Mathematical modeling of infectious diseases

Insights and limitations

Jonathan Dushoff, McMaster University

2023

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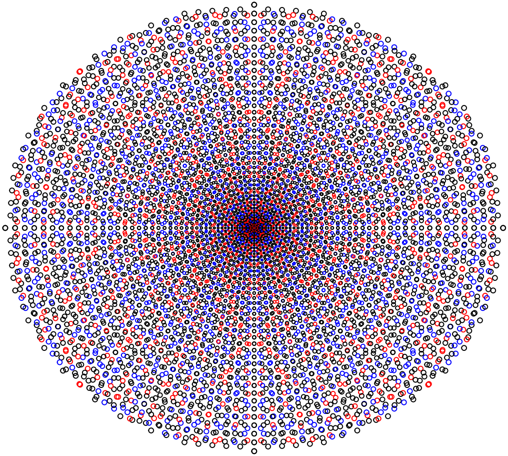
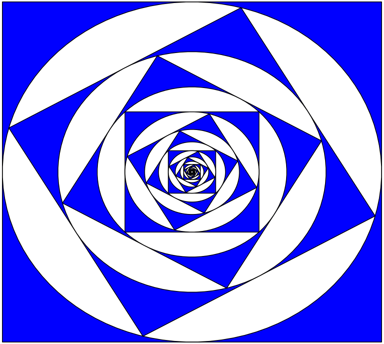
大家茶事

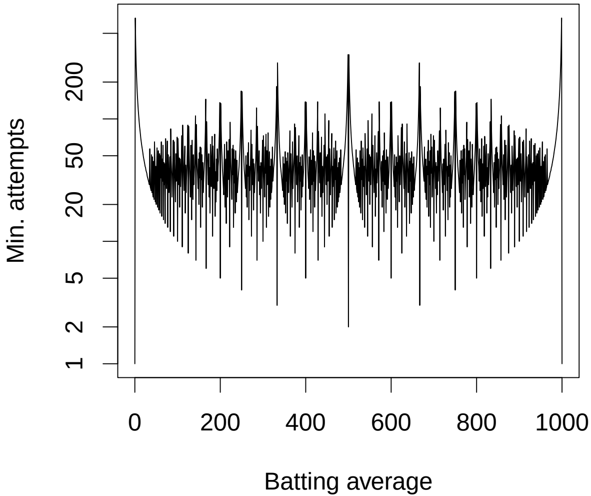


What is the pattern of Pythagorean triples of integers
$a^2 + b^2 = c^2$?



Divide a square and a circle each into two complementary subsets that are pairwise similar

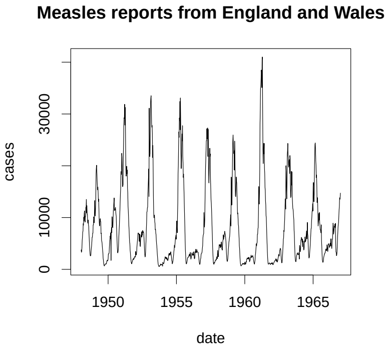
Batting average (安打率)



Outline

Dynamical modeling connects scales

Measles reports 麻疹病例報告



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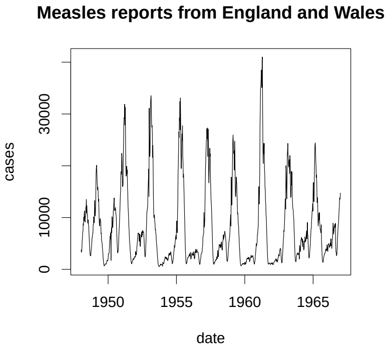

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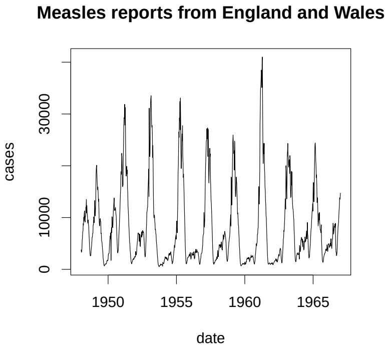

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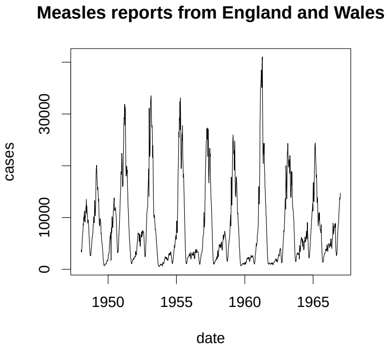

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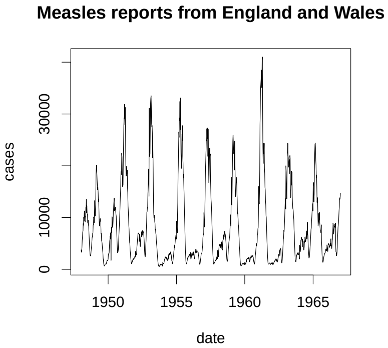

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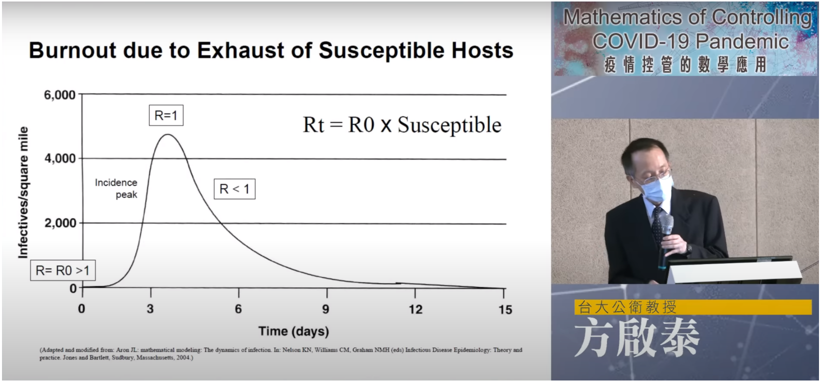
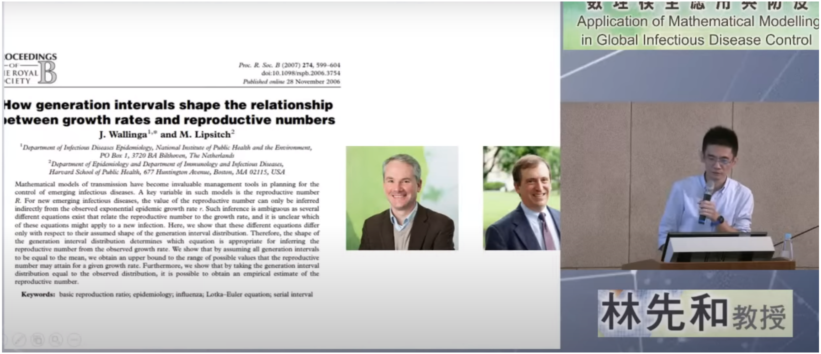

Burnout due to Exhaust of Susceptible Hosts
6,000
4,000
2,000
0
Infectives/square mile
R=1
Rt = R0 x Susceptible
Incidence peak
R < 1
R= R0 >1
0
3
6
9
12
15
Time (days)
(Adapted and modified from: Aron JL: mathematical modeling: The dynamics of infection. In: Nelson KN, Williams CM, Graham NMH (eds) Infectious Disease Epidemiology: Theory and practice. Jones and Bartlett, Sudbury, Massachusetts, 2004.)
Mathematics of Controlling COVID-19 Pandemic
疫情控管的數學應用
台大公衛教授
方啟泰



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How generation intervals shape the relationship between growth rates and reproductive numbers

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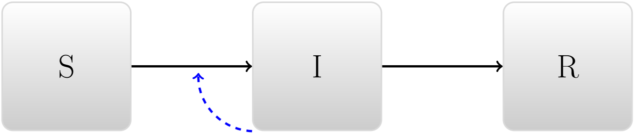
Mathematical models of transmission have become invaluable management tools in planning for the control of emerging infectious diseases. A key variable in such models is the reproductive number R. For new emerging infectious diseases, the value of the reproductive number can only be inferred indirectly from the observed exponential epidemic growth rate r. Such inference is ambiguous as several different equations exist that relate the reproductive number to the growth rate, and it is unclear which of these equations might apply to a new infection. Here, we show that these different equations differ only with respect to their assumed shape of the generation interval distribution. Therefore, the shape of the generation interval distribution determines which equation is appropriate for inferring the reproductive number from the observed growth rate. We show that by assuming all generation intervals to be equal to the mean, we obtain an upper bound to the range of possible values that the reproductive number may attain for a given growth rate. Furthermore, we show that by taking the generation interval distribution equal to the observed distribution, it is possible to obtain an empirical estimate of the reproductive number.

Keywords: basic reproduction ratio; epidemiology; influenza; Lotka–Euler equation; serial interval

Outline

Simple dynamical models use compartments

Divide people into categories:



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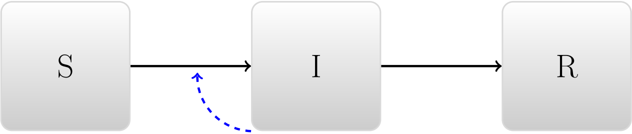

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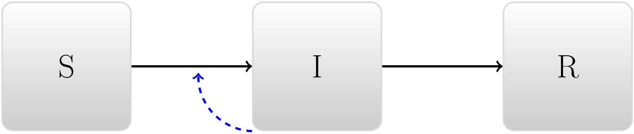

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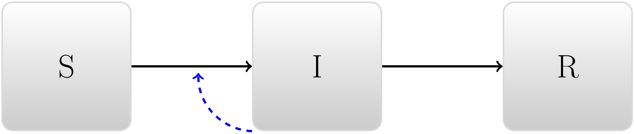

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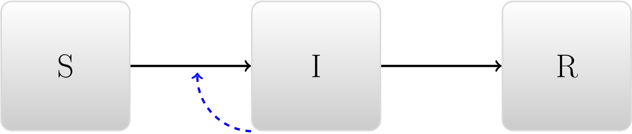
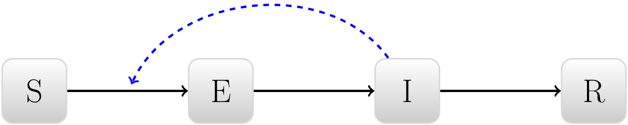
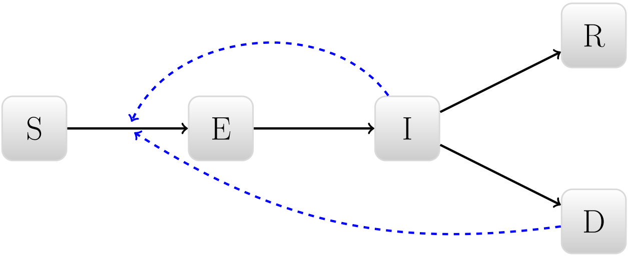


$$
\begin{aligned}
\frac{dS}{dt} &= \mu N - \beta \frac{SI}{N} - \mu S \\
\frac{dI}{dt} &= \beta \frac{SI}{N} - \gamma I - \mu R \\
\frac{dR}{dt} &= \gamma I - \mu R
\end{aligned}
$$

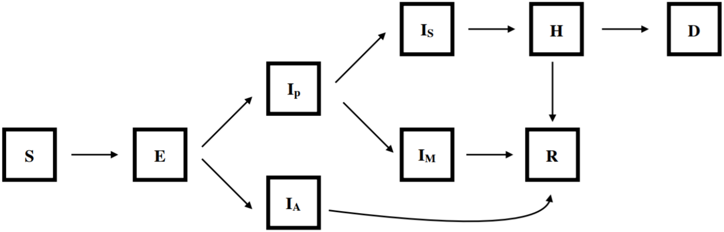
Delayed infectiousness



Ebola 伊波拉



COVID-19



I_p = pre-symptomatic
I_A = asymptomatic
I_S = symptomatic, severe case
I_M = symptomatic, minor case

S = susceptible
E = exposed

H = hospitalized
R = recovered
D = dead

Childs et al., http://covid-measures.stanford.edu/

Lessons

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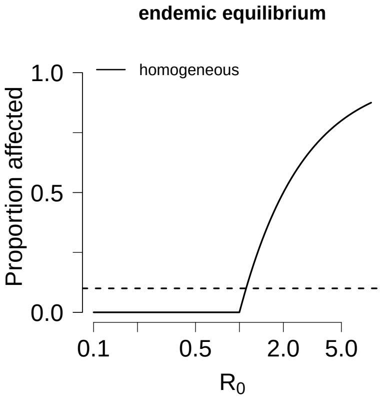

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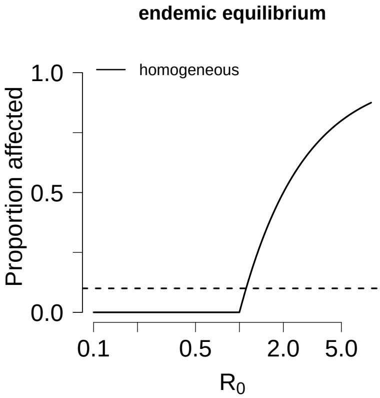

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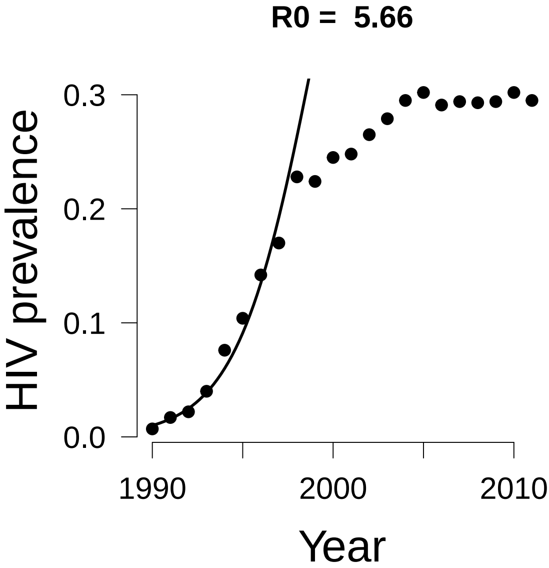

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Transmission intervals


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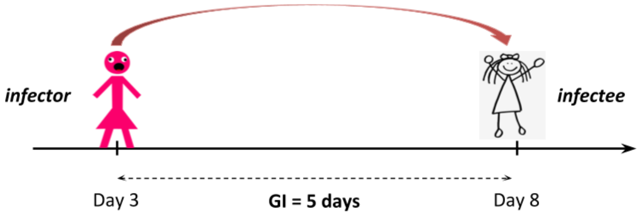
How long is a disease generation?

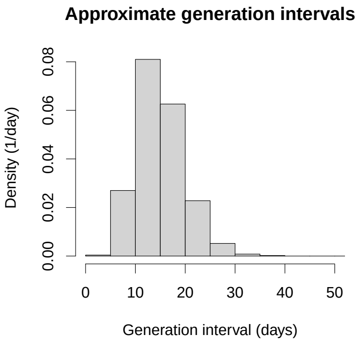
Definition

Generation Interval:

Interval between the time that an individual is infected by an infector and the time this infector was infected



Generation-interval distributions



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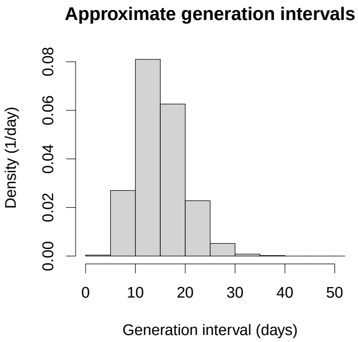

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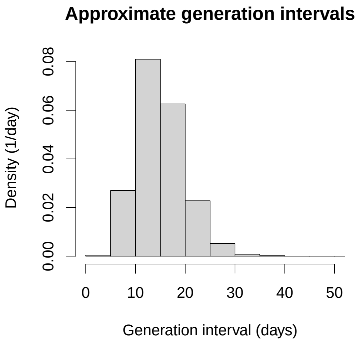

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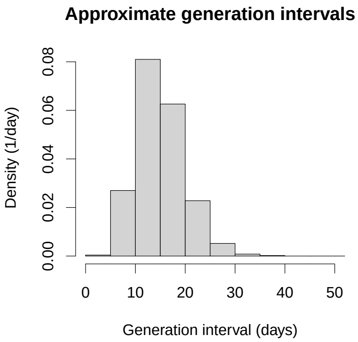

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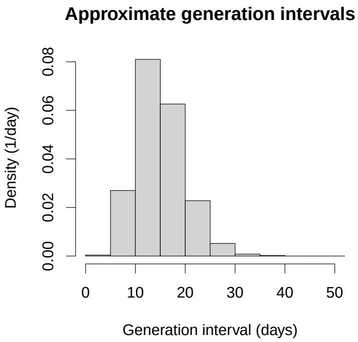

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Mechanistic perspective
知道了是規則

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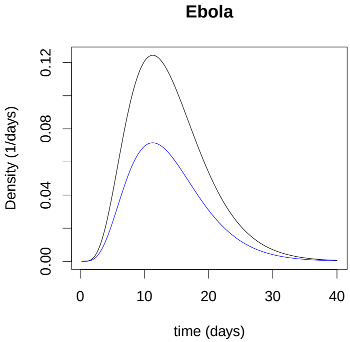

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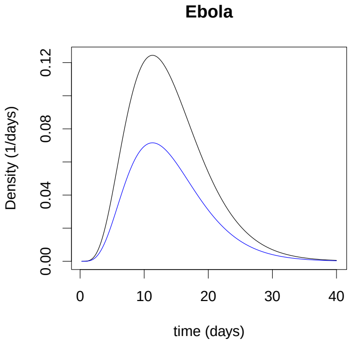

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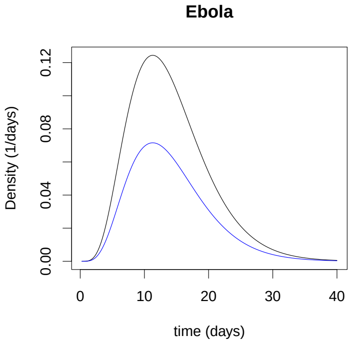
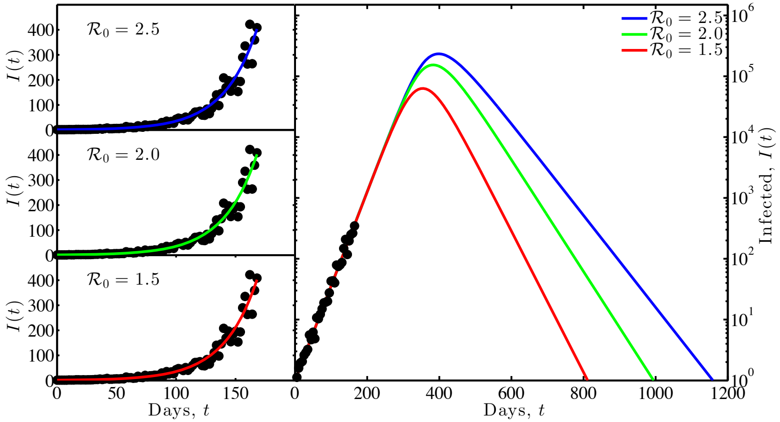


Ebola outbreak



Phenomenological perspective
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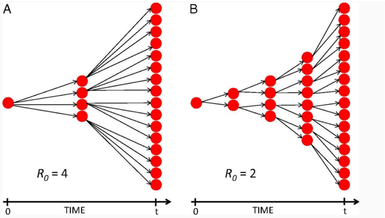

Powers et al., *https://www.pnas.org/content/111/45/15867*

Phenomenological perspective

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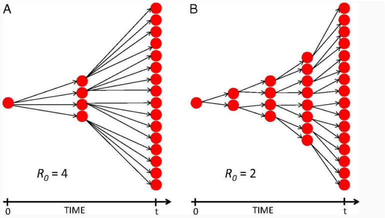
- Population-level speed r is observed
- Generation-interval distribution $g(\tau)$ can be estimated



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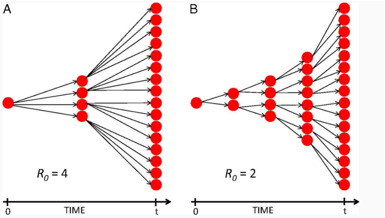

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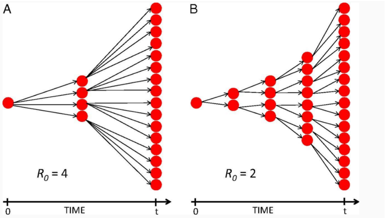

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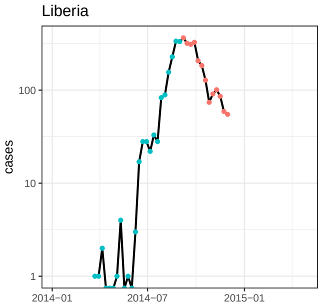

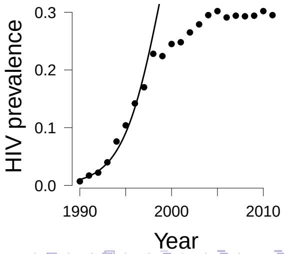

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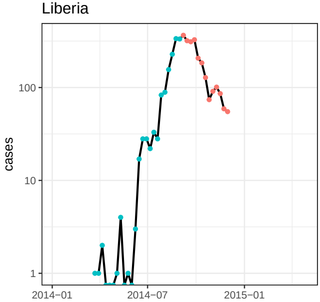

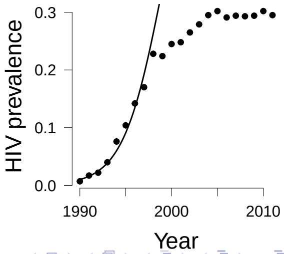

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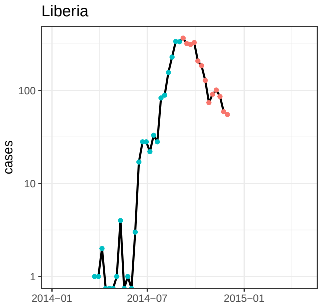

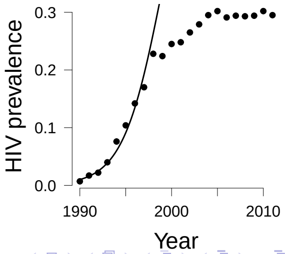

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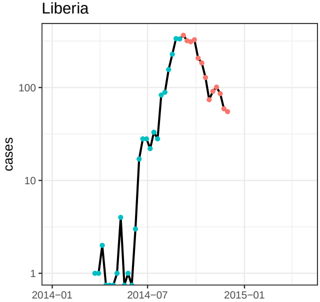

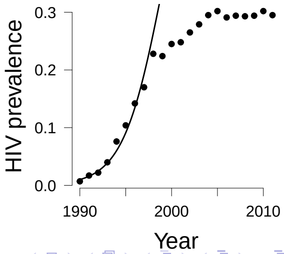

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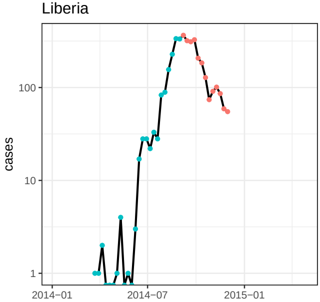

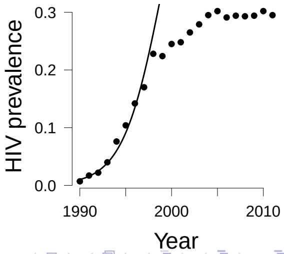

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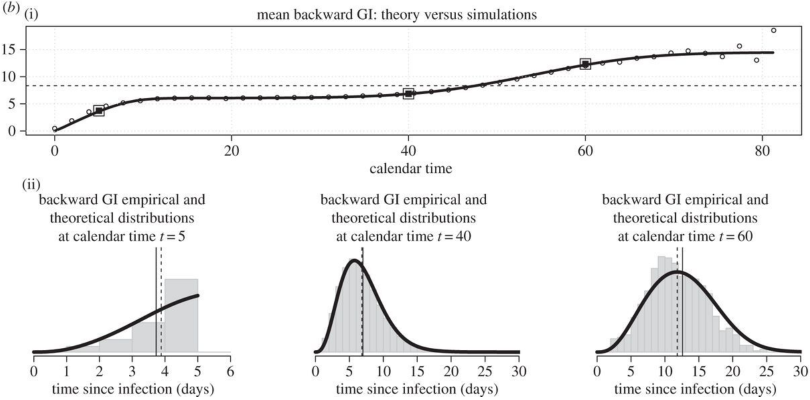

Champredon and Dushoff, 2015. DOI:10.1098/rspb.2015.2026

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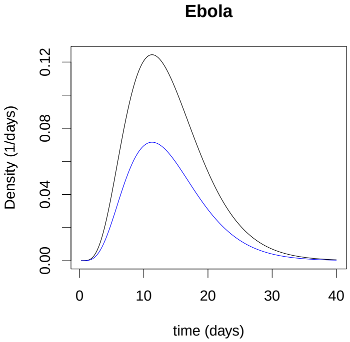

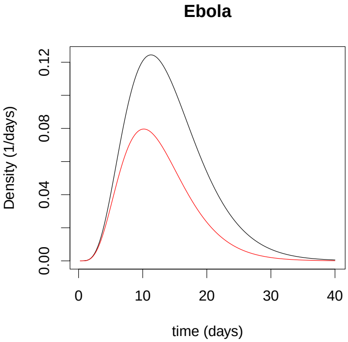

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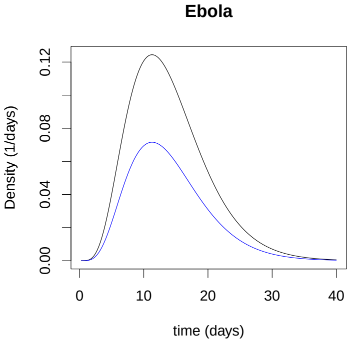

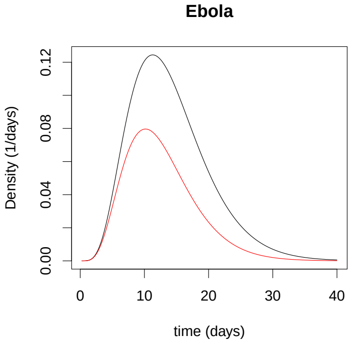

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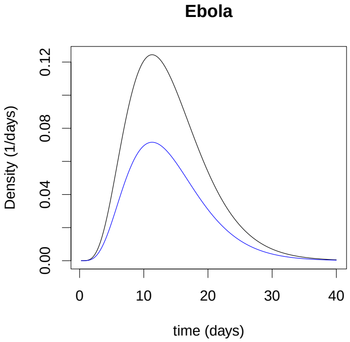

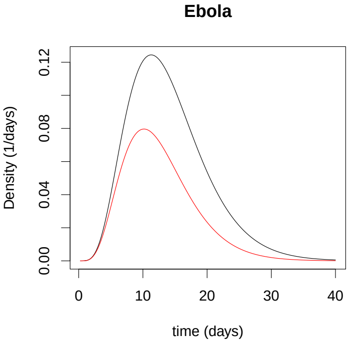

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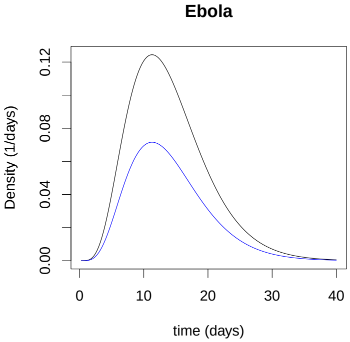

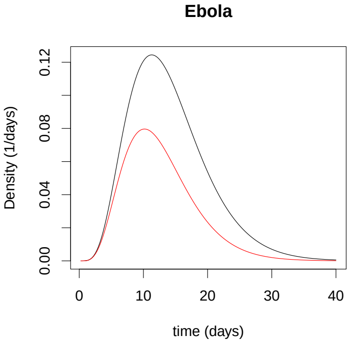

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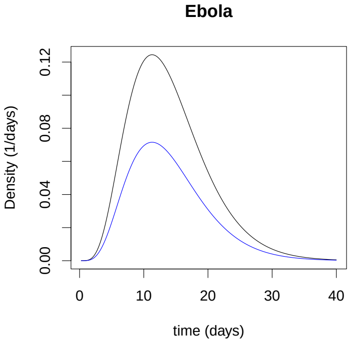

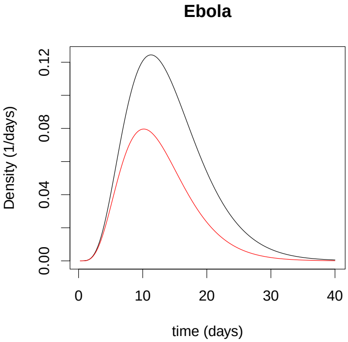

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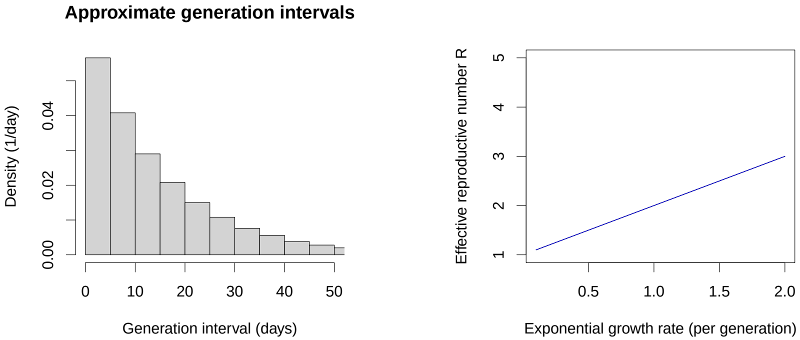

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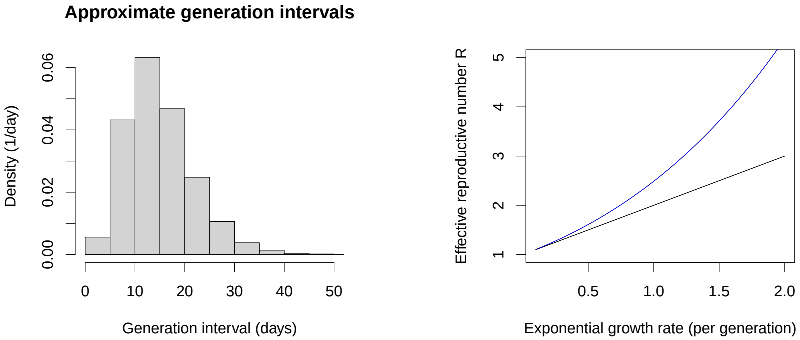

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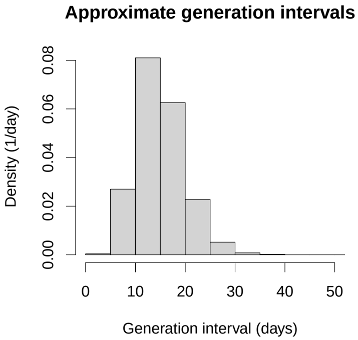

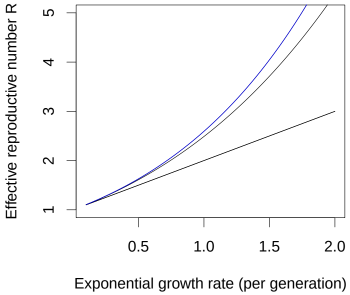

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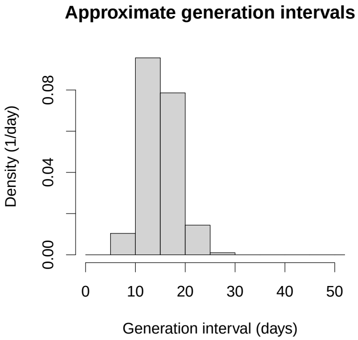
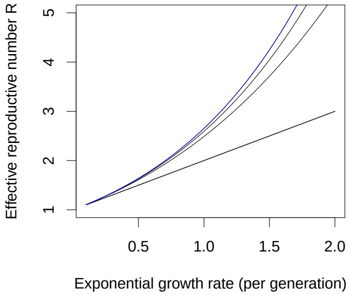
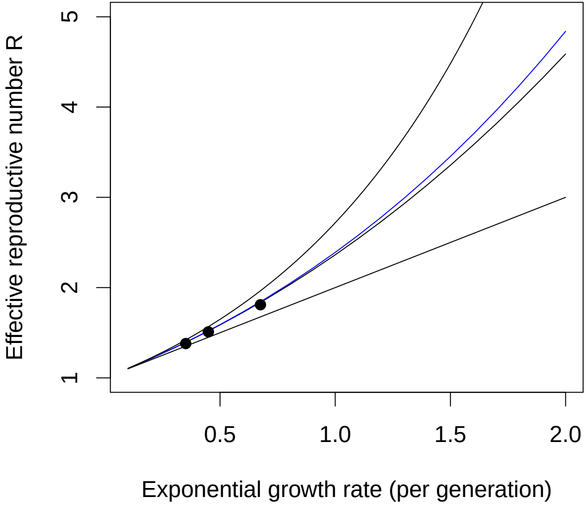




Approximating the $r\mathcal{R}$ relationship



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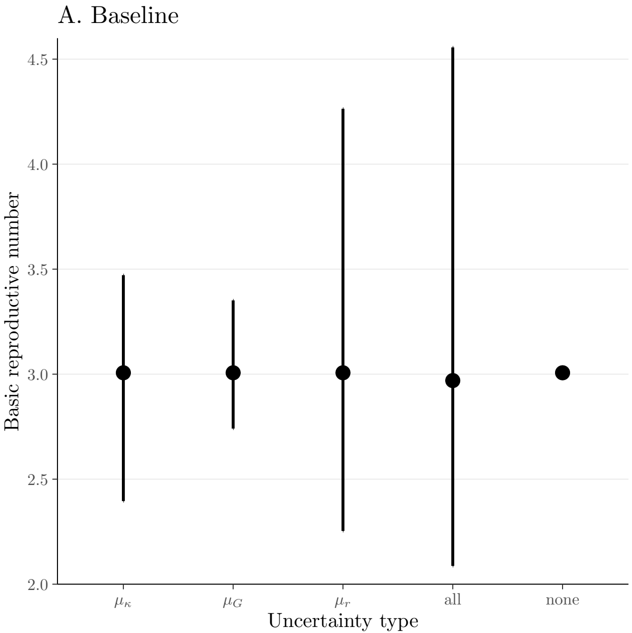

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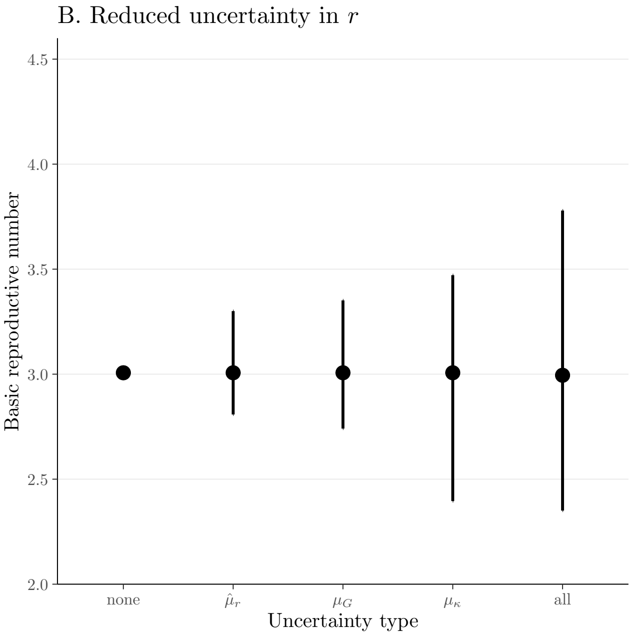
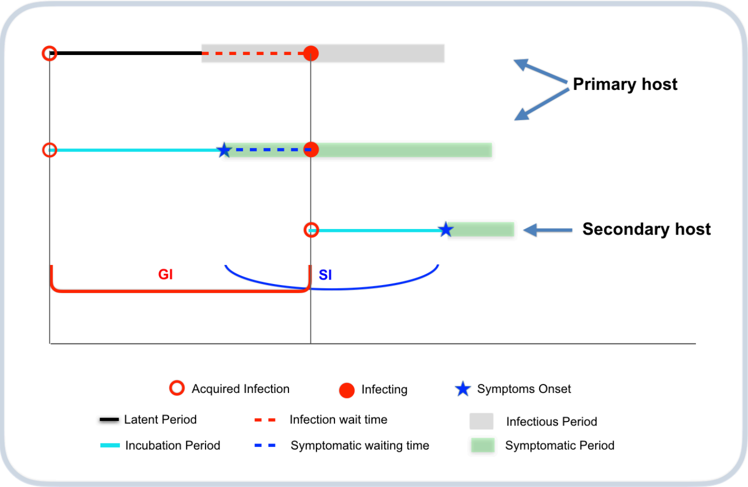


Outline

Serial-interval distributions



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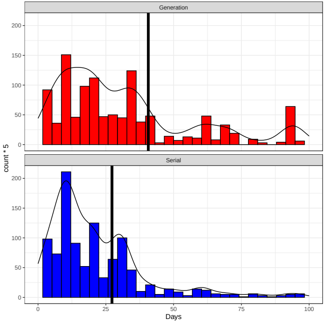

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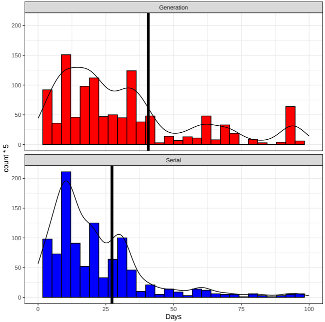

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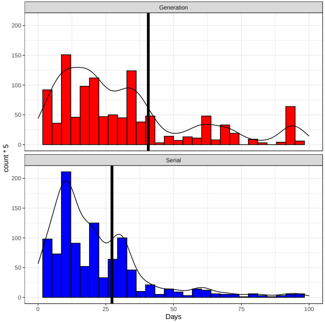

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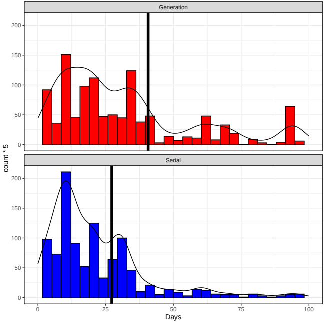

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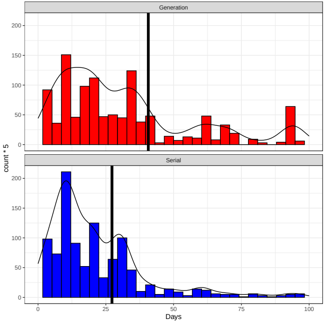

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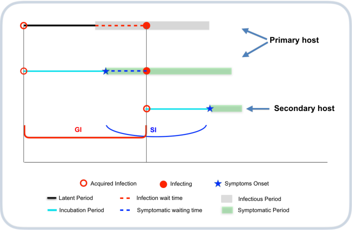
Differences between individuals



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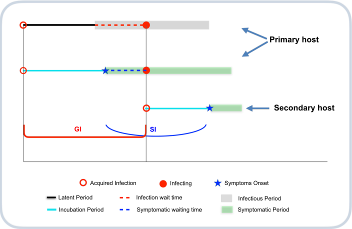

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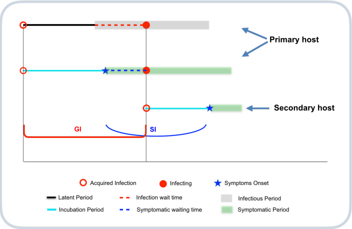

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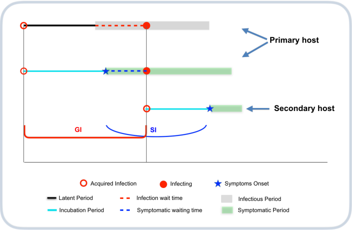

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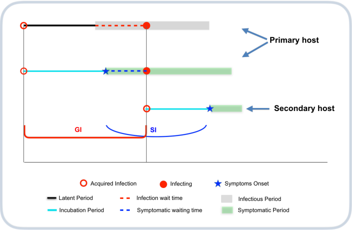

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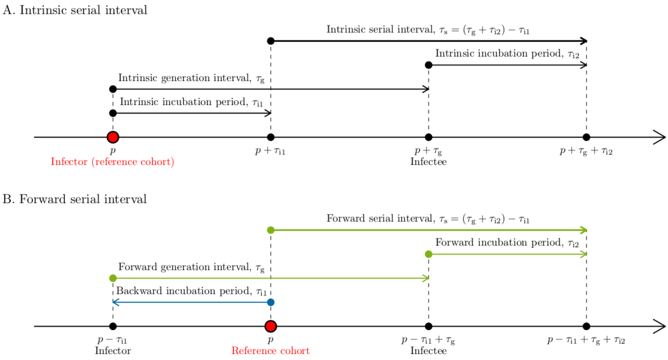

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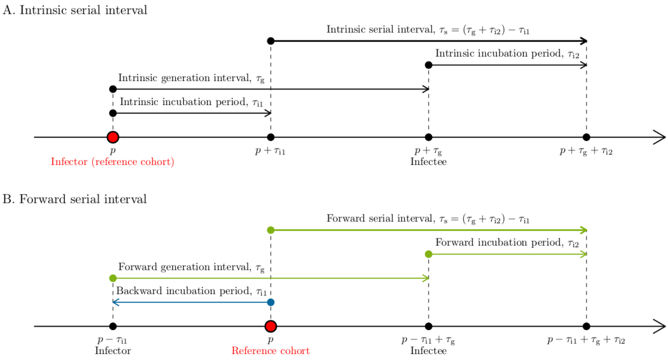

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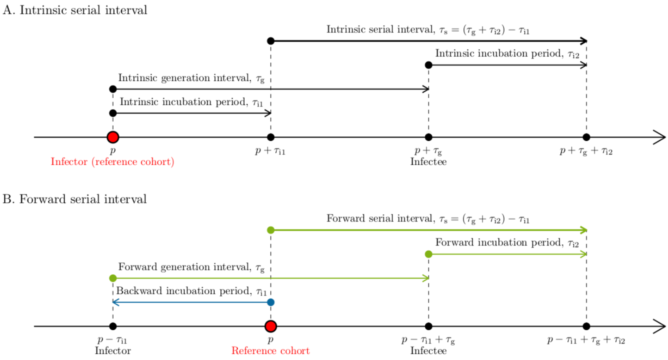

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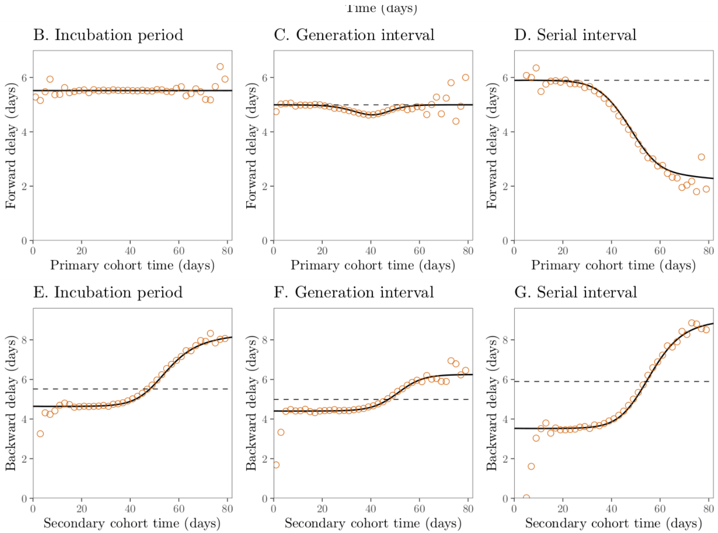

Park et al. https://doi.org/10.1101/2020.06.04.20122713

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