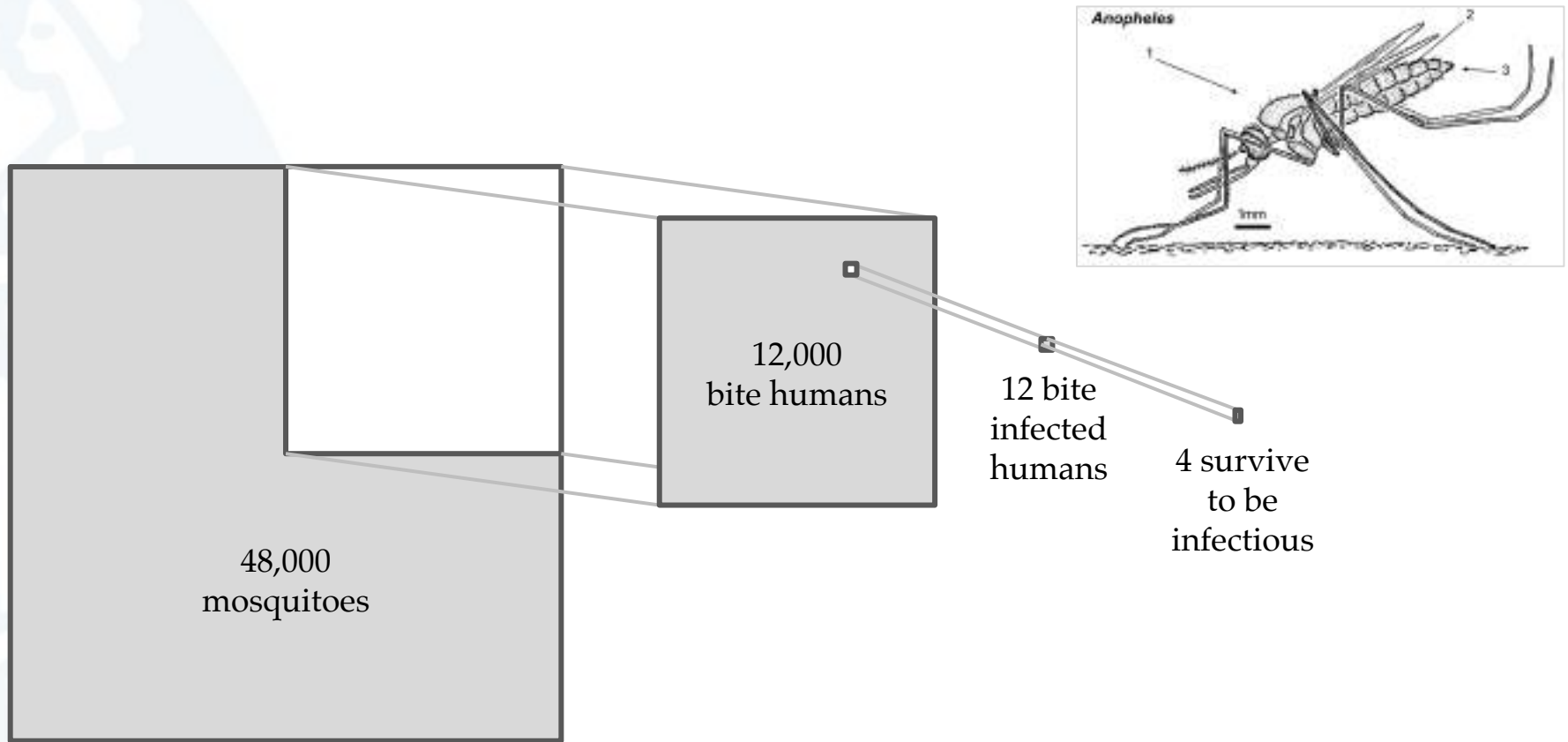
Village with 1,000 people and one person infected with malaria



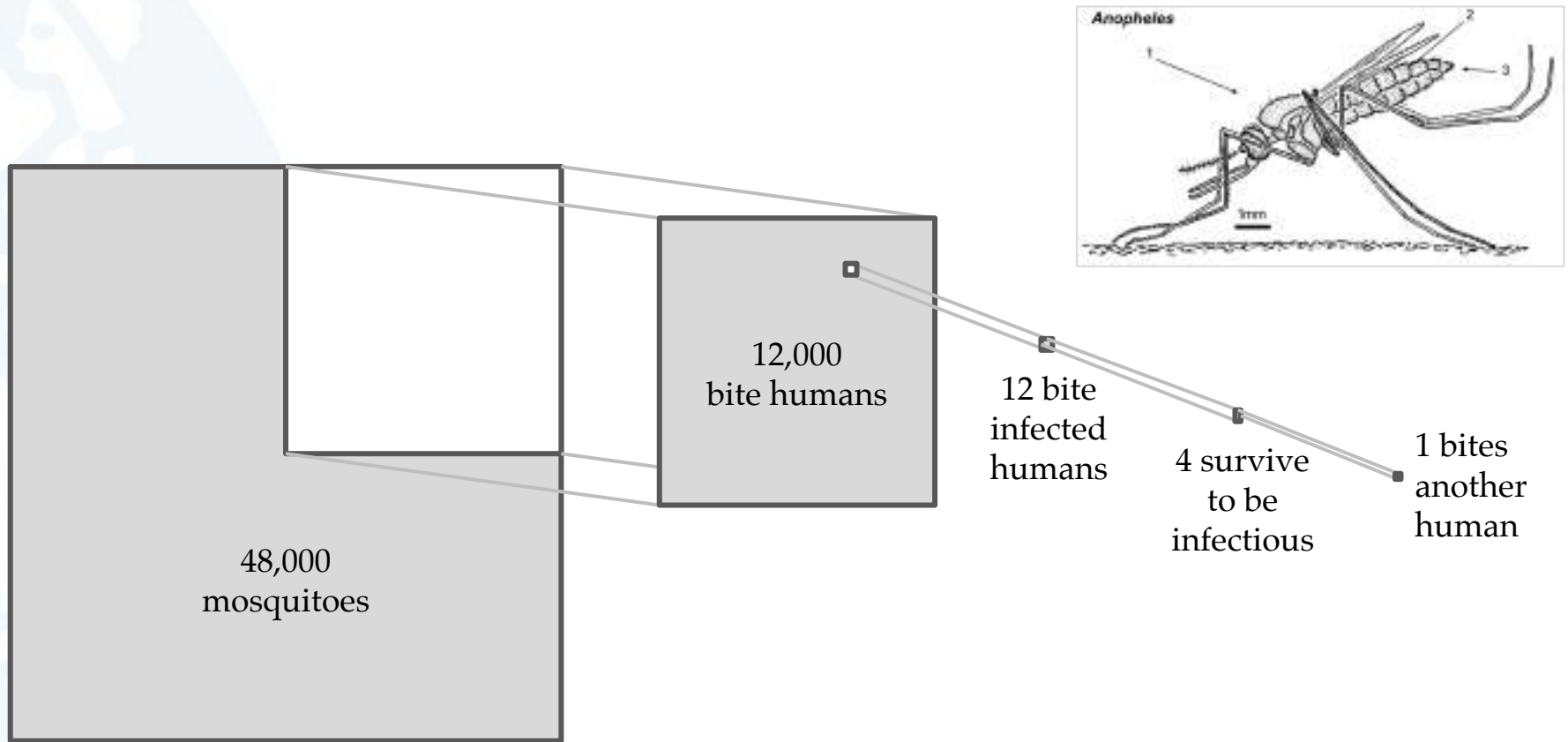
Village with 1,000 people and one person infected with malaria




Village with 1,000 people and one person infected with malaria



Village with 1,000 people and one person infected with malaria





“Basic Reproduction Rate of malaria, definition.
The number of infections distributed in a
community as the direct result of the presence in
it of a single primary non-immune case.”

– George MacDonald, 1952

(not actually a rate)



“Basic Reproduction Rate of malaria, definition. The number of infections distributed in a community as the direct result of the presence in it of a single primary non-immune case.”

– George MacDonald, 1952

Reproduction number

'R'

New cases

Initial
cases

Time



New cases

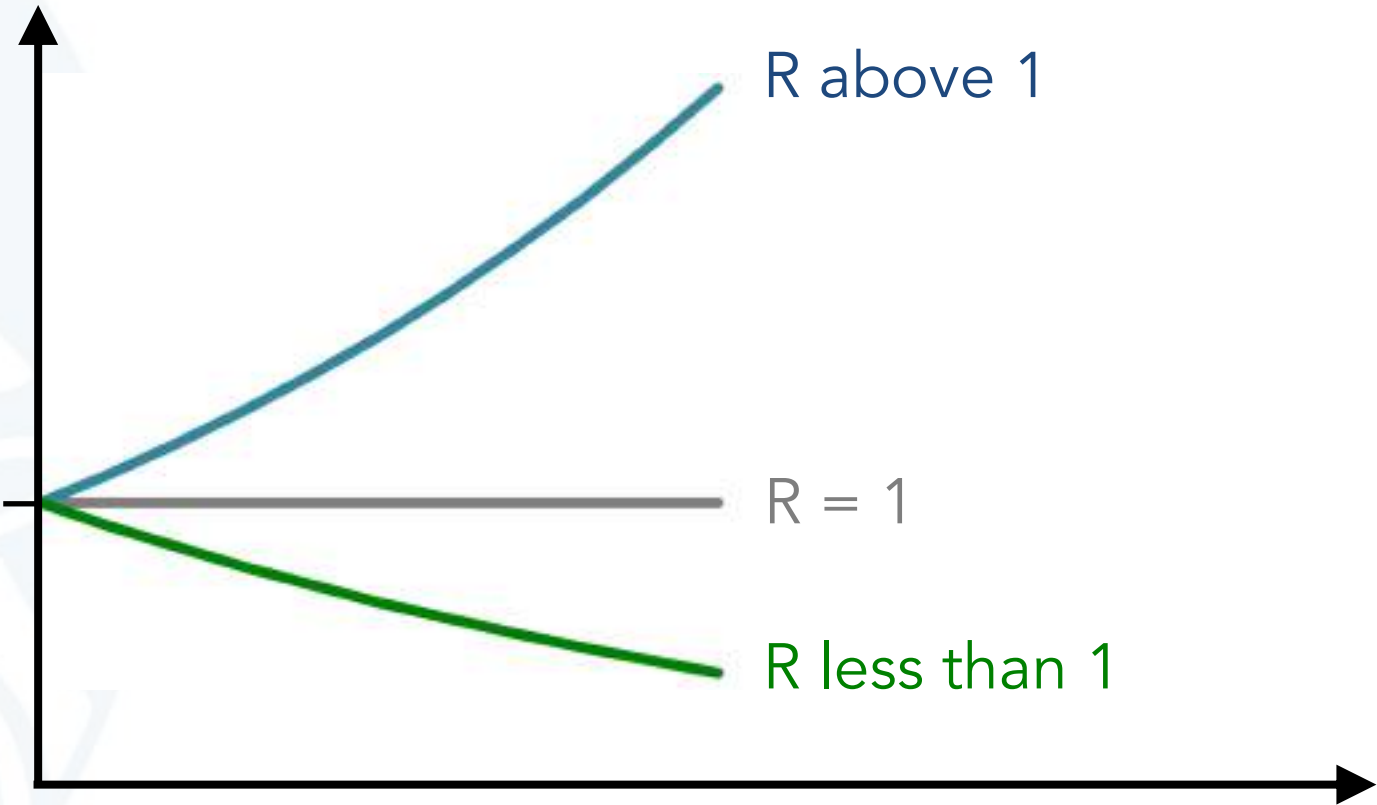
Initial cases

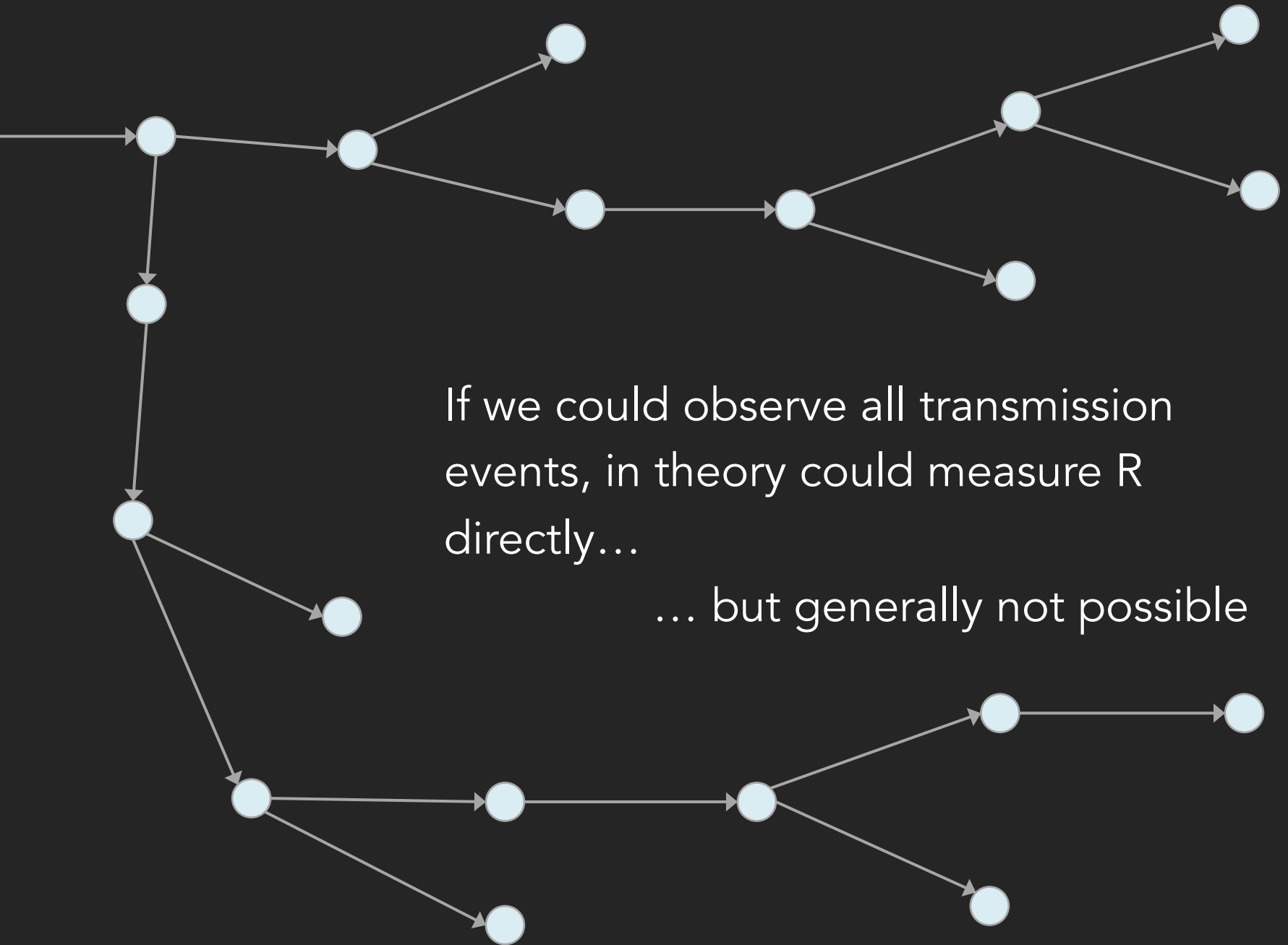
R above 1

R = 1

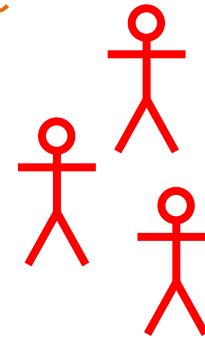
R less than 1

Time





Delay from case showing symptoms to person they infect showing symptoms given by the 'serial interval'

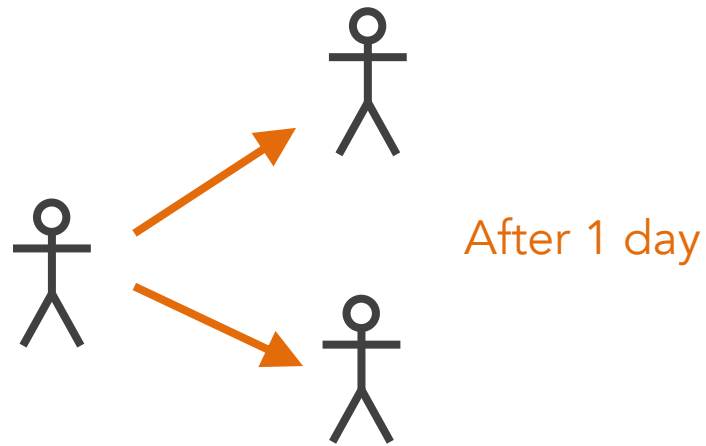


Average growth in cases during this period given by R

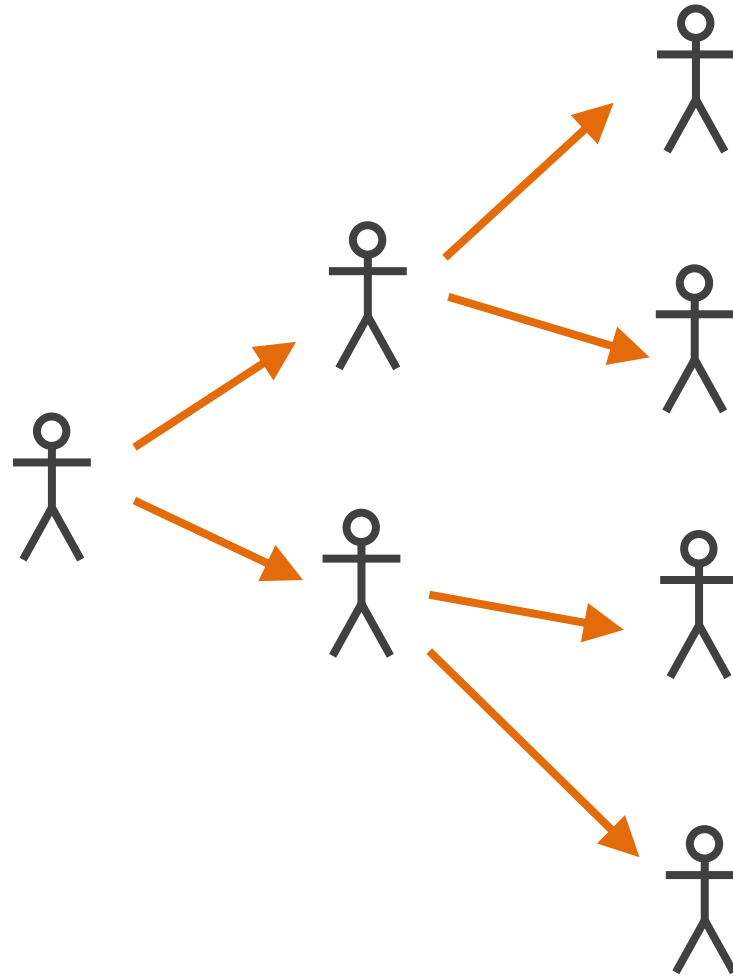
If serial interval is 1 day and
 $R=2...$



If serial interval is 1 day and
 $R=2$...

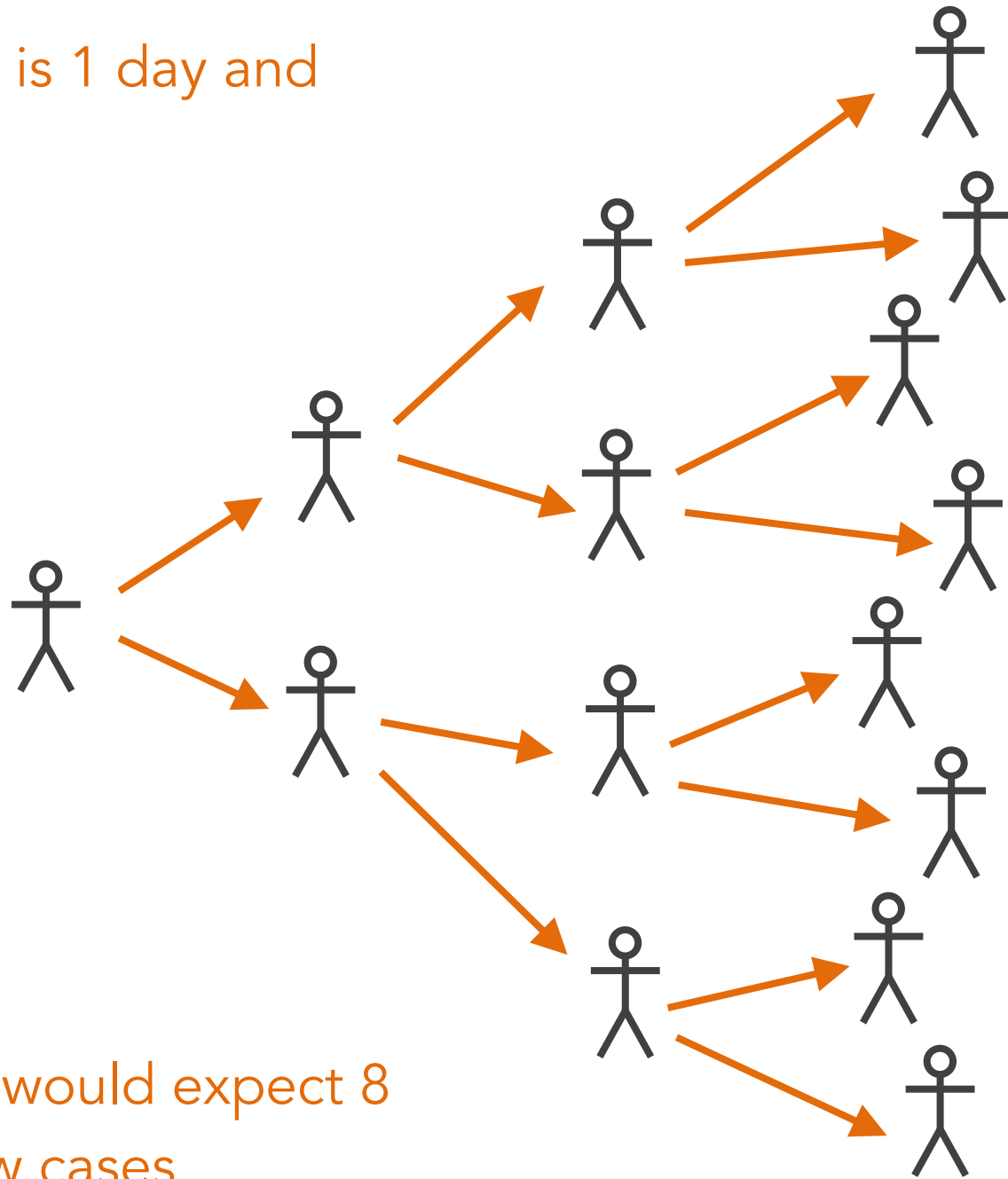


If serial interval is 1 day and
 $R=2...$



After 2 days

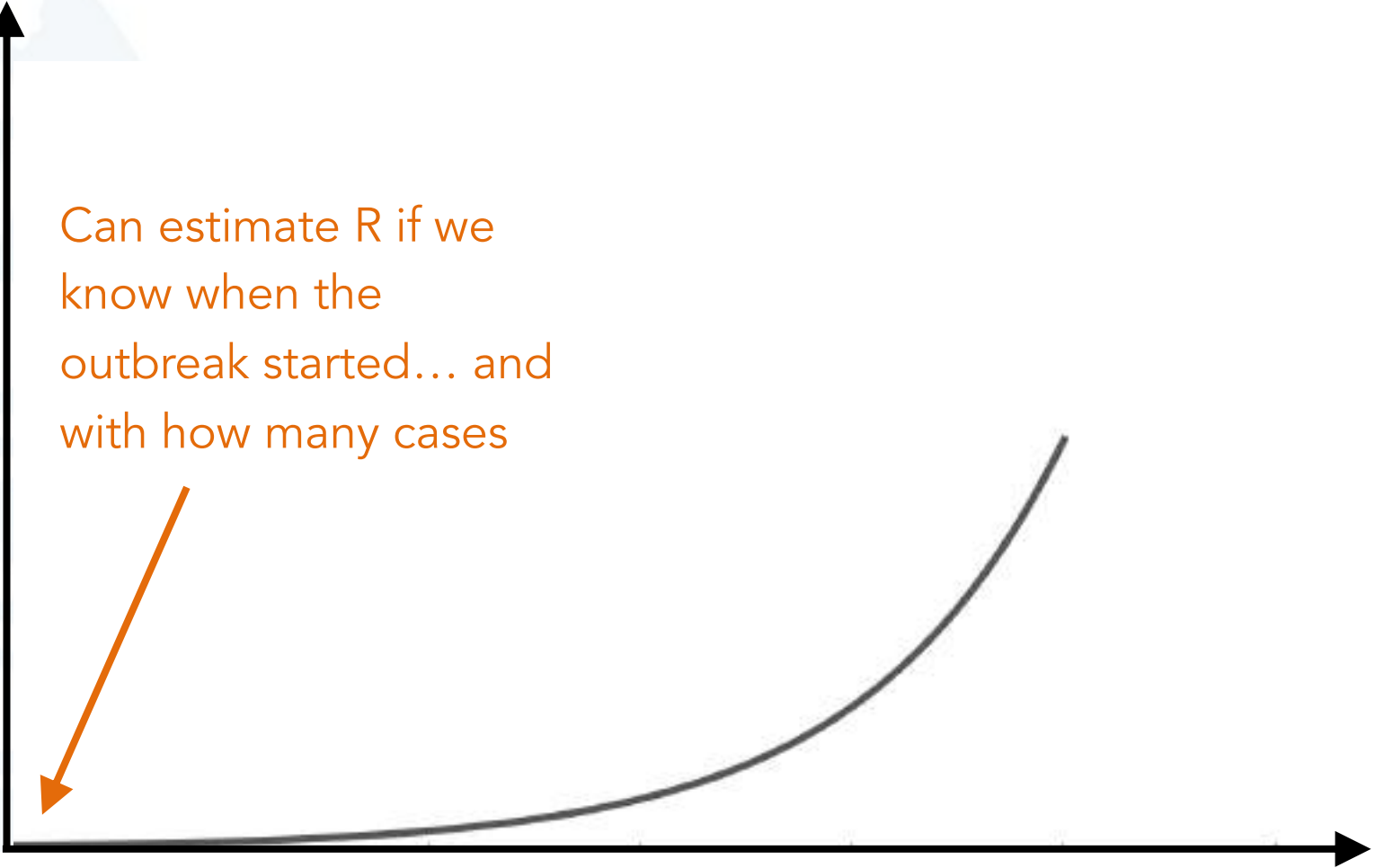
If serial interval is 1 day and
 $R=2$...



... after 3 days would expect 8
times more new cases

Cases

Can estimate R if we know when the outbreak started... and with how many cases



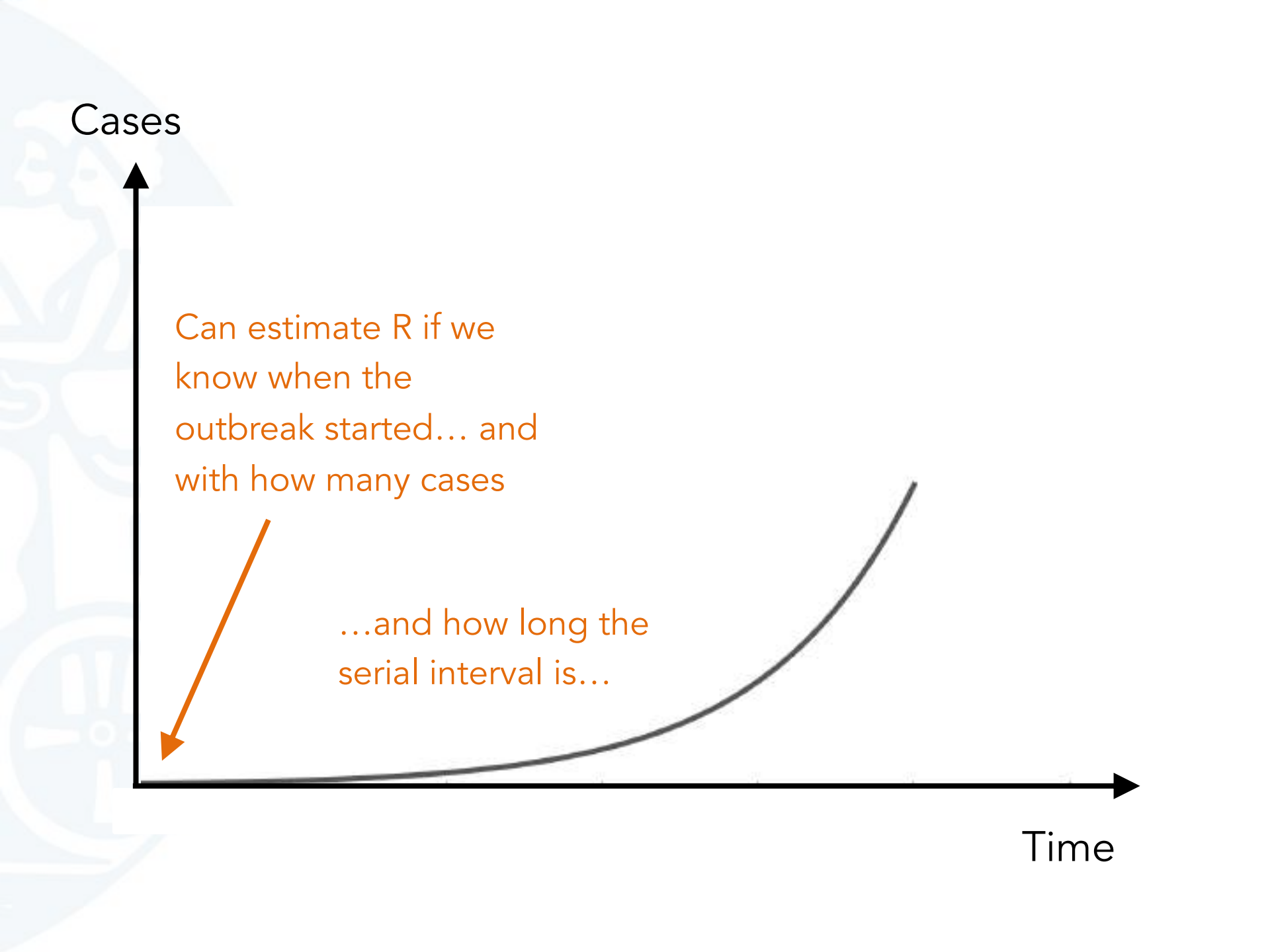
Time

Cases

Can estimate R if we know when the outbreak started... and with how many cases

...and how long the serial interval is...

Time



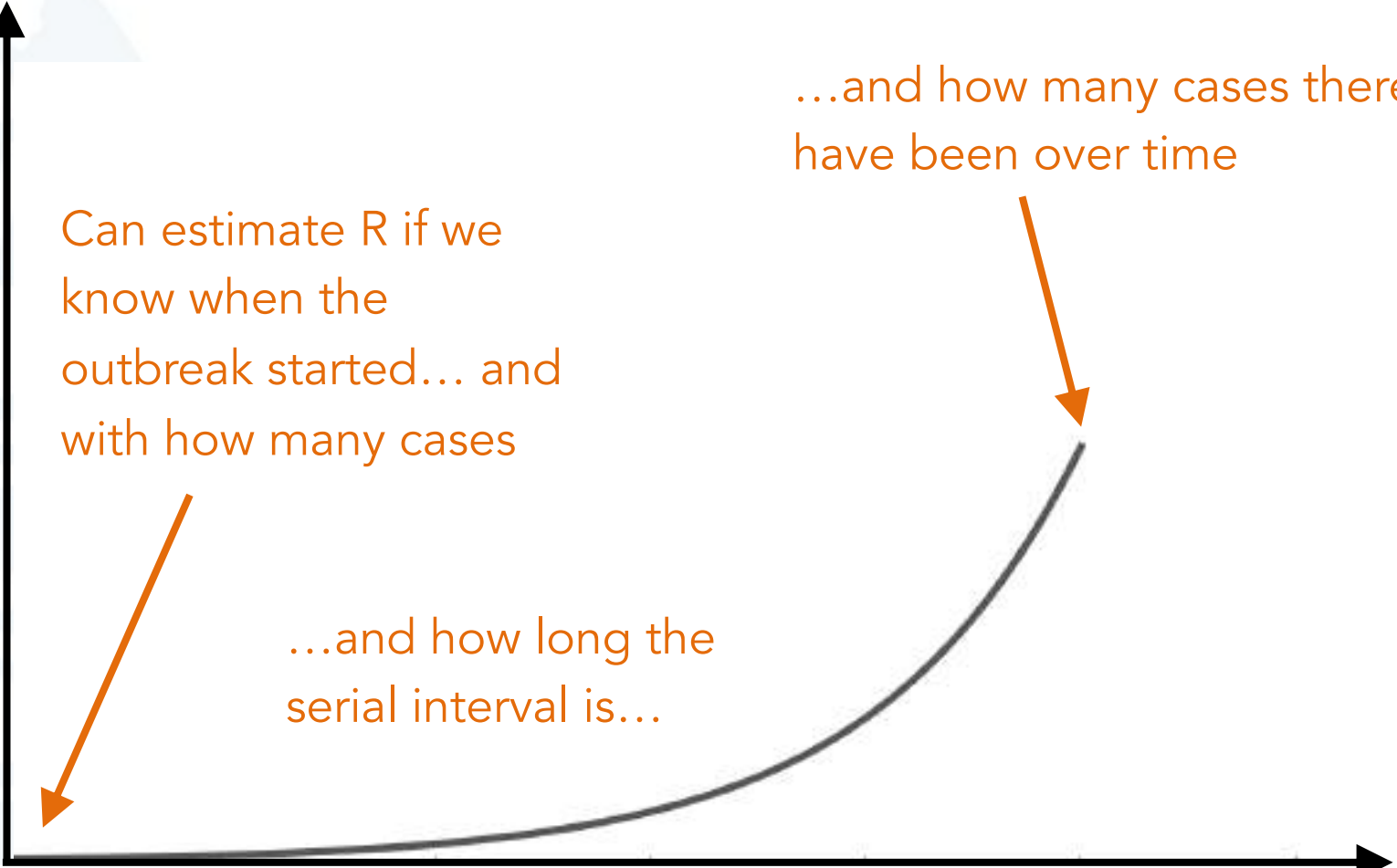
Cases

Can estimate R if we know when the outbreak started... and with how many cases

...and how long the serial interval is...

...and how many cases there have been over time

Time



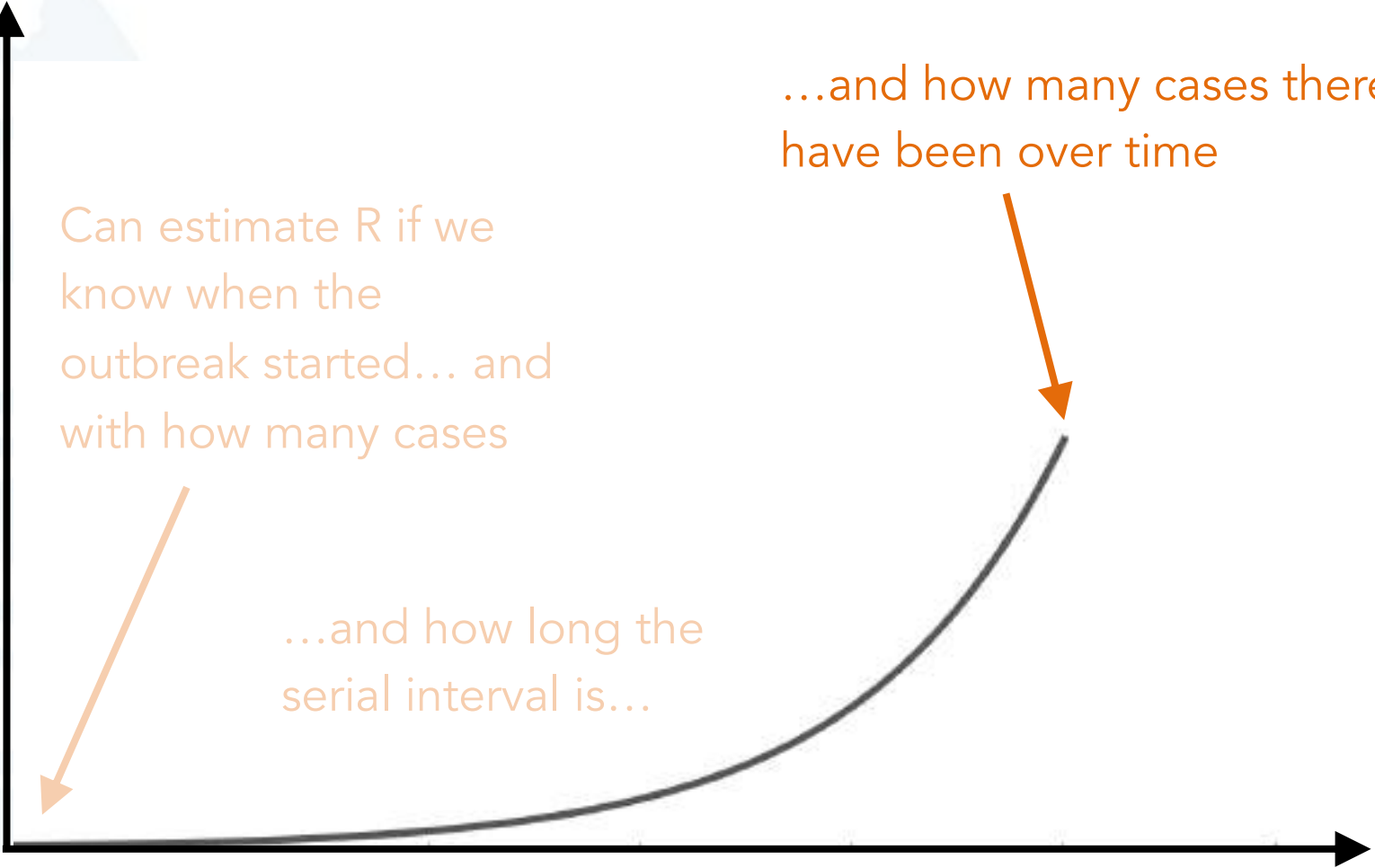
Cases

Can estimate R if we know when the outbreak started... and with how many cases

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Time



- By 16th January, 41 confirmed COVID-19 cases in Wuhan, China.
- Three cases detected abroad (2 in Thailand, 1 in Japan).

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- Three cases detected abroad (2 in Thailand, 1 in Japan).

Based on flight patterns, likely to already been thousands of cases in Wuhan



Woman returning from Iran is B.C.'s sixth case of new coronavirus

The Canadian Press

Feb 21, 2020 • Last Updated 4 months ago • 2 minute read

EDITORS' PICK | 53,417 views | Mar 6, 2020, 04:49pm EST

Most Of Canada's New Cases Of COVID-19 Are Linked To The U.S.

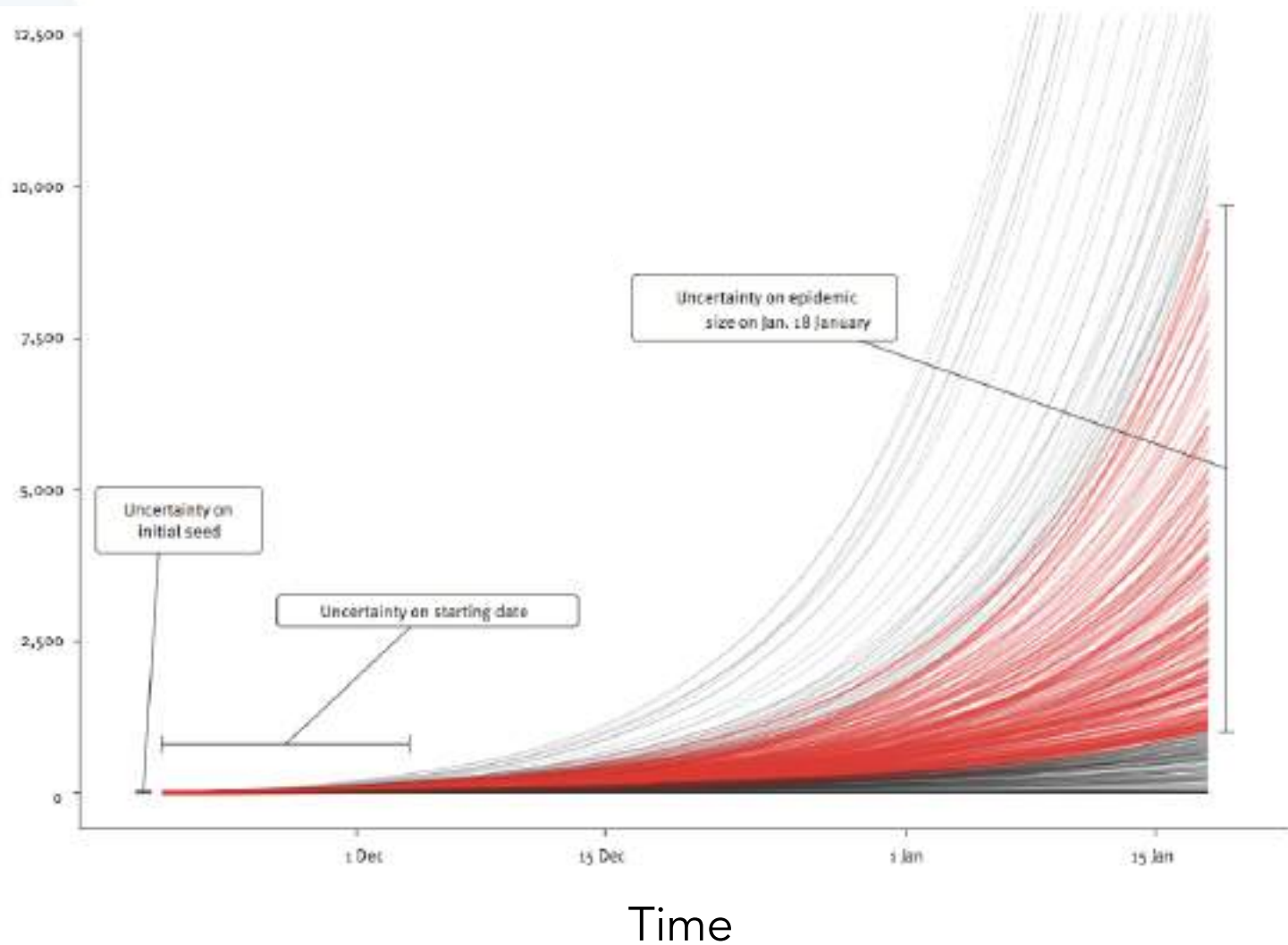
CASE 154

Case 154 is an imported case involving a 52-year-old British man.

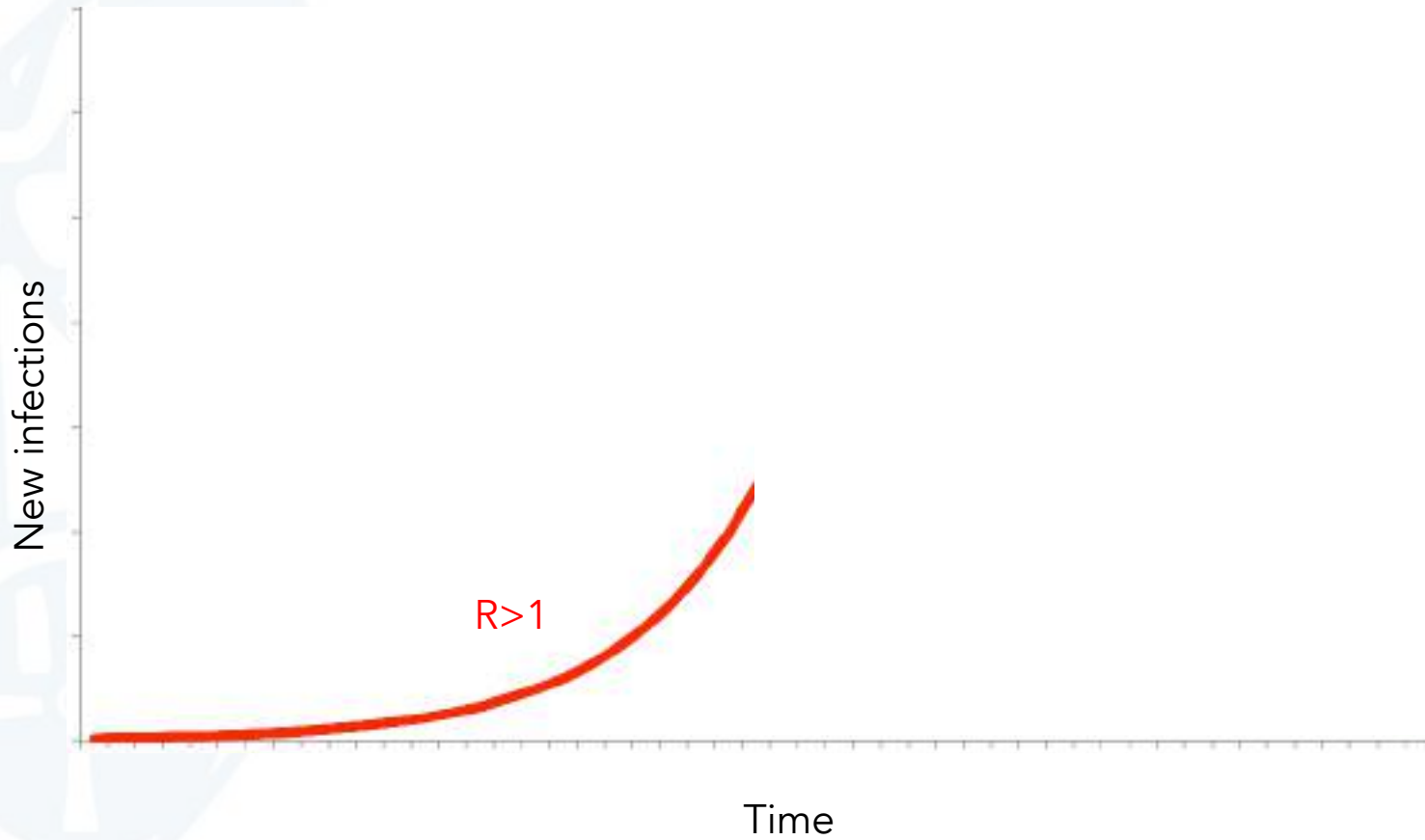
He arrived in Singapore on Mar 6 and was confirmed to have COVID-19 infection on Mar 9 morning and is currently warded in an isolation room at NCID.

Early estimates suggested $R = 2.2$ (90% CI: 1.4–3.8)

Total cases

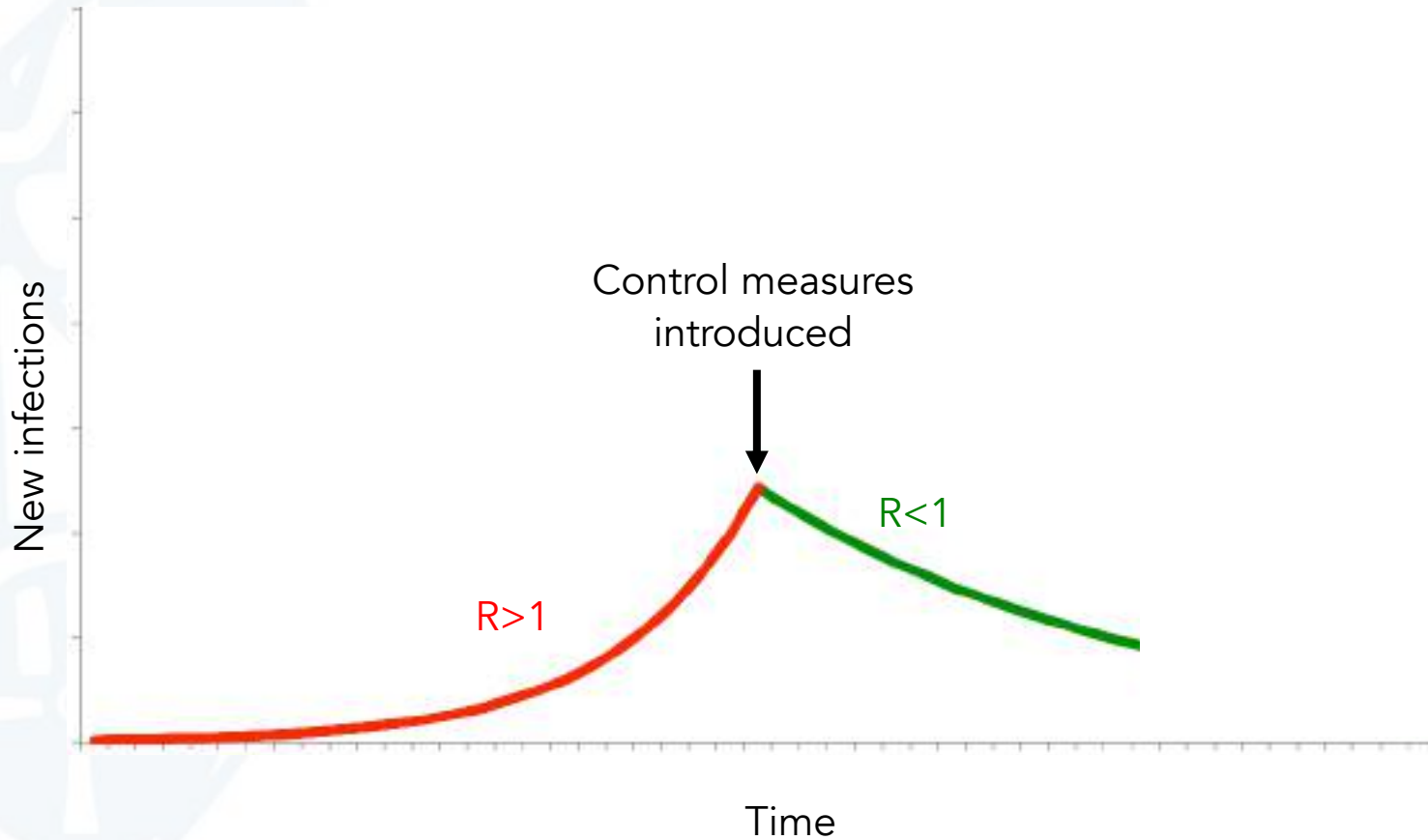


R can change over time



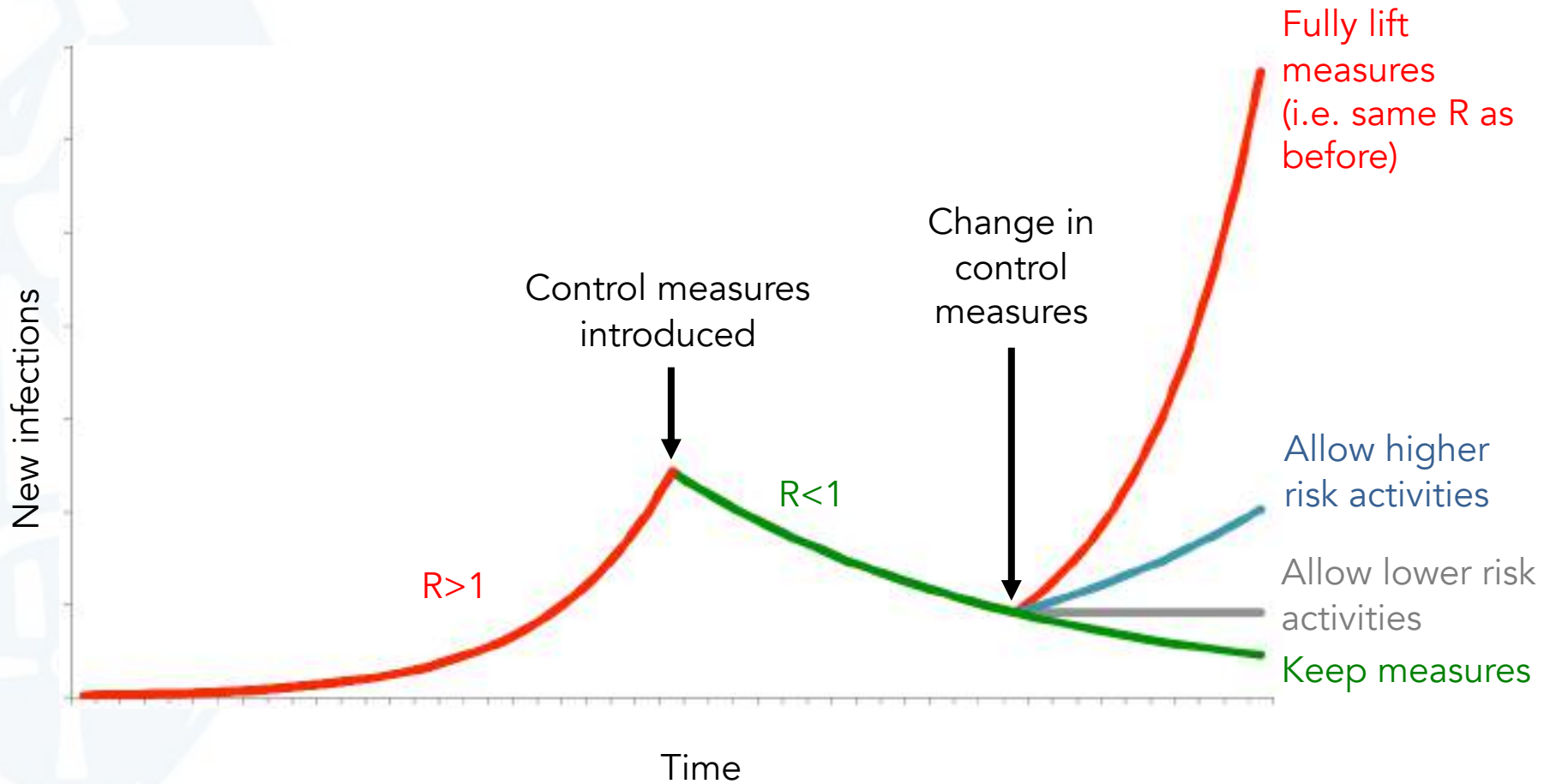
Note: illustrative figure only!

R can change over time



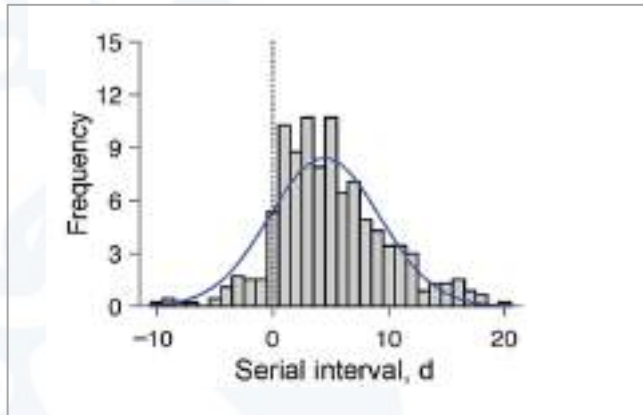
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R can change over time

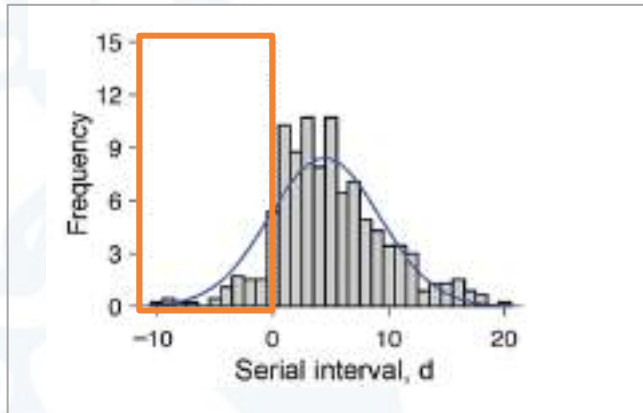


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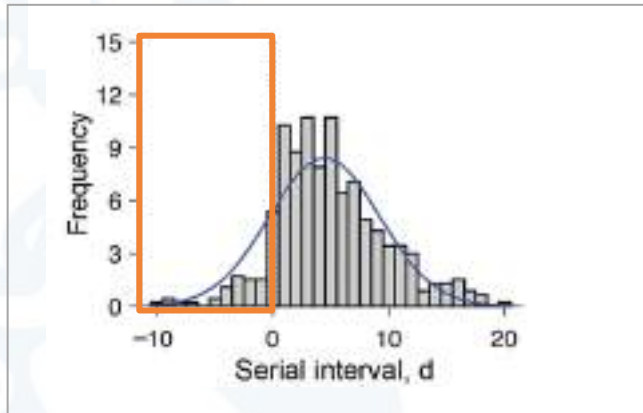
Serial interval vs generation time



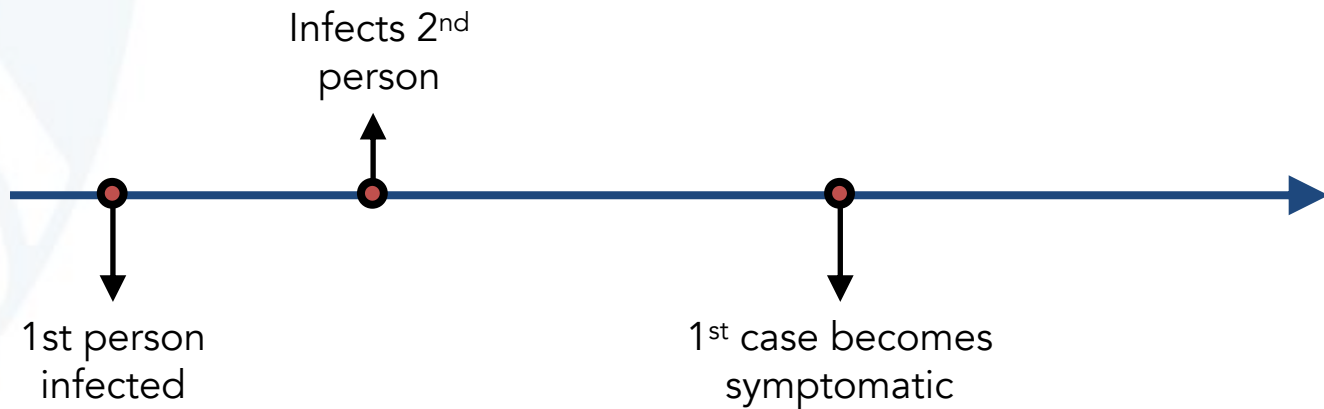
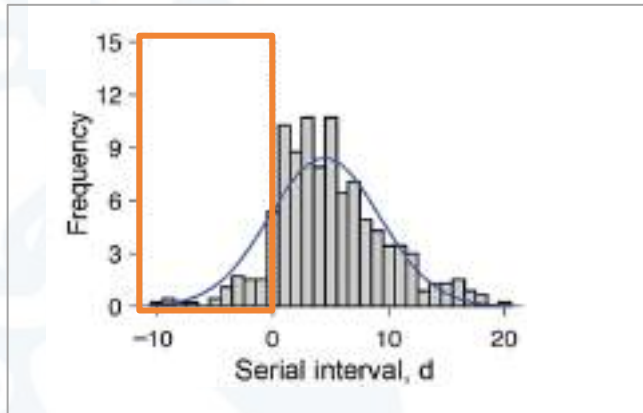
Serial interval vs generation time



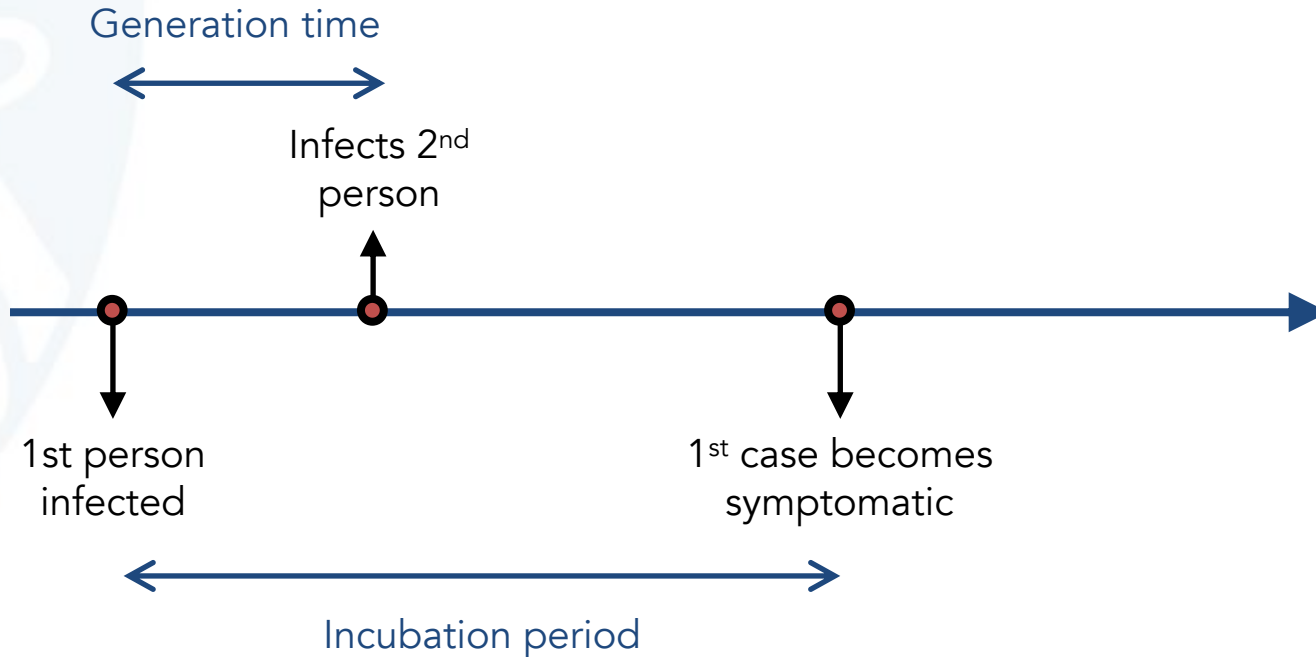
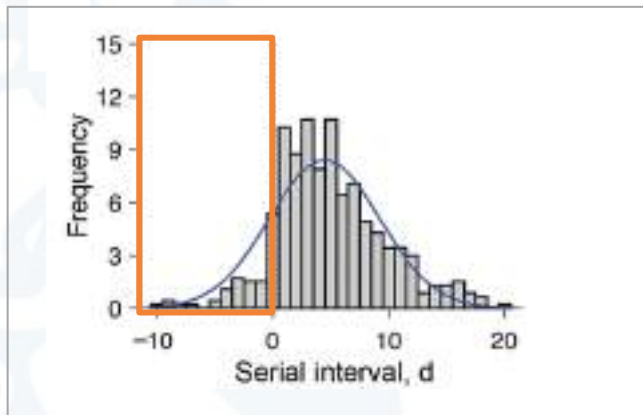
Serial interval vs generation time



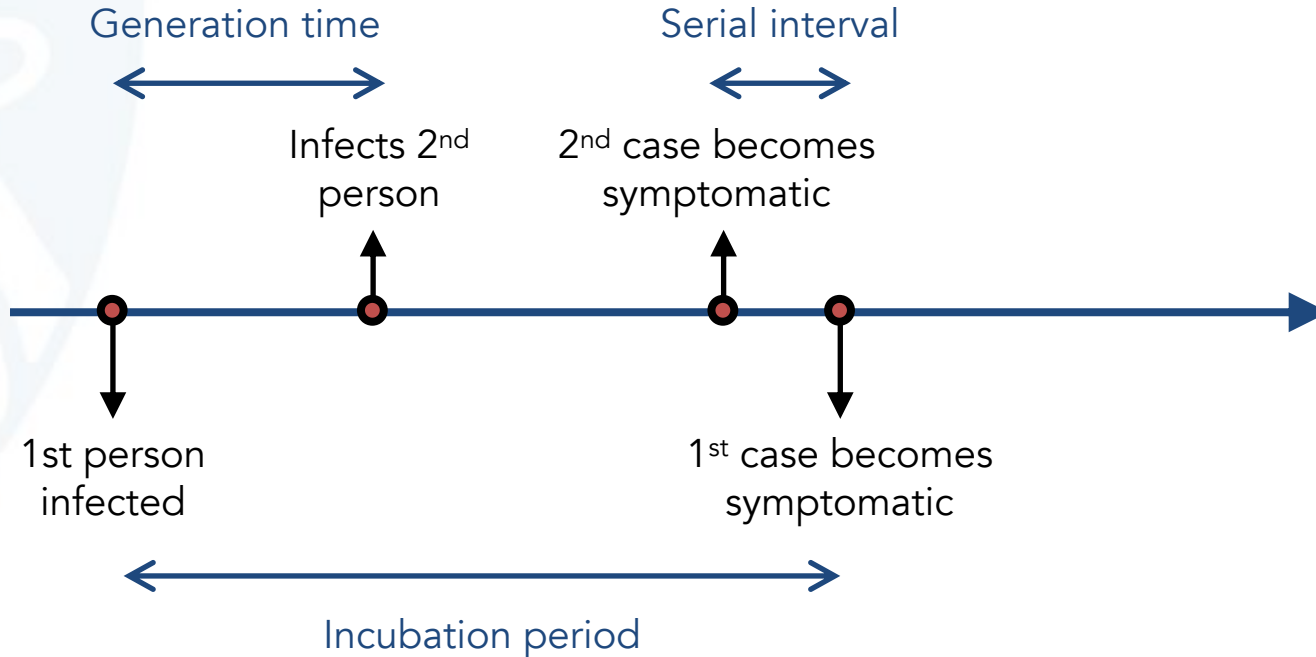
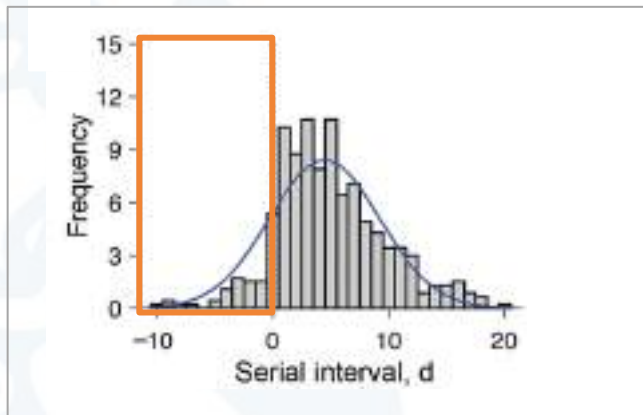
Serial interval vs generation time



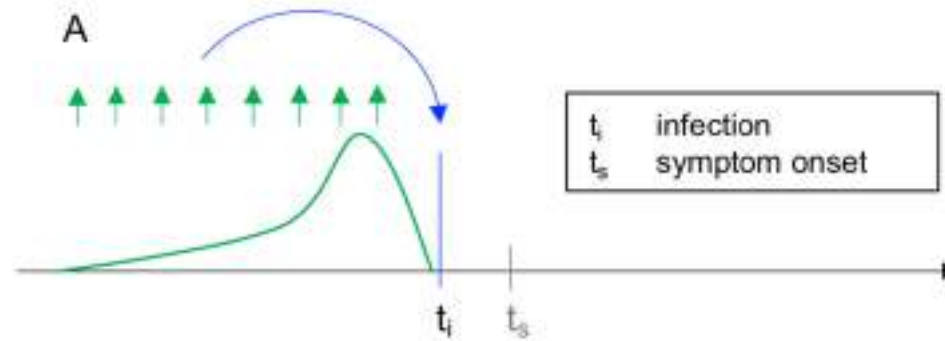
Serial interval vs generation time



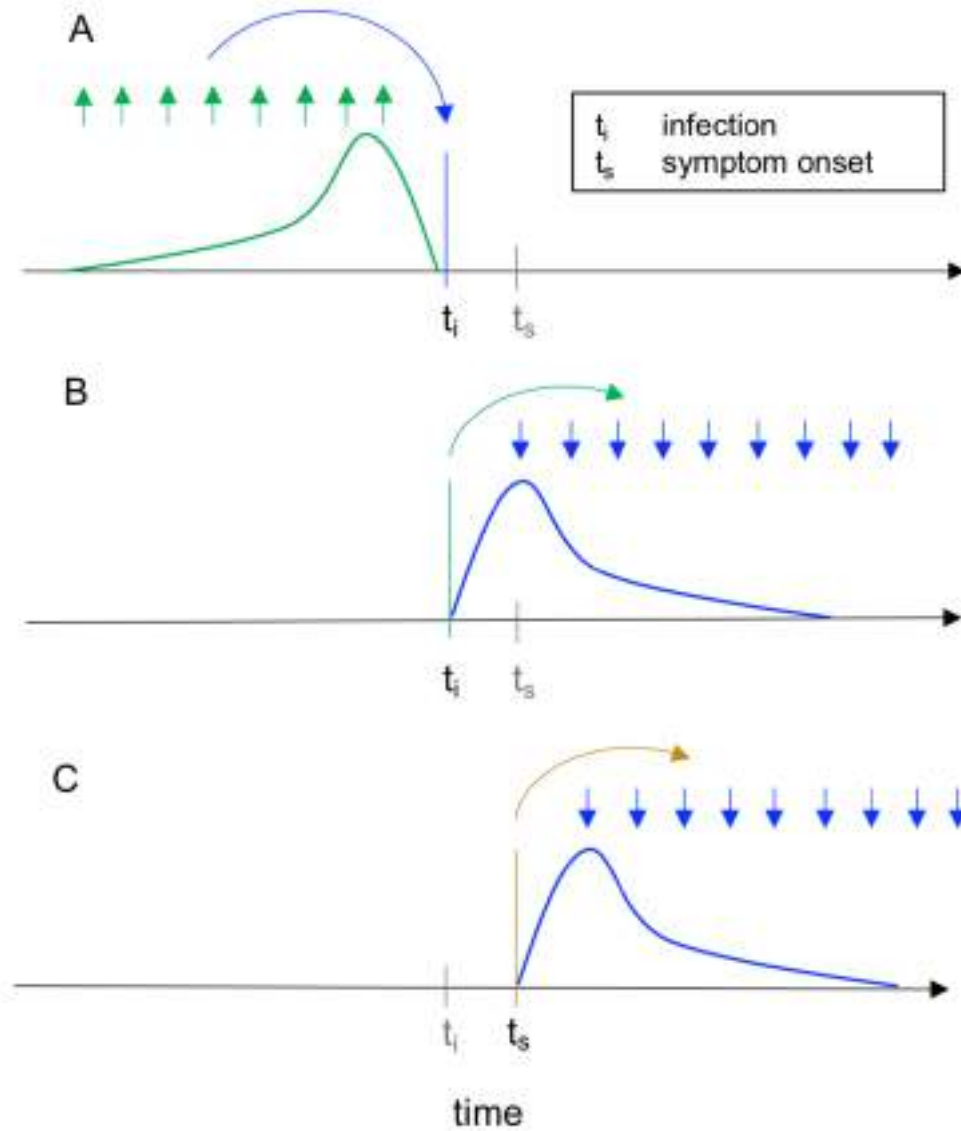
Serial interval vs generation time



Two methods for calculation

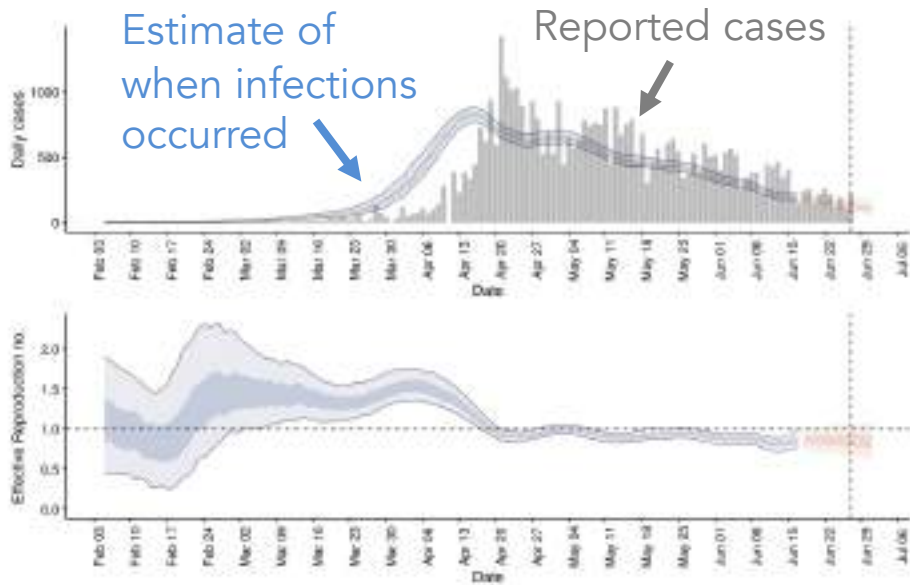


Two methods for calculation

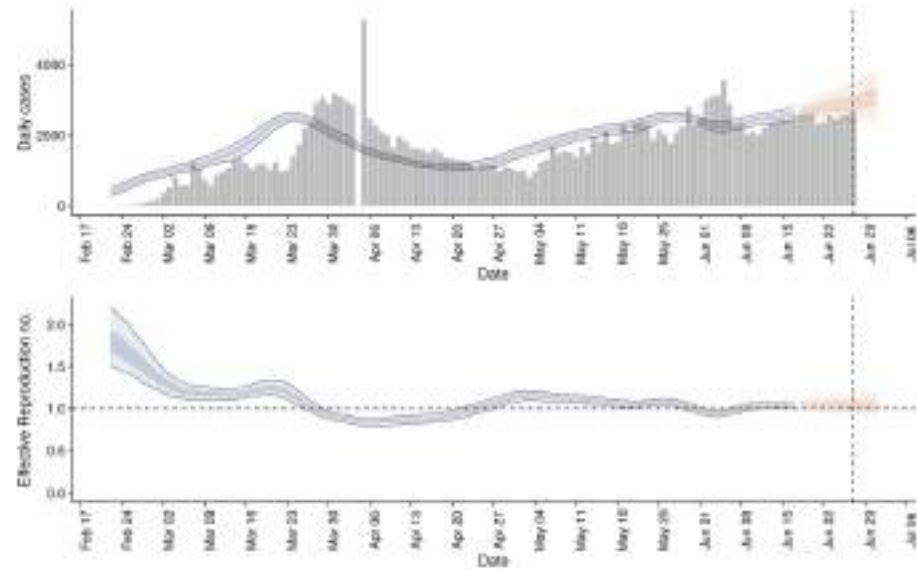


Estimating R over time

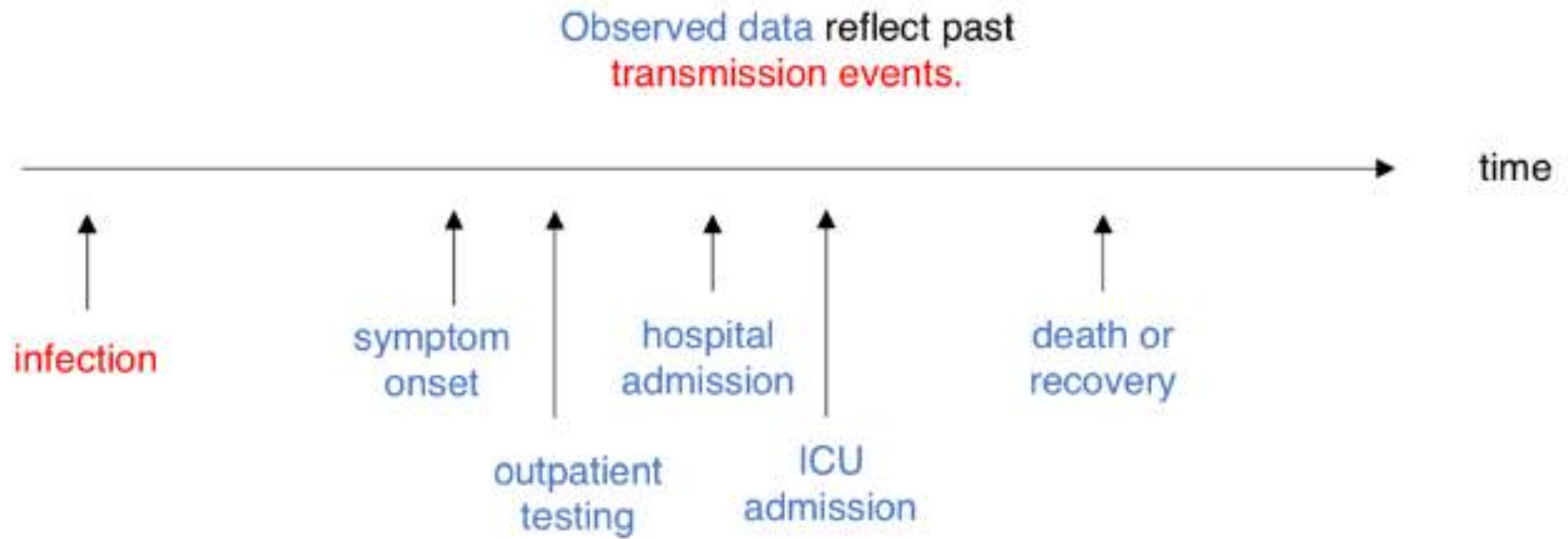
Singapore



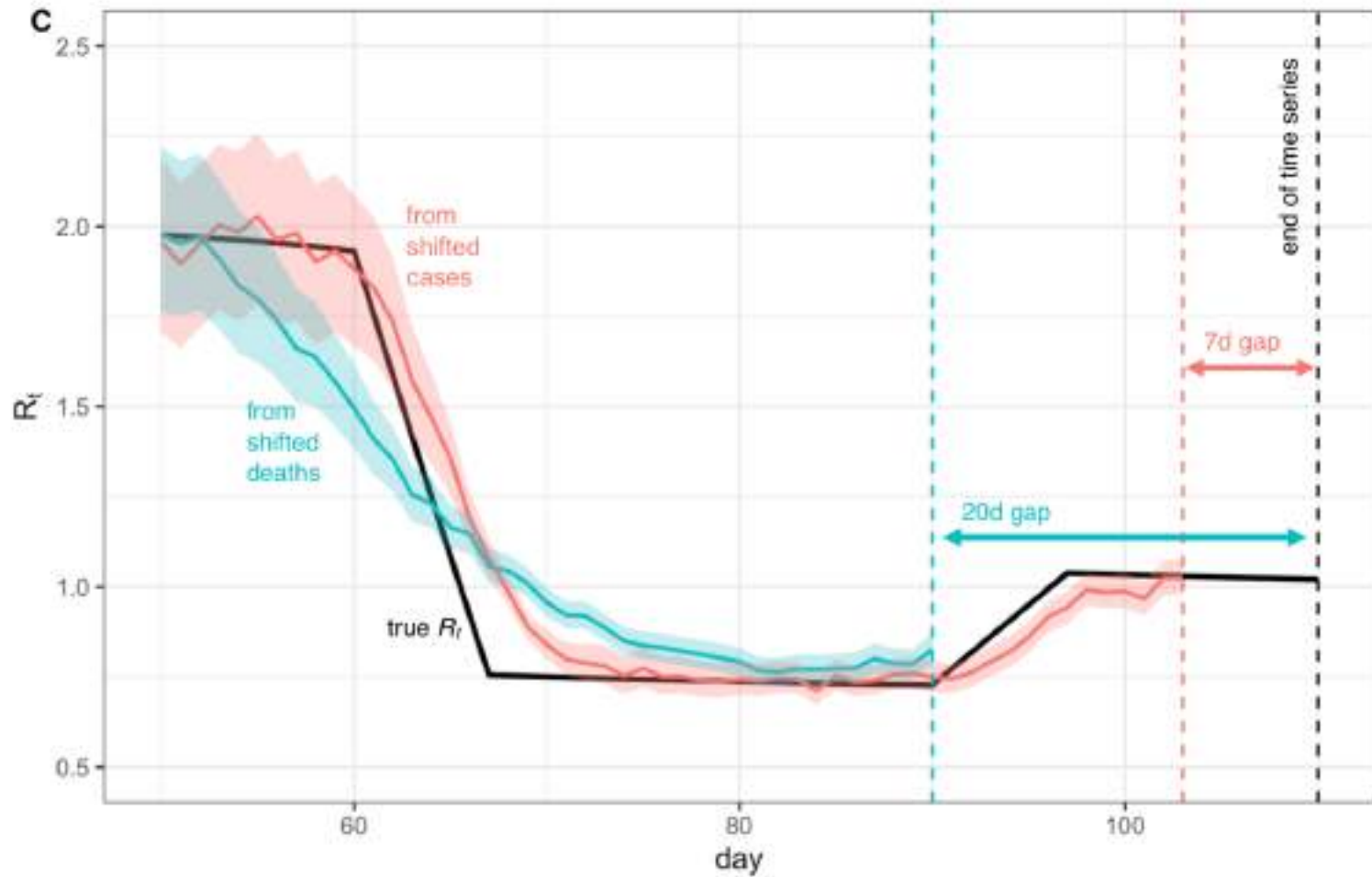
Iran



Data generally reflects the past

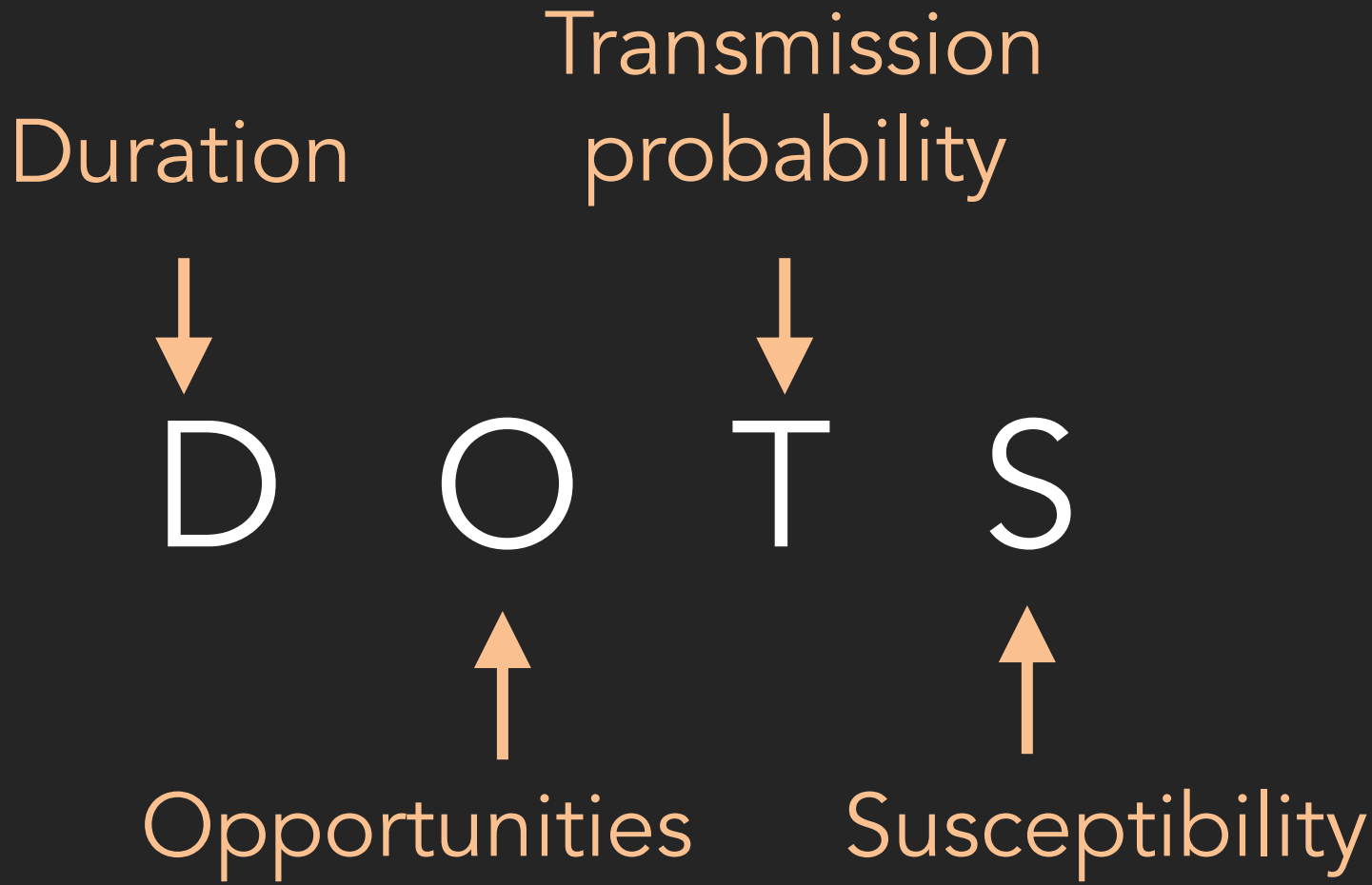


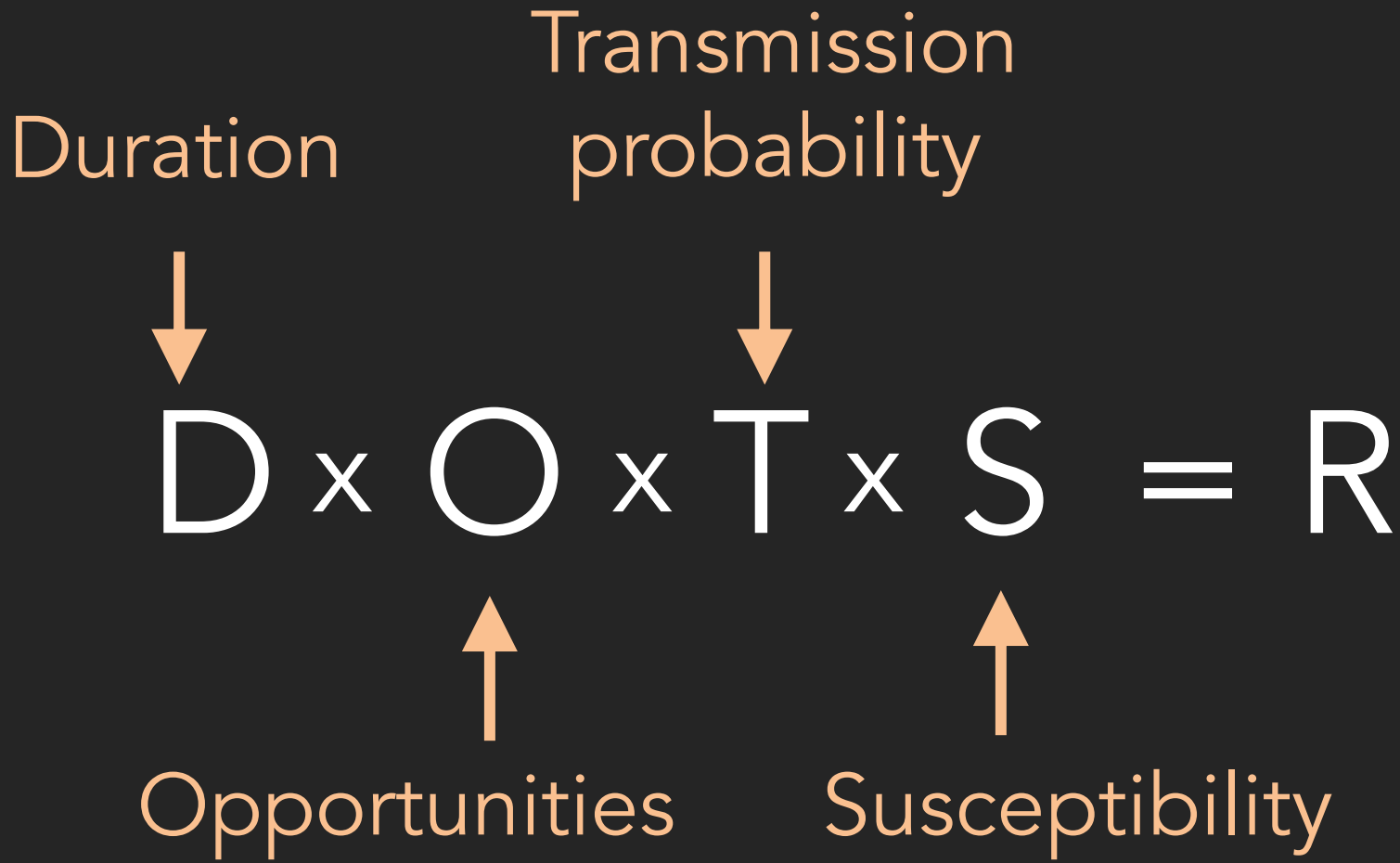
Adjusting to look back in time can 'smooth' estimates

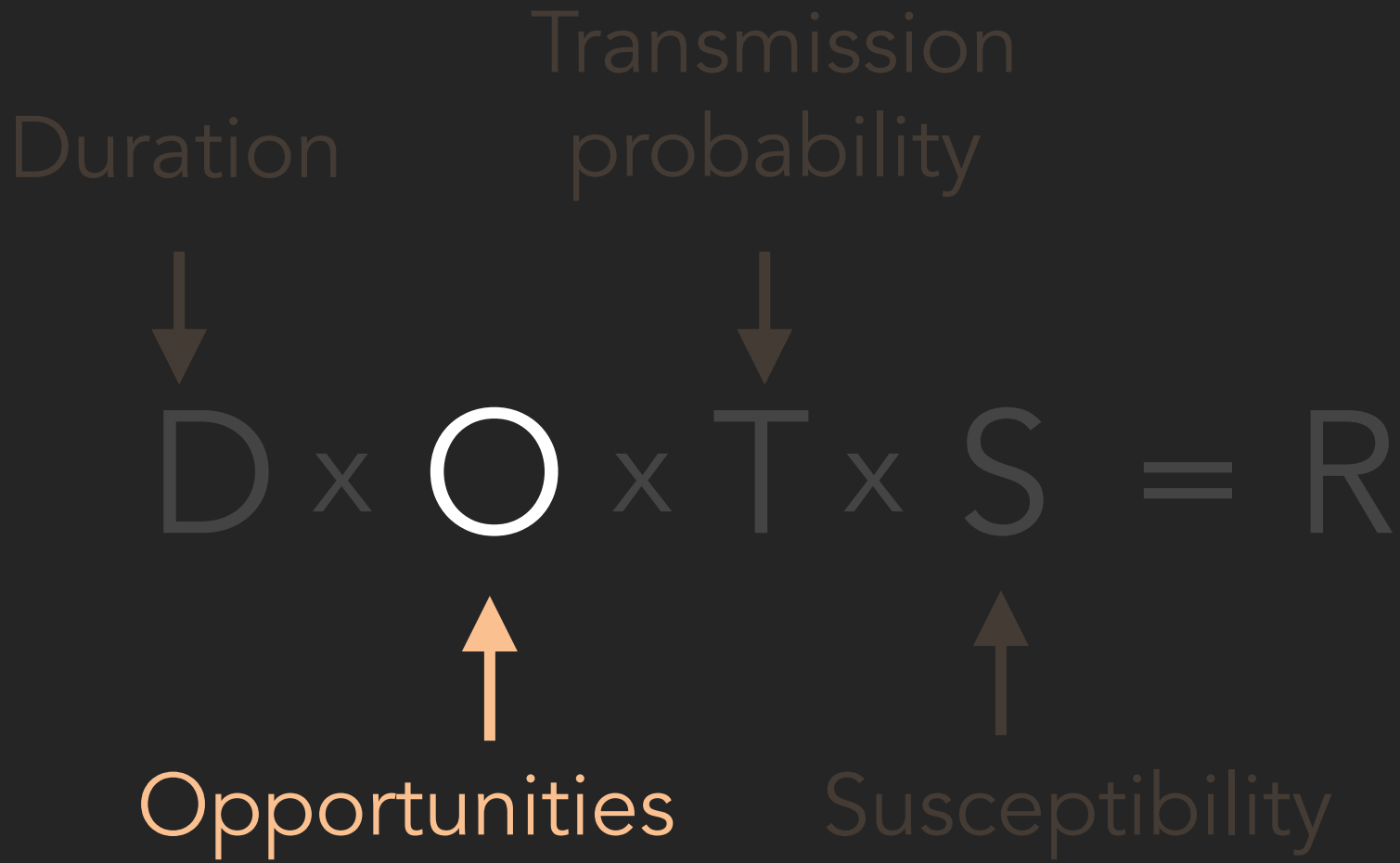


What influences R?

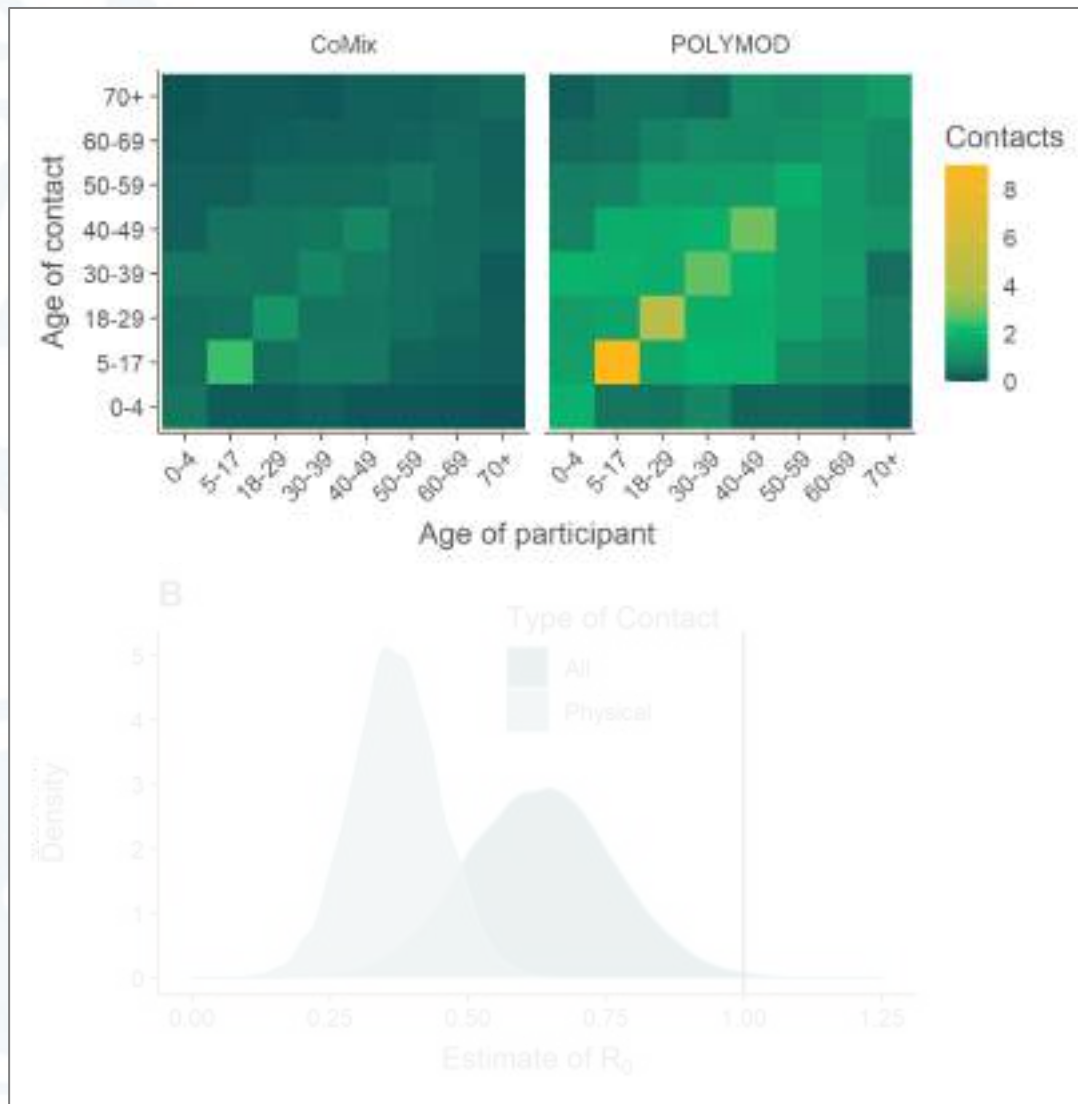
D O T S





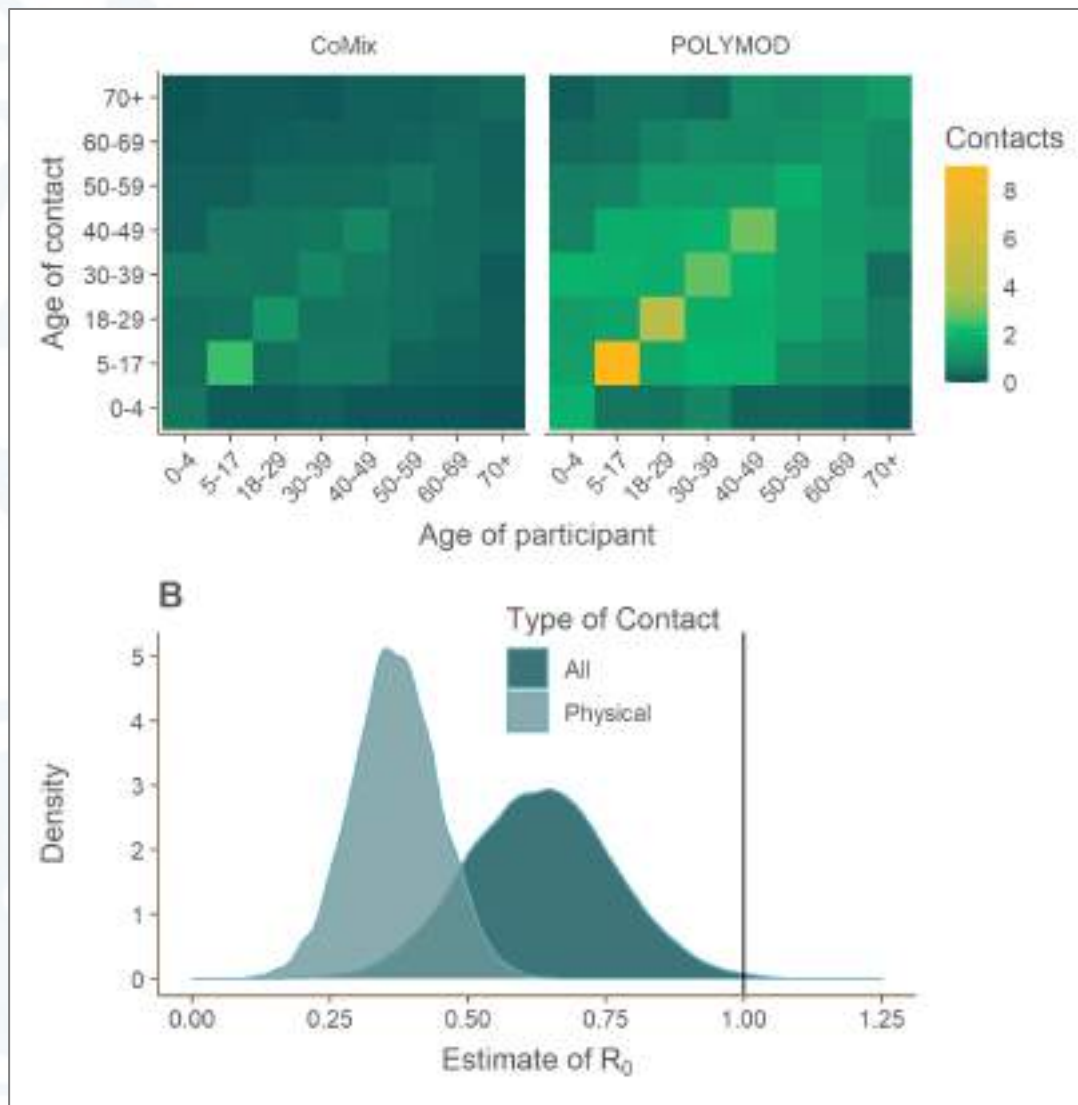


Can use real-time social mixing data to estimate R



Post-lockdown in UK:
“We found a 74%
reduction in the
average daily number
of contacts observed
per participant (from
10.8 to 2.8).”

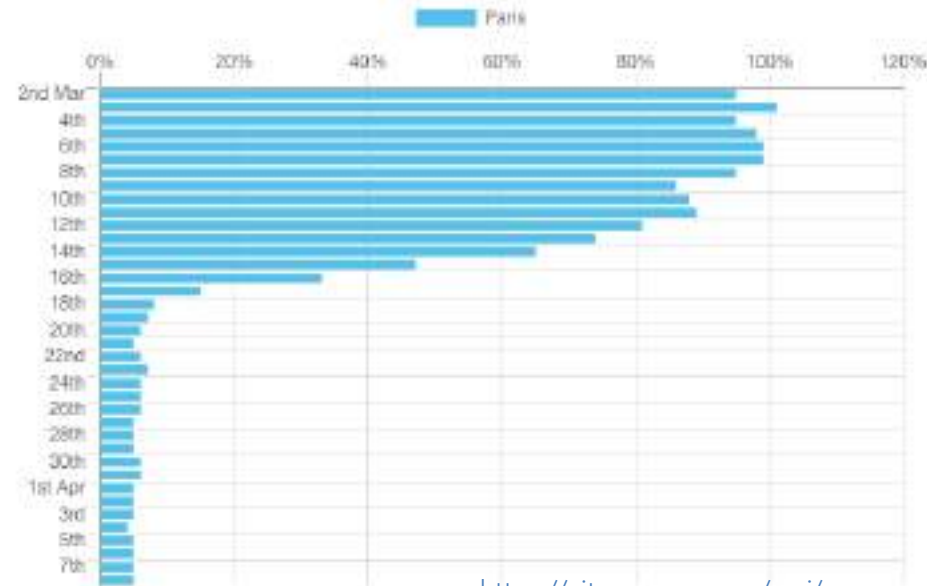
Can use real-time social mixing data to estimate R



Post-lockdown in UK:
“We found a 74% reduction in the average daily number of contacts observed per participant (from 10.8 to 2.8).”

Other digital data sources

Citymapper Mobility Index



<https://citymapper.com/cmi/compare>

Google Community Mobility Reports

Retail & recreation

-91% compared to baseline

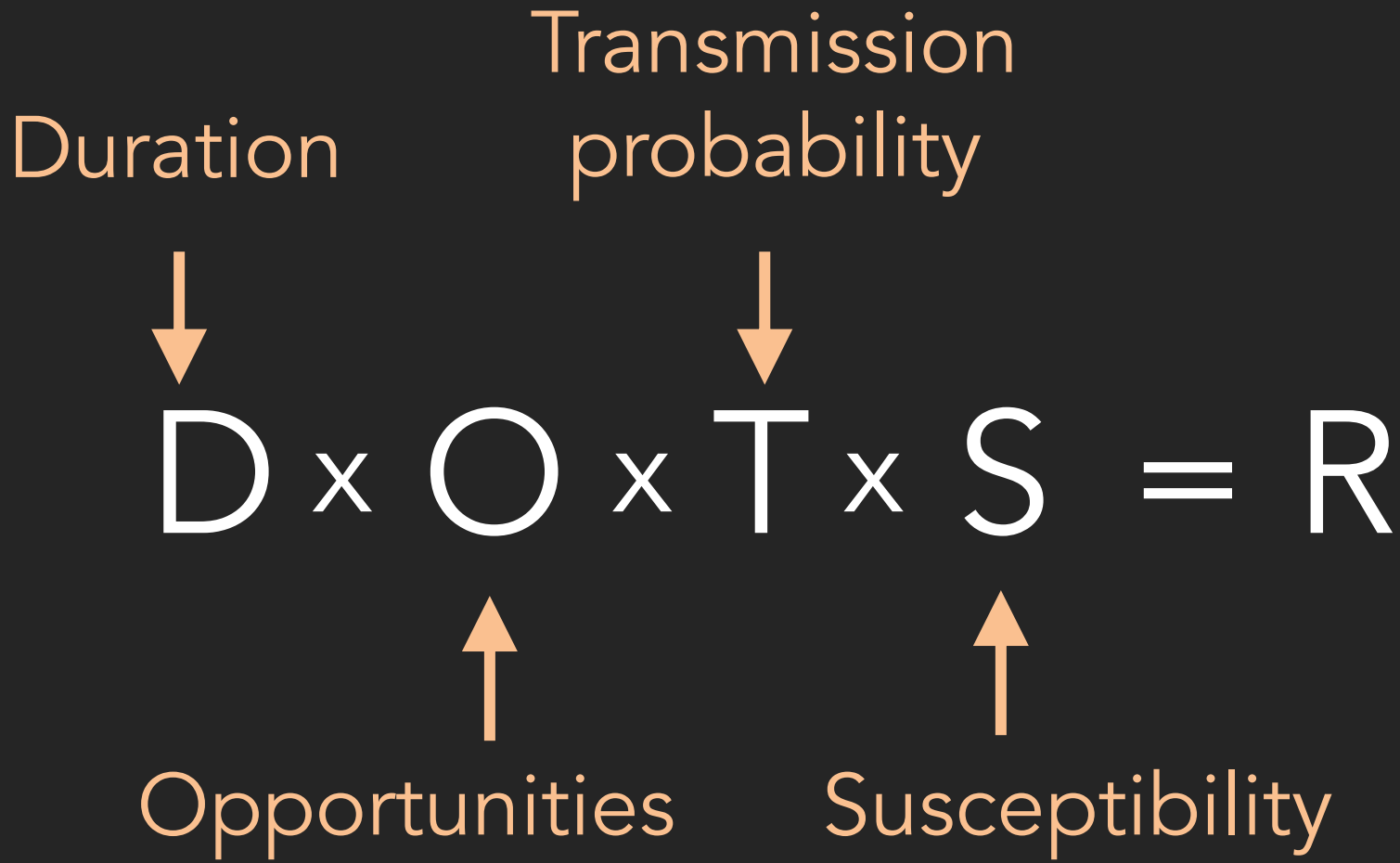


Grocery & pharmacy

-69% compared to baseline



<https://www.google.com/covid19/mobility/>



Example: controlling HIV

Treatment

Safe sex



D

x

O

x

T

x

S

=

R



Fewer
partners



PrEP

Example: controlling COVID-19

Isolation

Masks/PPE



$$D \times O \times T \times S = R$$



Social
distancing

Vaccine?

Basic reproduction number

$$\boxed{D \times O \times T} \times S = R$$

$= R_0$...hence $R_0 \times S = R$

If $R_0 \times R = S$

...then $R < 1$ when $S < 1/R_0$

If $R_0 \times R = S$

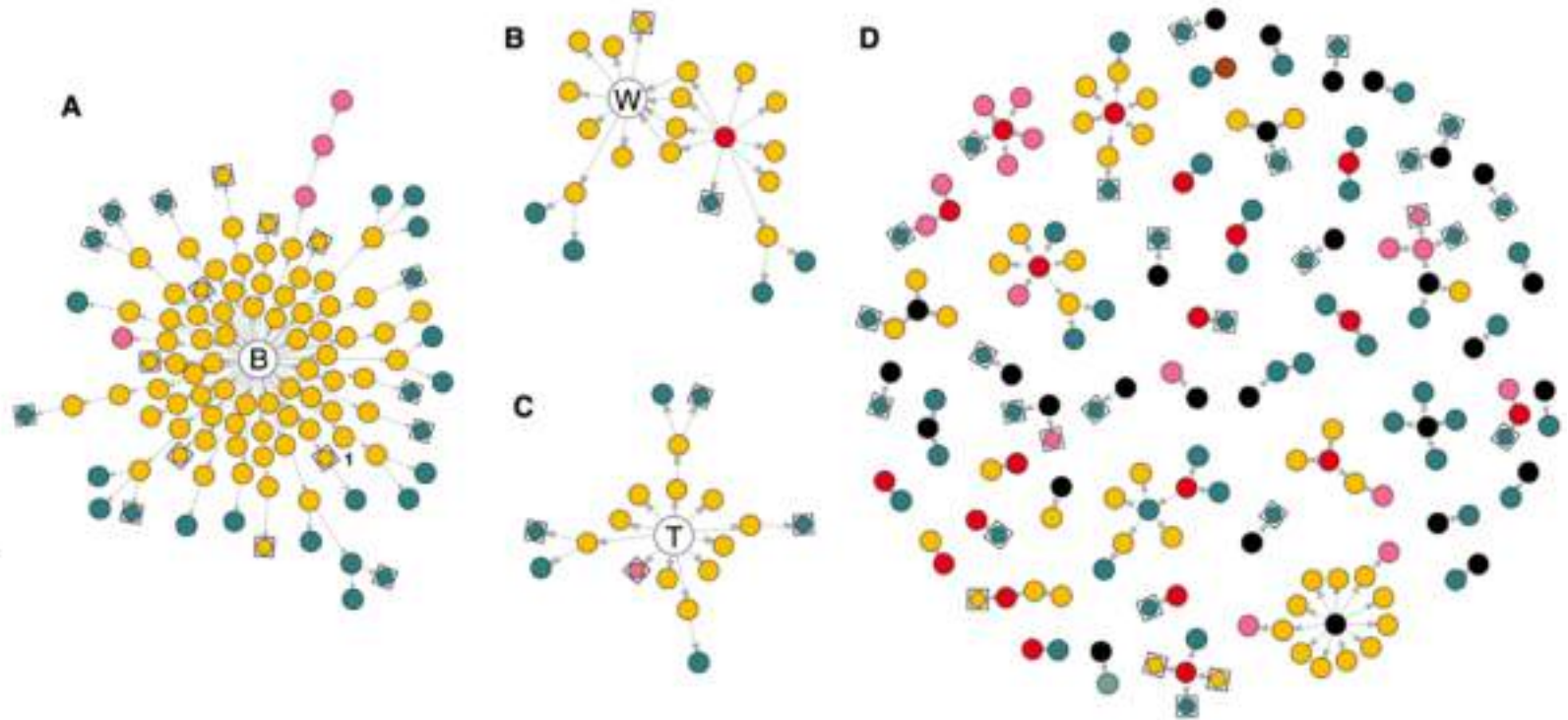
...then $R < 1$ when $S < 1/R_0$

...so wouldn't expect epidemics if proportion immune is above "herd immunity threshold" of $1 - 1/R_0$

i.e. if $R_0 = 2$, threshold would be 50%

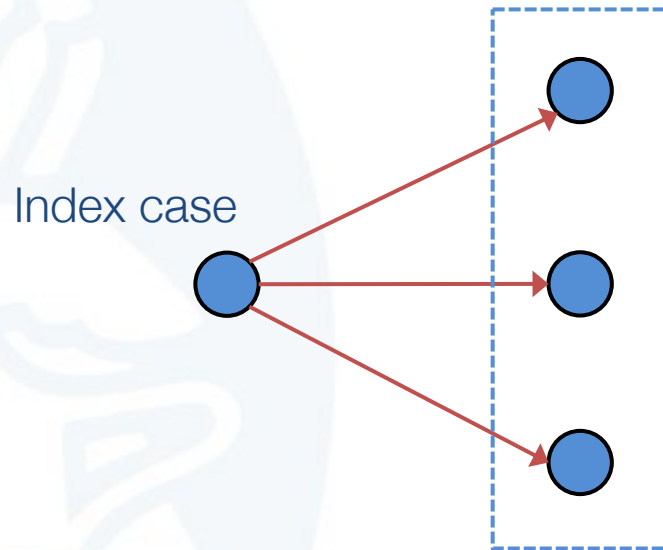
Individual-level variation in transmission

COVID-19 transmission chains in Hong Kong



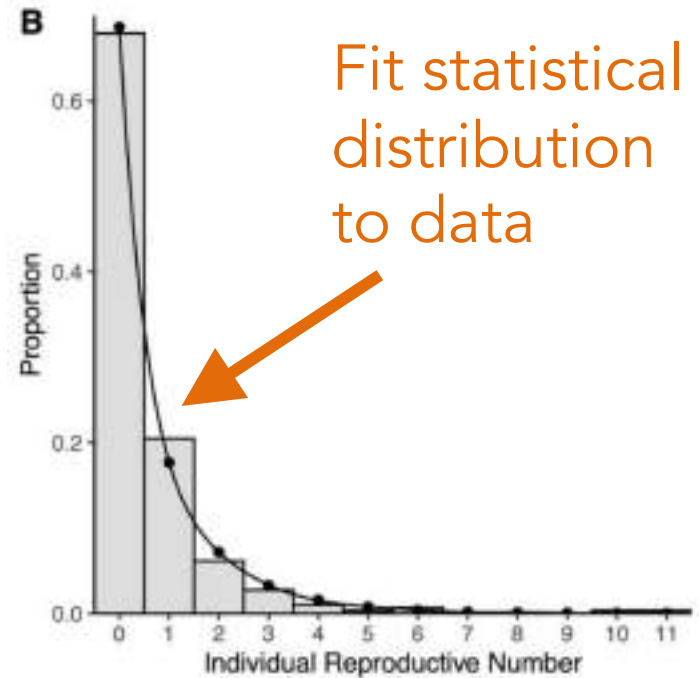
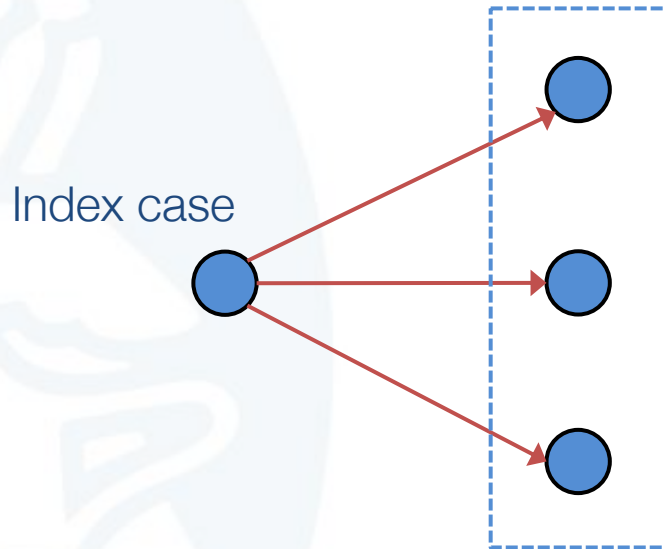
Estimating variation in transmission (method 1)

Secondary cases



Estimating variation in transmission (method 1)

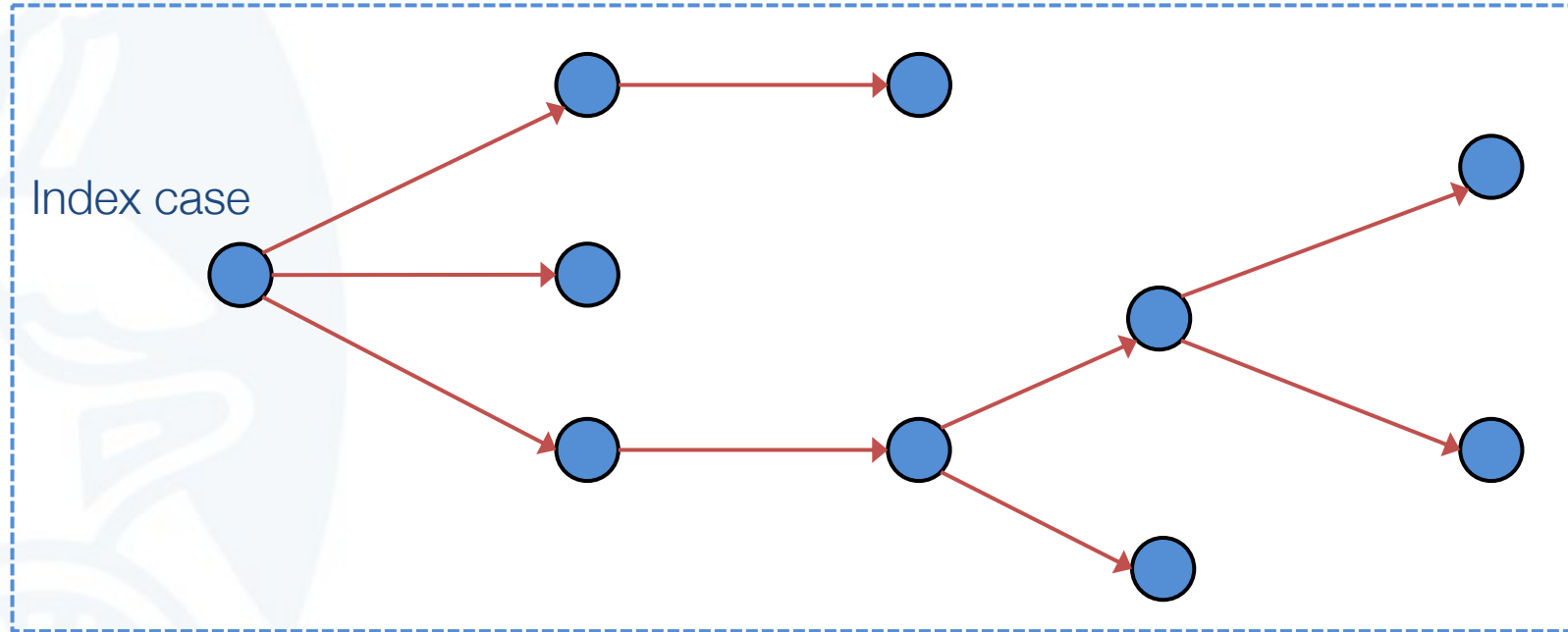
Secondary cases



80% of transmission generated by around 20% of infections

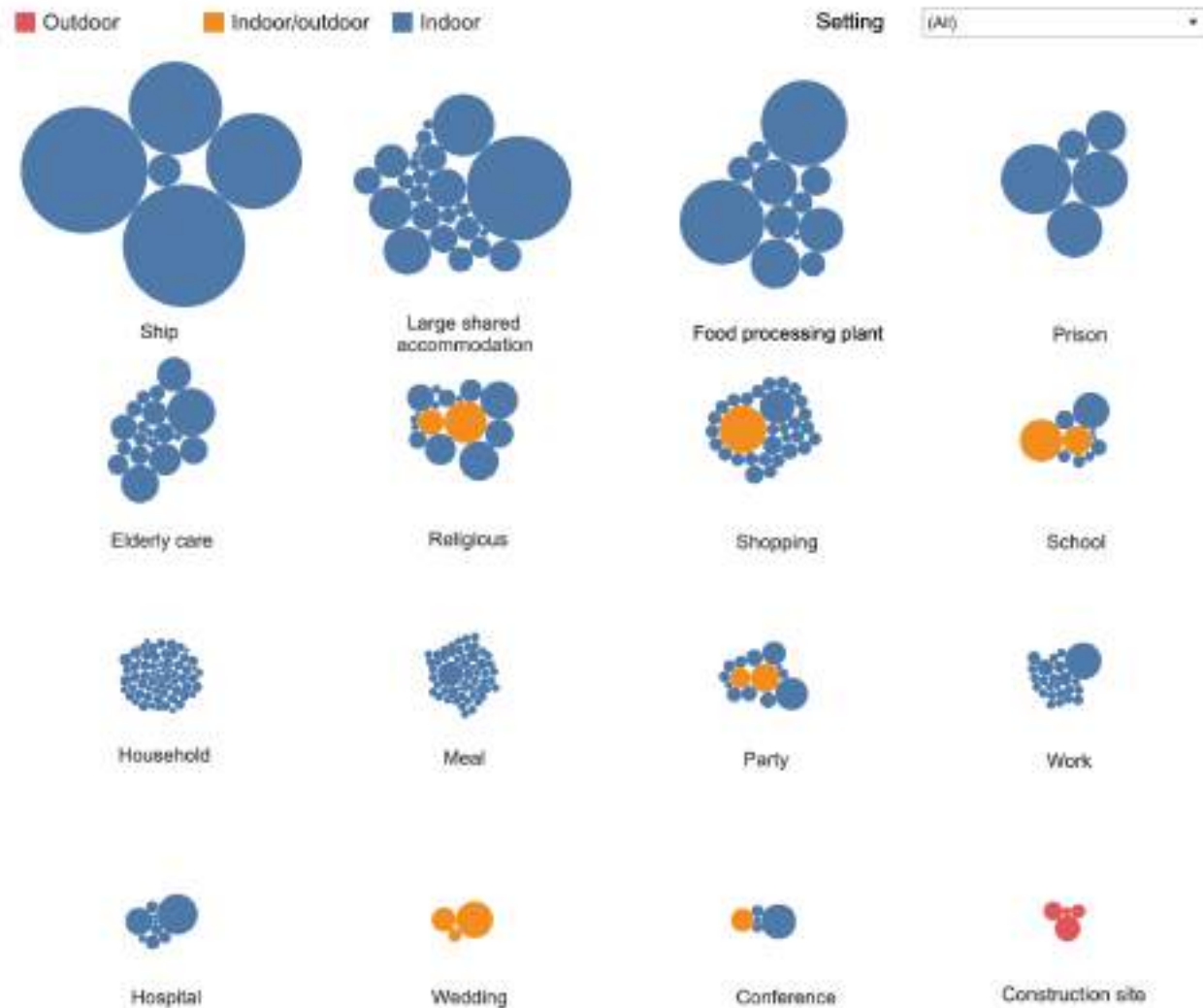
Estimating variation in transmission (method 2)

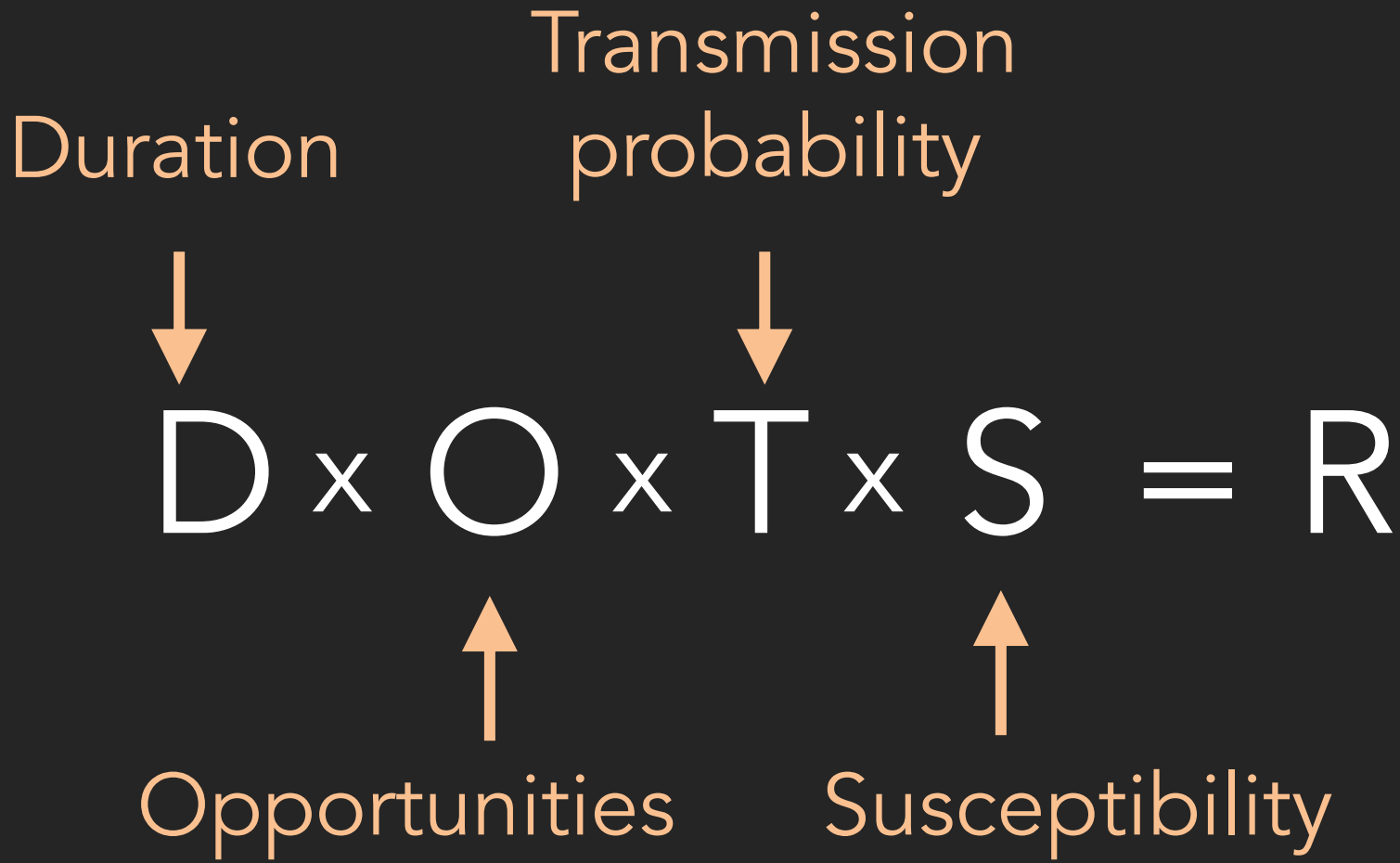
Outbreak size



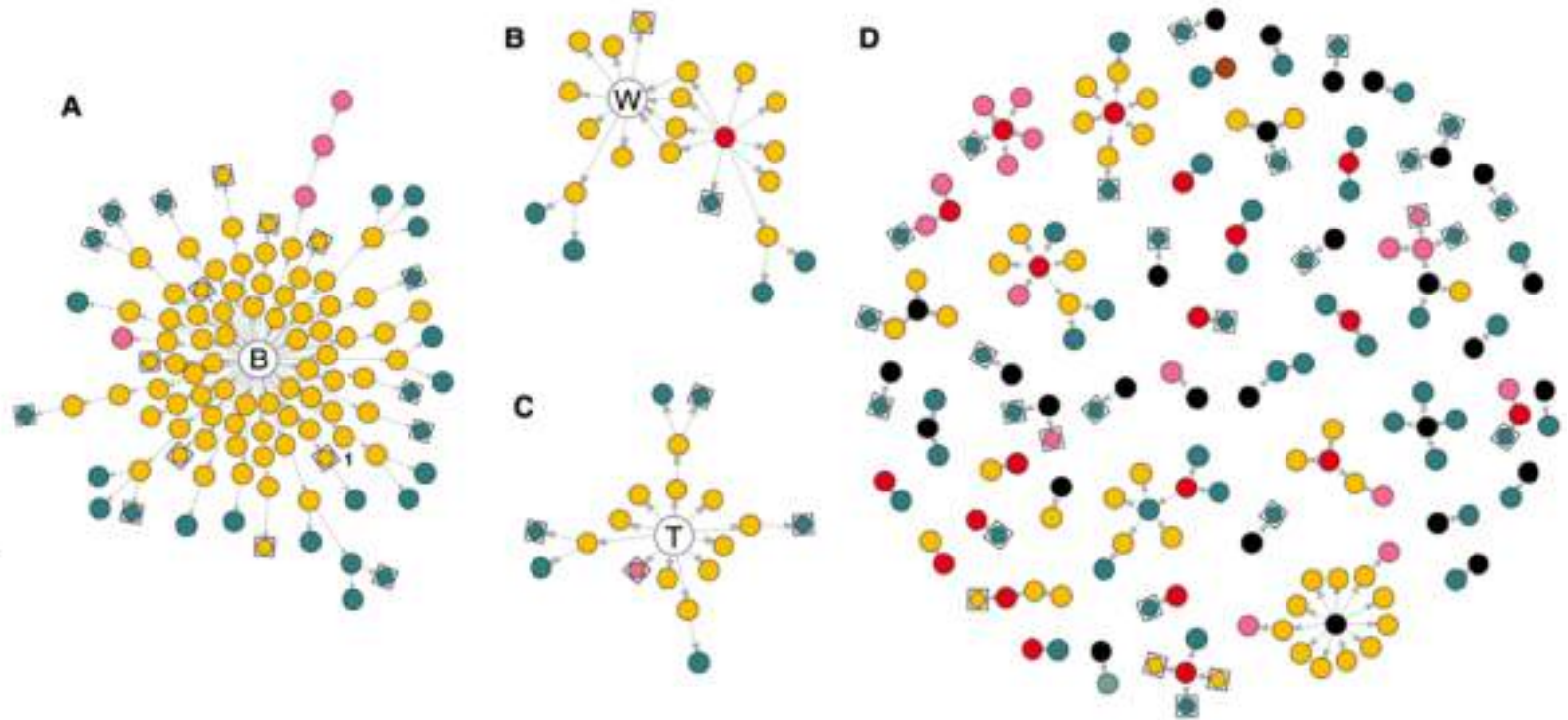
80% of transmission generated by around 10 – 20% of infections

Where are transmission clusters reported?

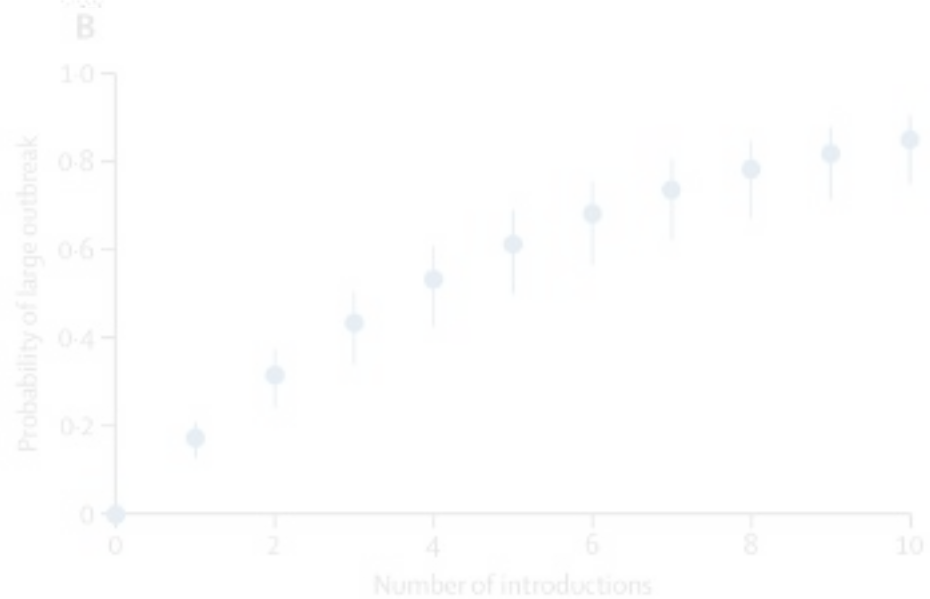
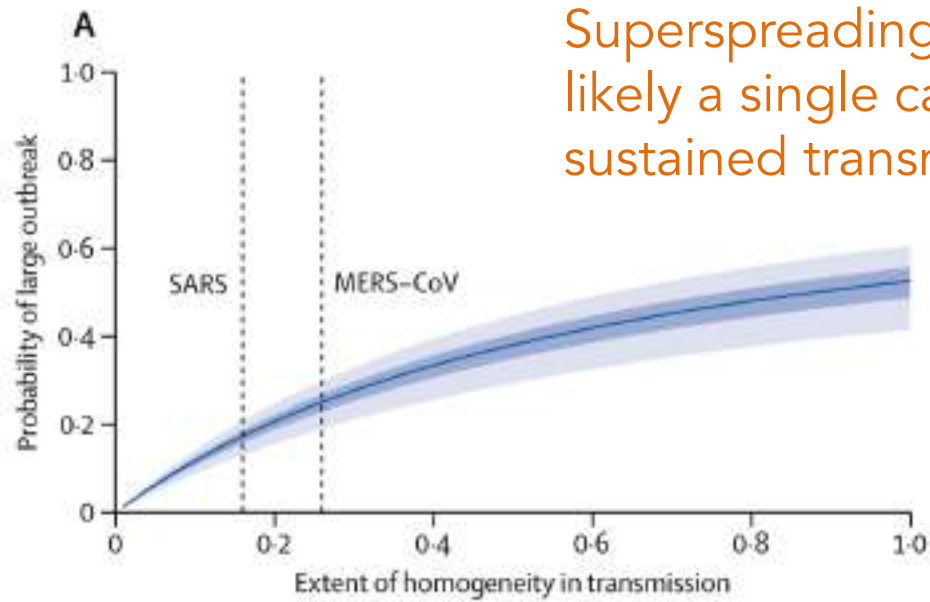




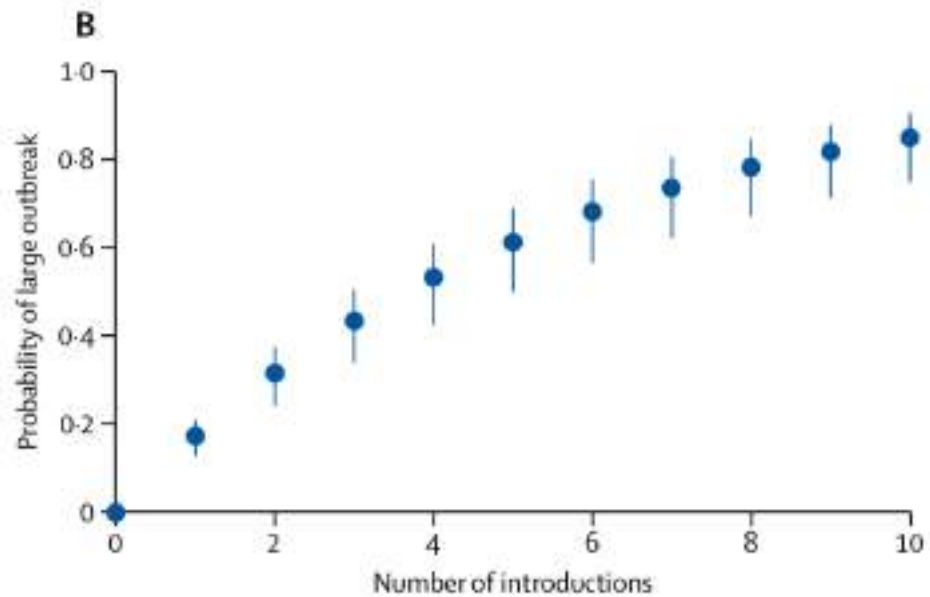
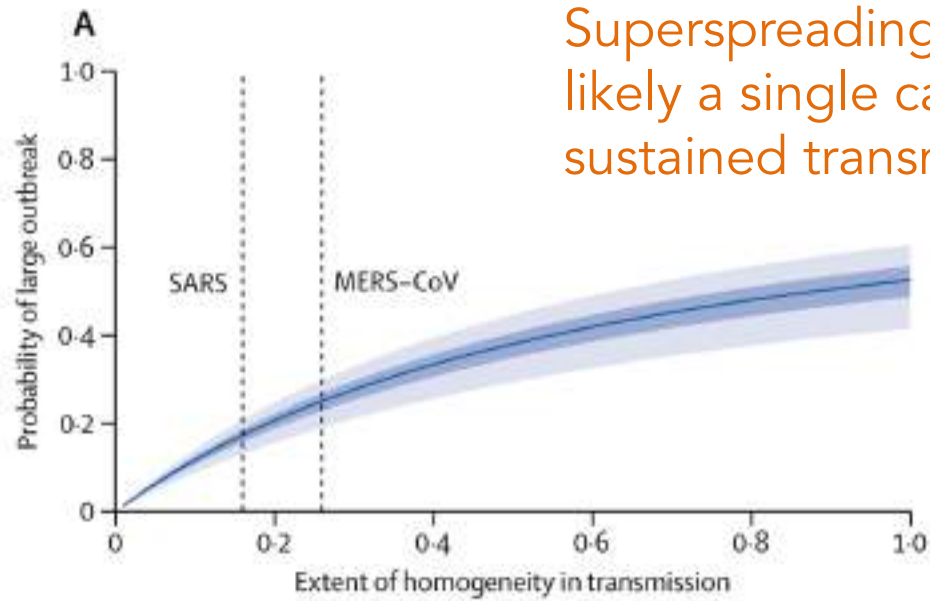
COVID-19 transmission chains in Hong Kong

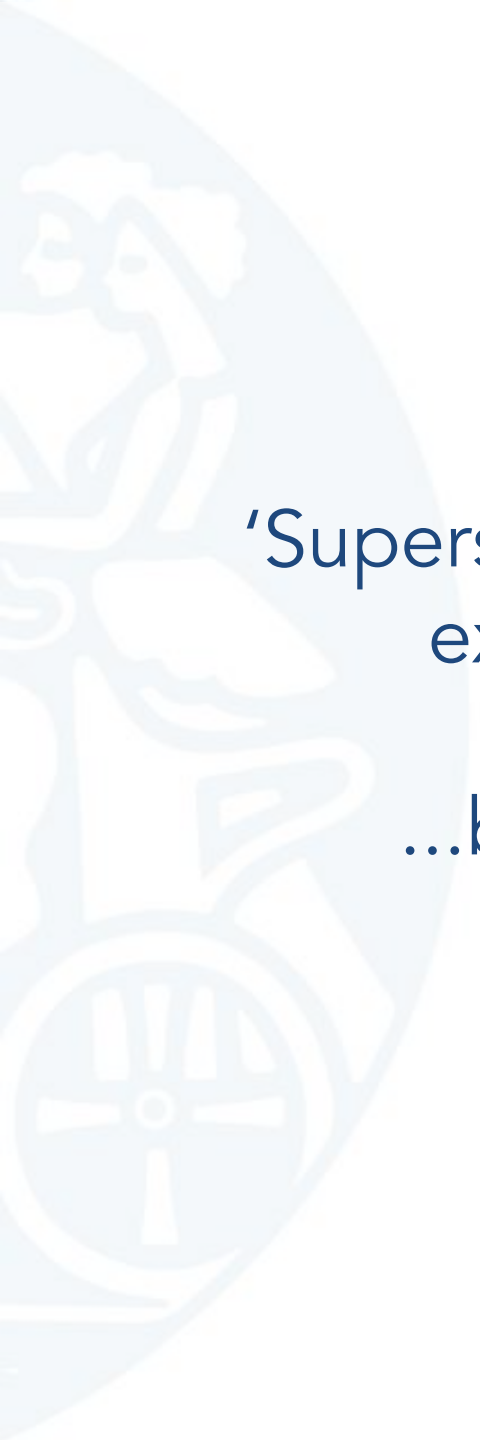


Superspreading makes it less likely a single case will lead to sustained transmission



Superspreading makes it less likely a single case will lead to sustained transmission



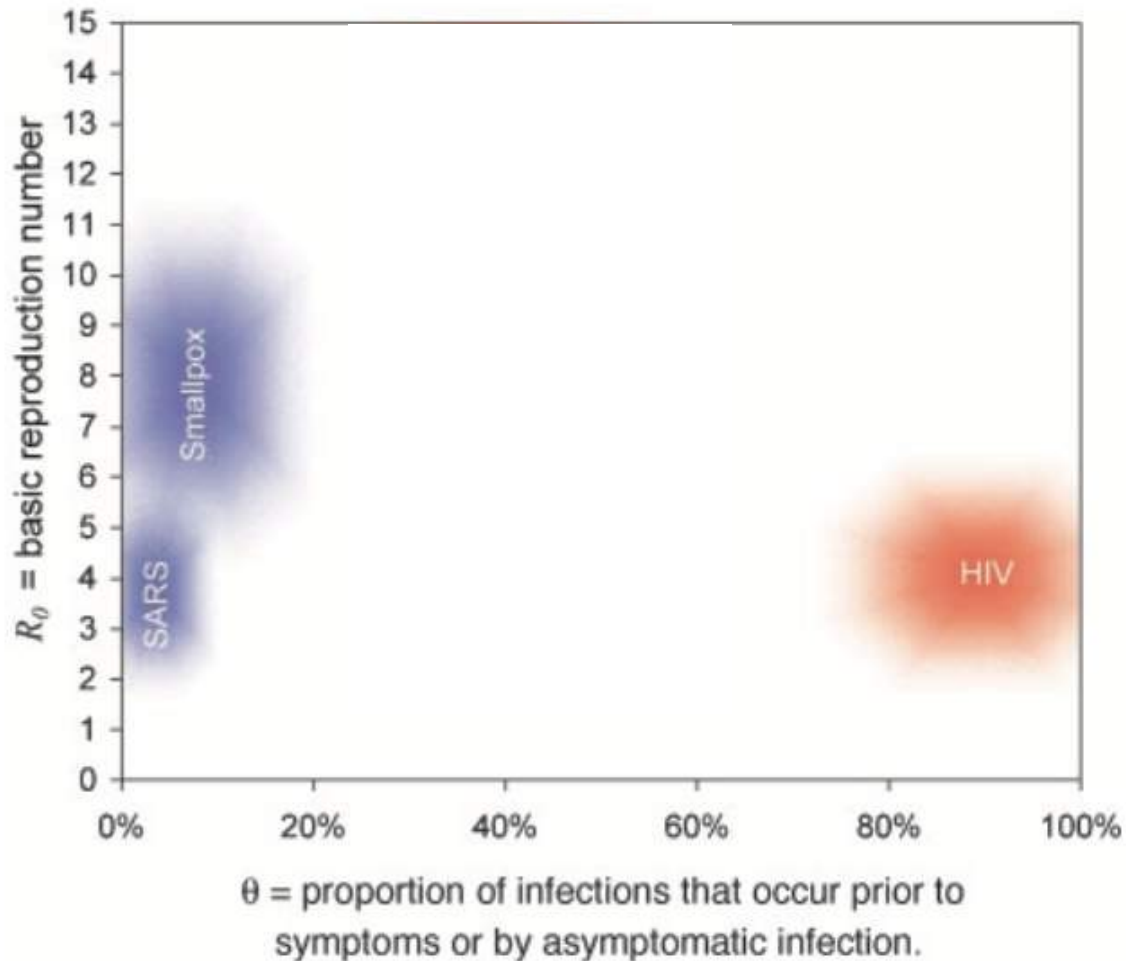


'Superspreading' makes outbreaks more explosive once they take off...

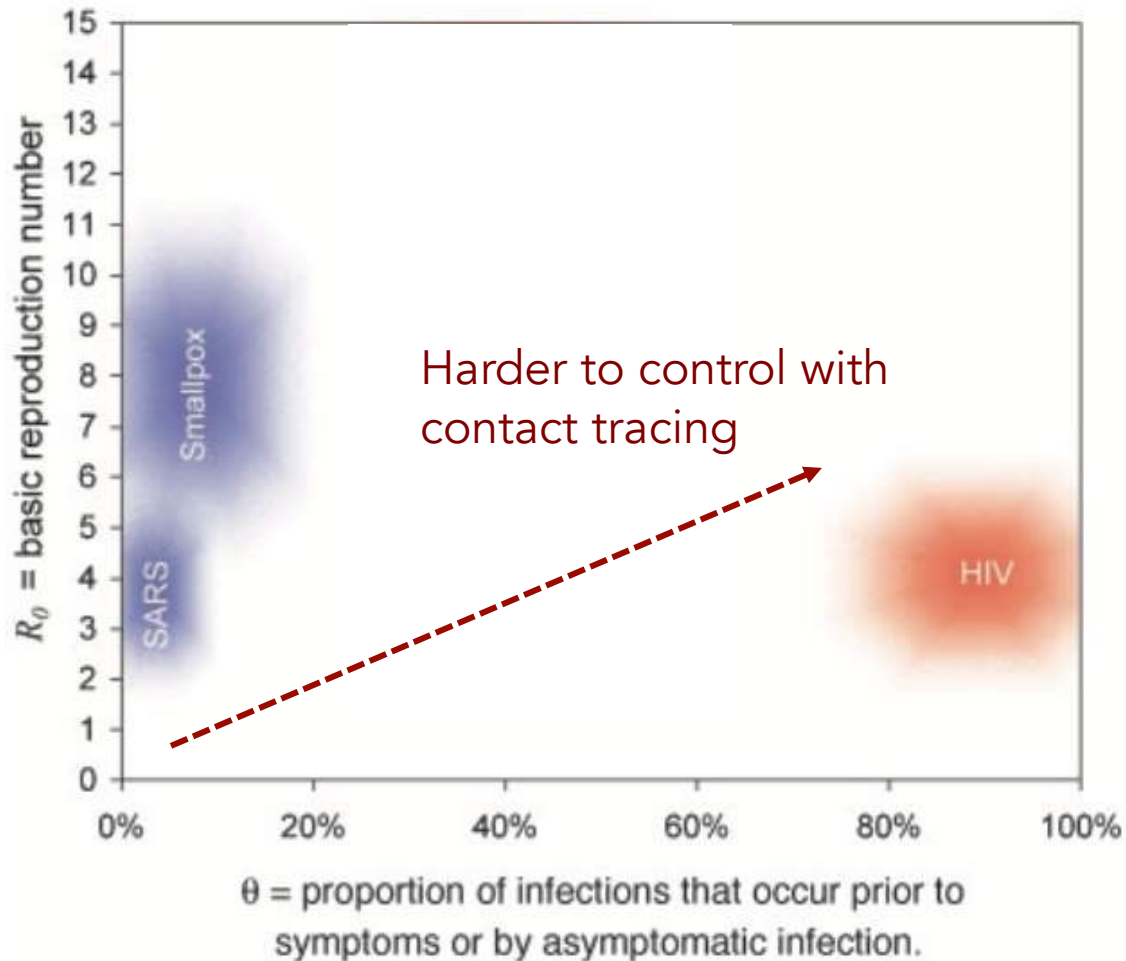
...but less likely to spark initially

Isolation & contact tracing

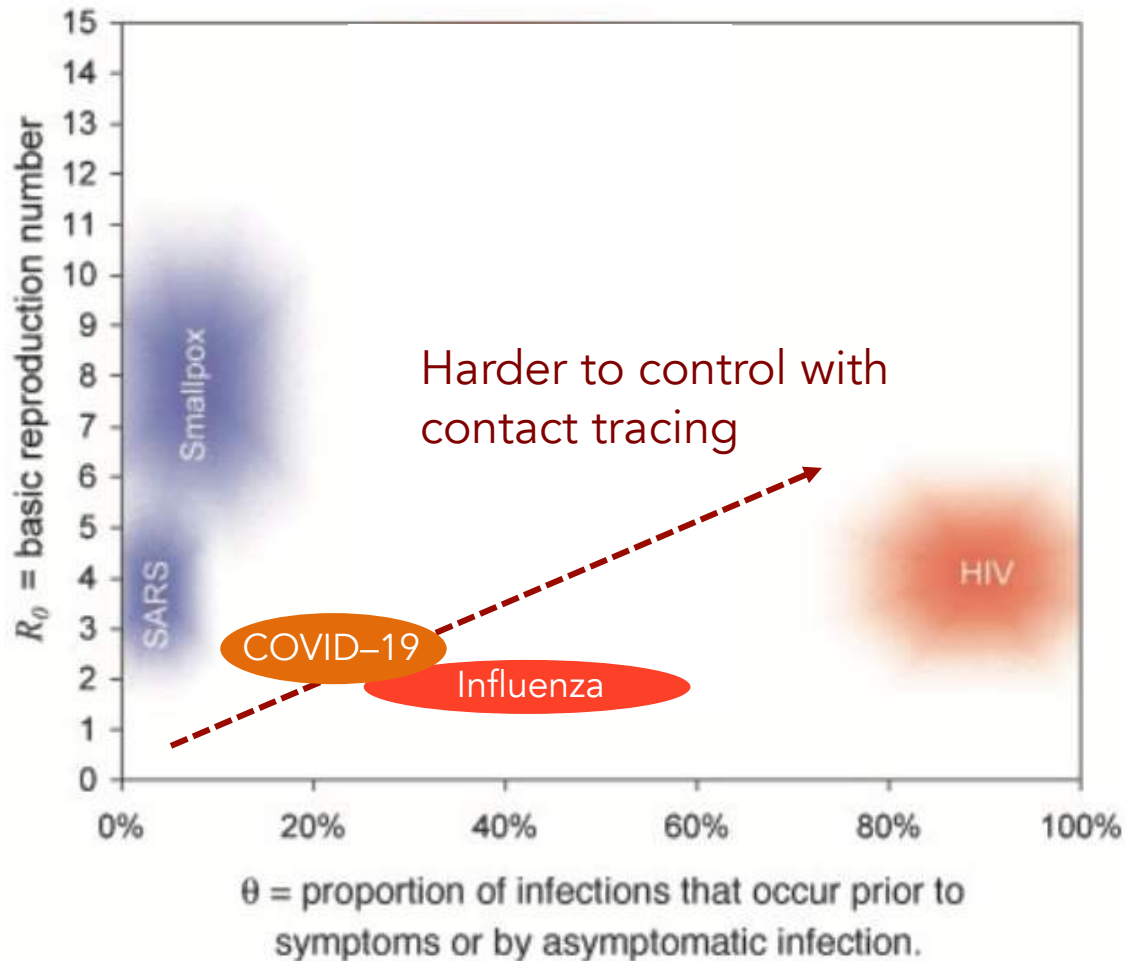
Isolation, contact tracing & quarantine more successful if infection less transmissible and clear symptoms while infectious

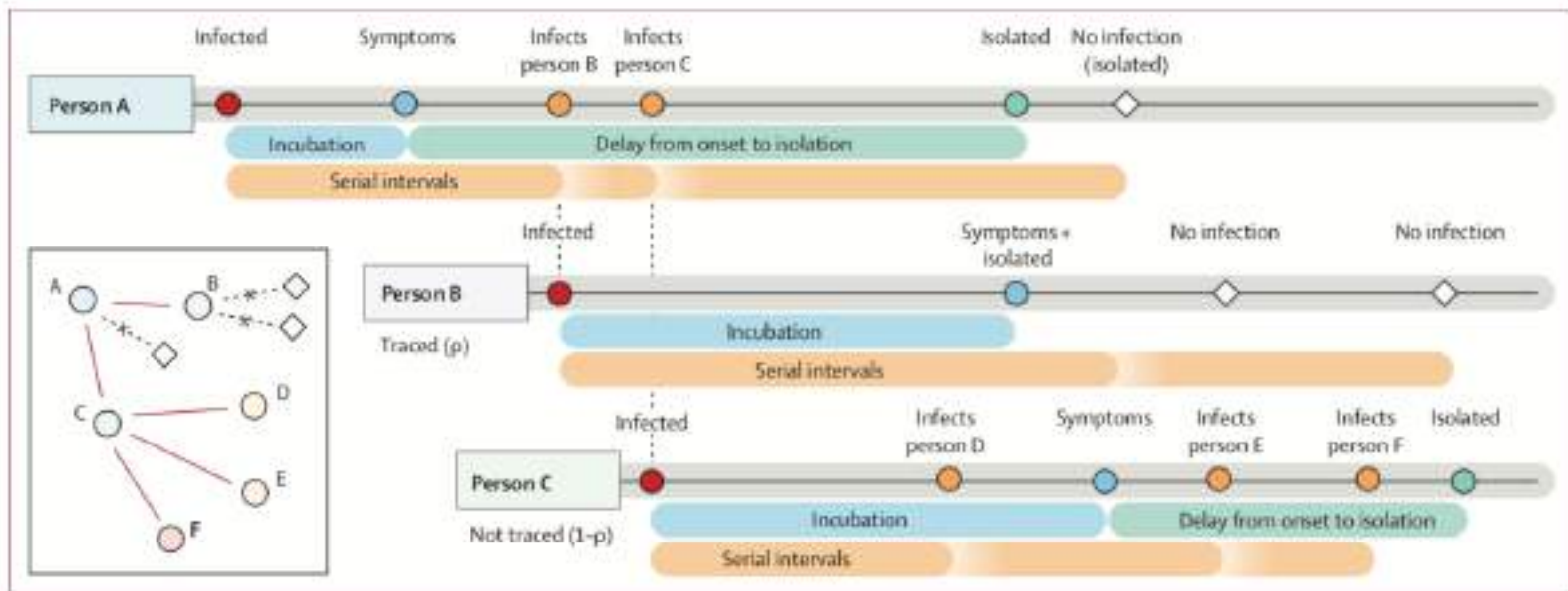


Isolation, contact tracing & quarantine more successful if infection less transmissible and clear symptoms while infectious

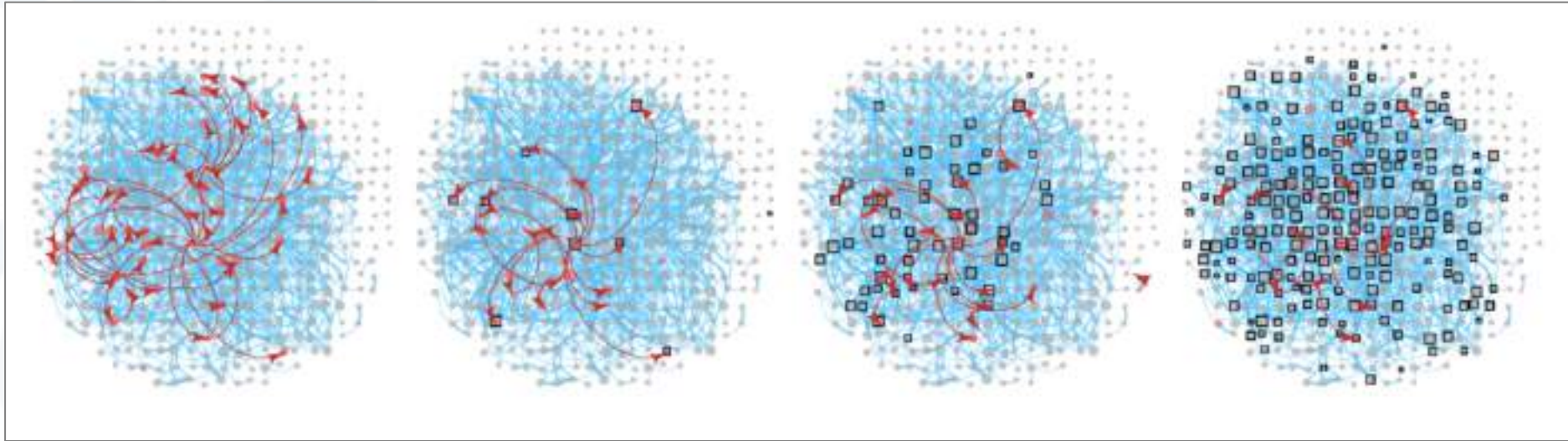
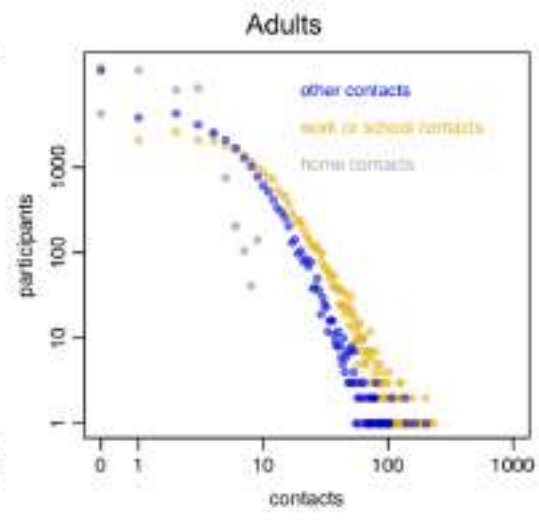
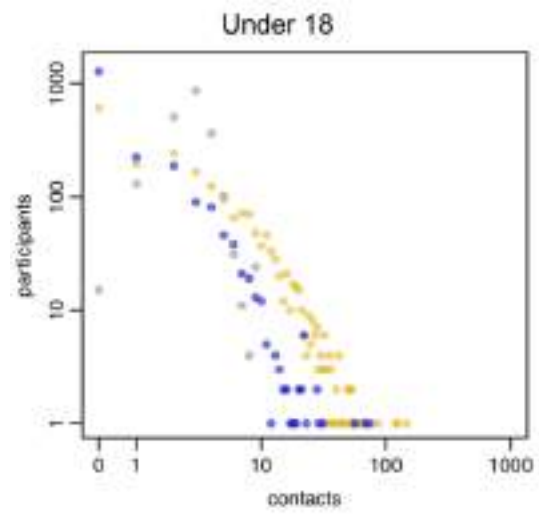


Isolation, contact tracing & quarantine more successful if infection less transmissible and clear symptoms while infectious



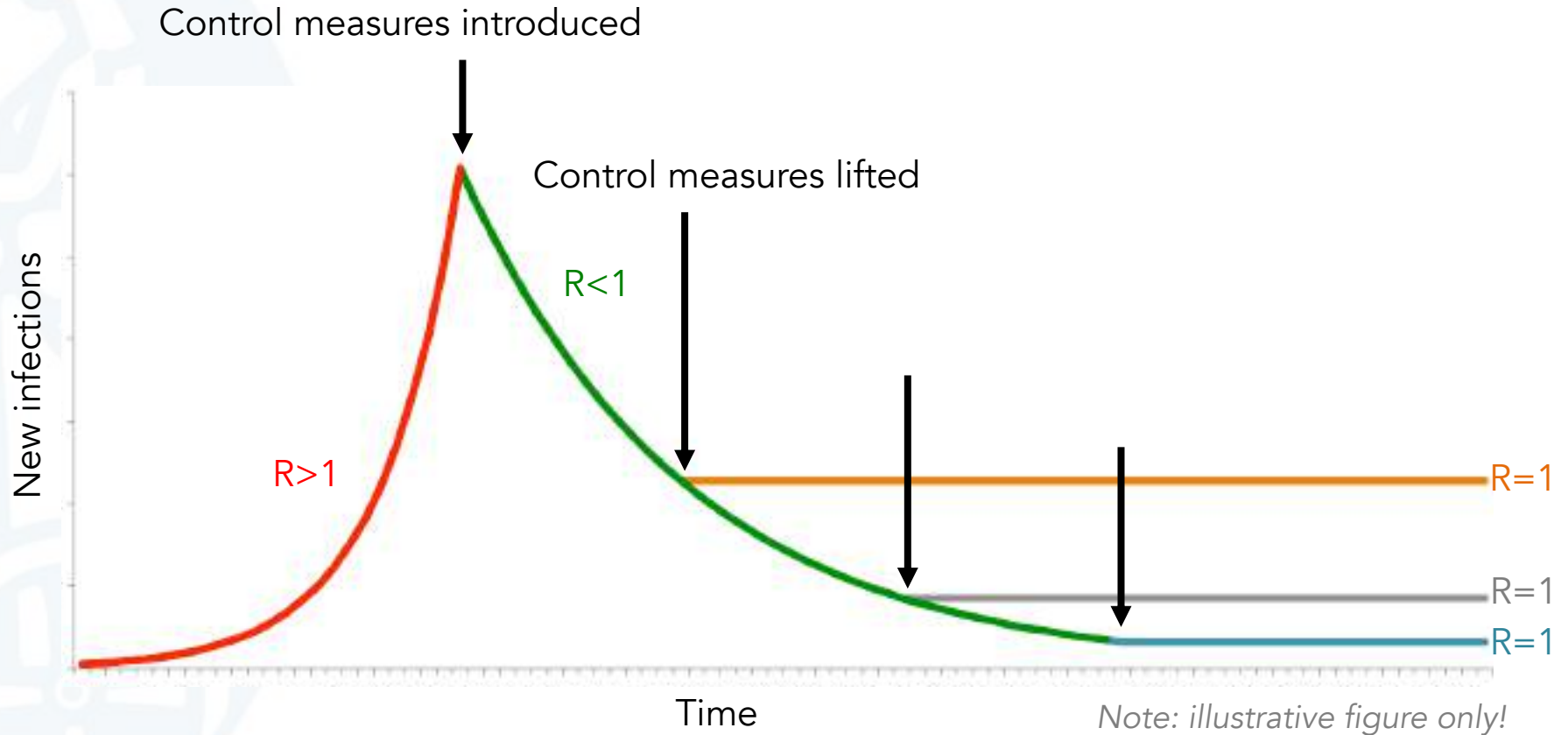


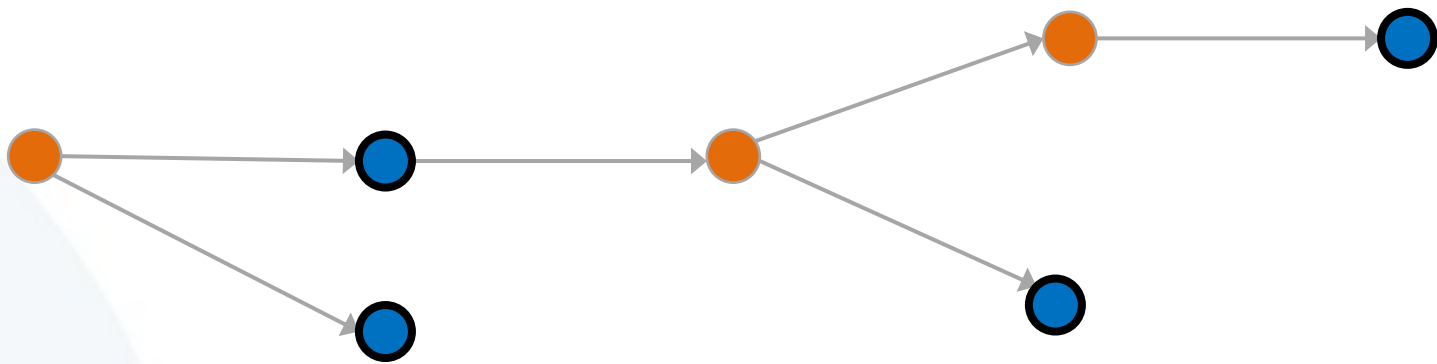
"The probability of control decreases with long delays from symptom onset to isolation, fewer cases ascertained by contact tracing, and increasing transmission before symptoms."



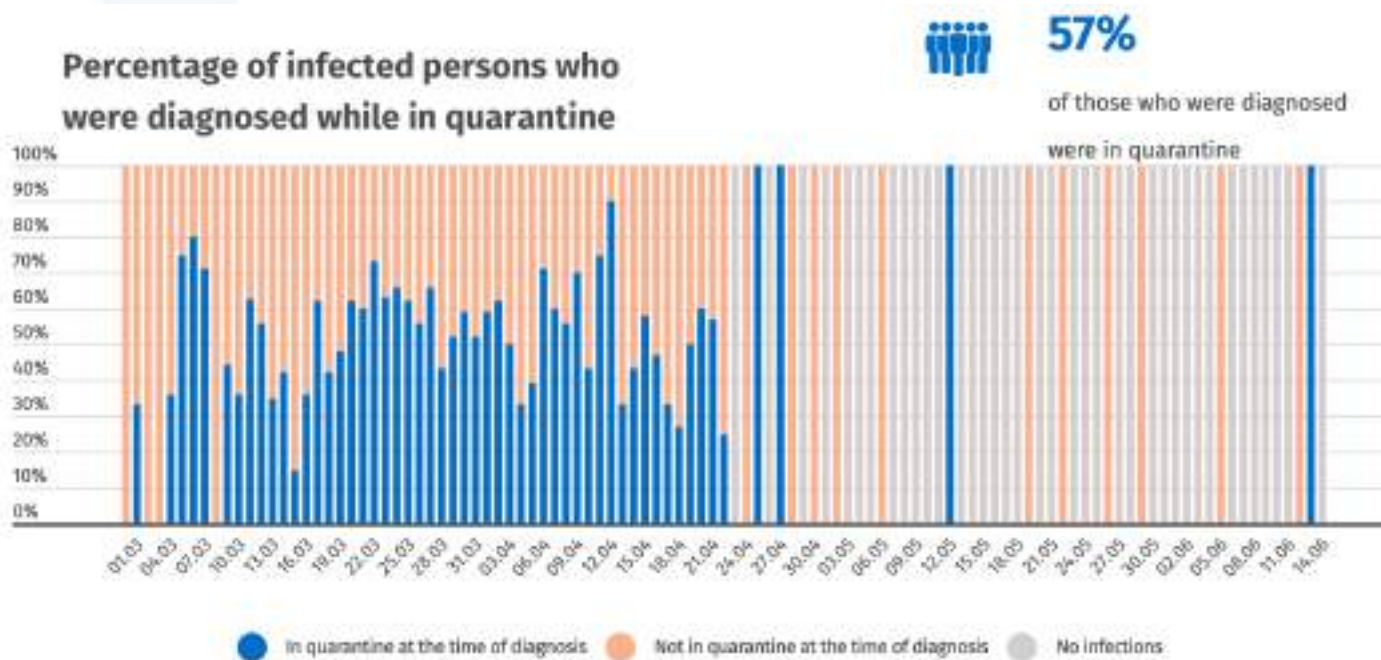
Klepac et al, *MedRxiv*, 2020
Kucharski et al, *Lancet ID*, 2020
Firth et al, *MedRxiv*, 2020

Need to consider level of infection as well as R





As infections decline, can focus more on transmission links



Finally

Thank you to all the public health teams, scientists and front-line medical staff working globally on COVID-19.

And all those whose rapid sharing of data and insights has provided an essential early evidence base.

For more on our group's work: cmmid.github.io/ncov

kucharski.io/academic



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