Transmission intervals in Disease Modeling

Jonathan Dushoff, McMaster University

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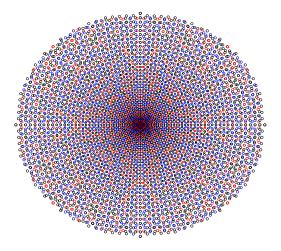
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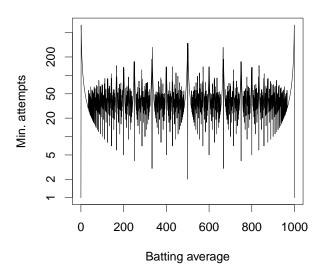
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What is the pattern of Pythagorean triples of integers $a^2 + b^2 = c^2$?

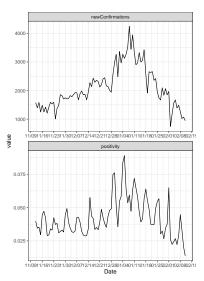




How many at-bats does it take to get a given batting average?



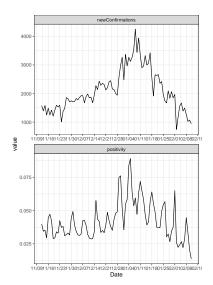
► How far and fast would it spread if unchecked?



https://wzmli.github.io/COVID19-Canada



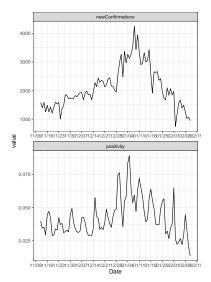
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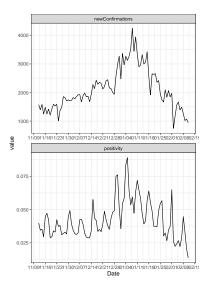
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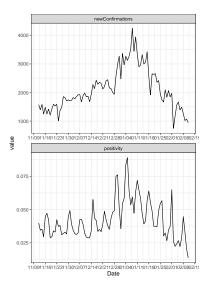
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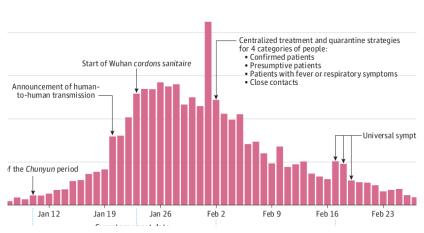


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Wuhan control measures



https://jamanetwork.com/journals/jama/fullarticle/2764658

Outline

Modeling approaches

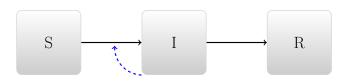
Transmission intervals

Linking rR

Evaluating interventions

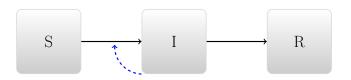
Summary

Divide people into categories:



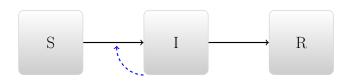
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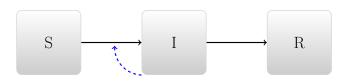
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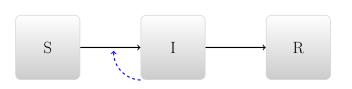


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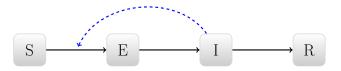


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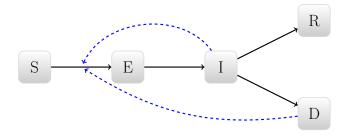


$$\begin{array}{ll} \frac{dS}{dt} & = & \mu N - \beta \frac{SI}{N} - \mu S \\ \frac{dI}{dt} & = & \beta \frac{SI}{N} - \gamma I - \mu R \\ \frac{dR}{dt} & = & \gamma I - \mu R \end{array}$$

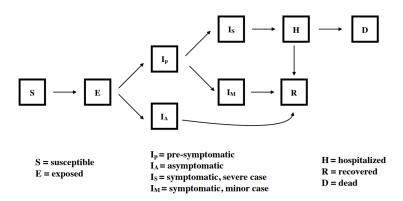
Delayed infectiousness



Ebola



Coronavirus



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

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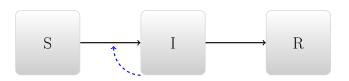
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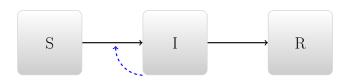
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Cohort modeling



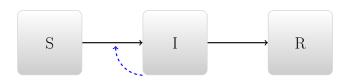
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Cohort modeling



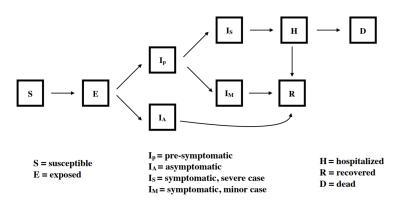
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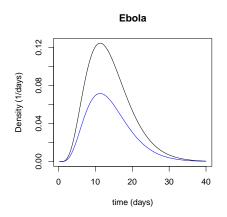
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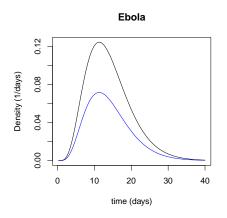
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Transmission kernel



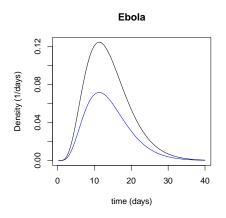
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Linking rR

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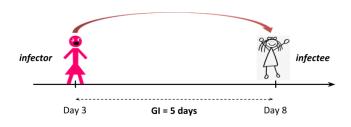
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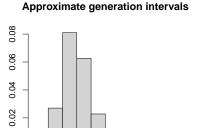
How long is a disease generation?

Definition

Generation Interval:

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





30

40

50

20

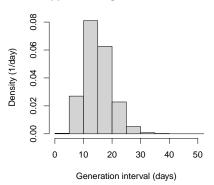
Generation interval (days)

10

Density (1/day)

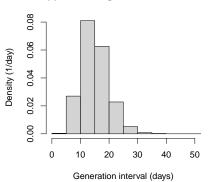
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Approximate generation intervals



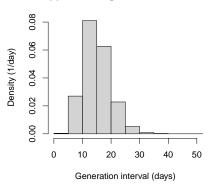
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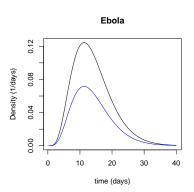
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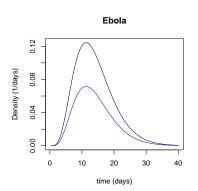
Mechanistic perspective

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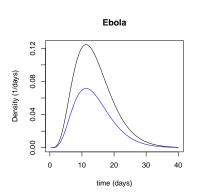
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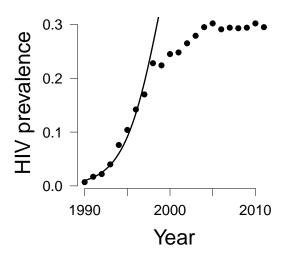


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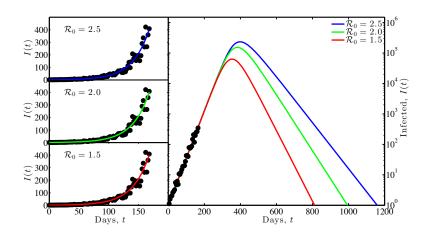


HIV in sub-Saharan Africa

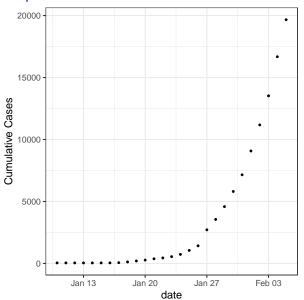


 $C \approx 18 \, \mathrm{month}$. Faster than expected.

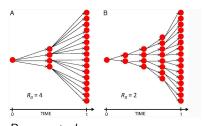
Ebola outbreak



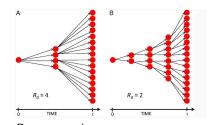
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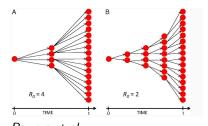
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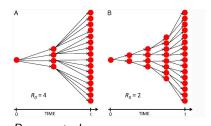
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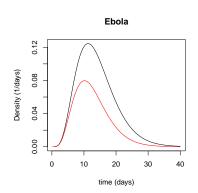
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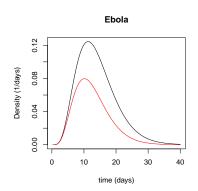
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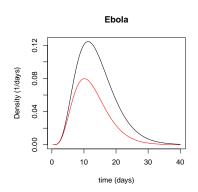
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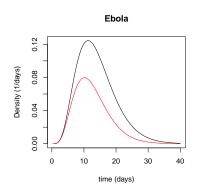
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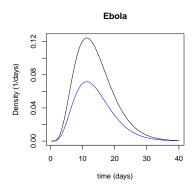
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- ► J Wallinga, M Lipsitch; DOI: 10.1098/rspb.2006.3754

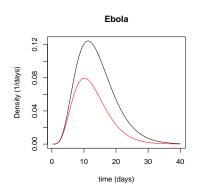


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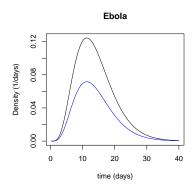
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- ► J Wallinga, M Lipsitch; DOI: 10.1098/rspb.2006.3754

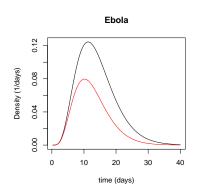




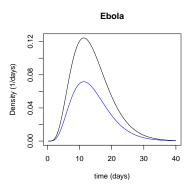


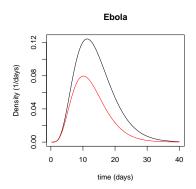
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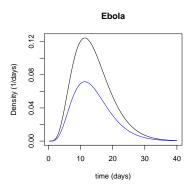


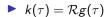


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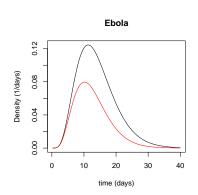
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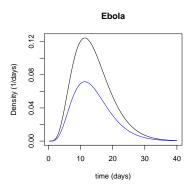


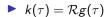
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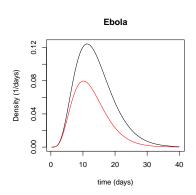
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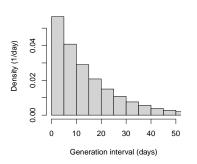
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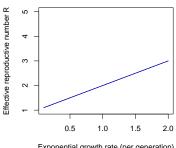
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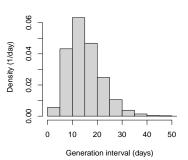
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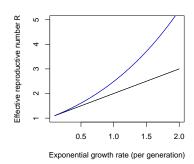
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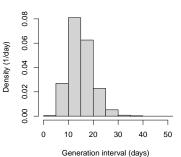
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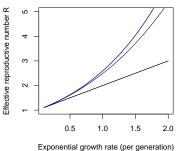


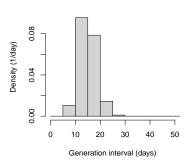


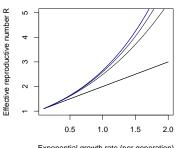




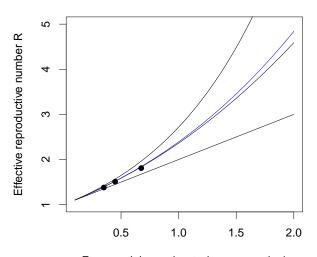








Approximating the rR relationship



Exponential growth rate (per generation)

Heuristics for \mathcal{R}

▶ Mechanistic: R = DcpS/N

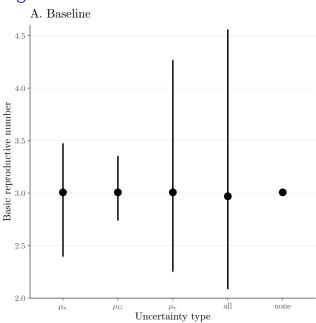
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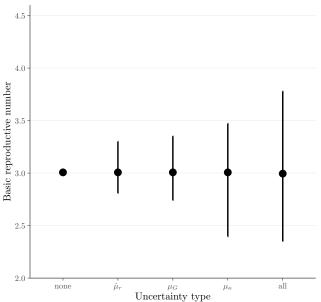
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Propagating error



Propagating error

B. Reduced uncertainty in r



Outline

Modeling approaches

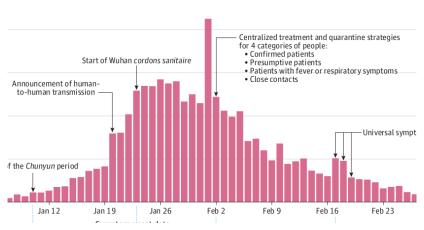
Transmission intervals

Linking rR

Evaluating interventions

Summary

Wuhan control measures



https://jamanetwork.com/journals/jama/fullarticle/2764658

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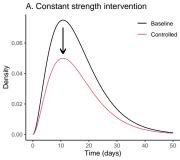
- Moving from reports to infections
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Time-varying reproductive numbers

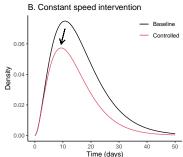
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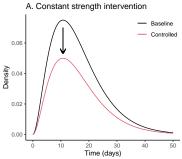
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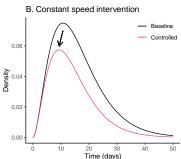
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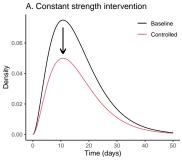


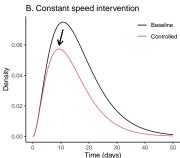




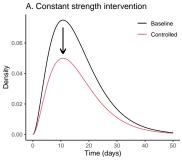


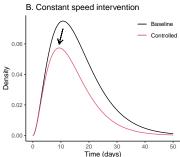
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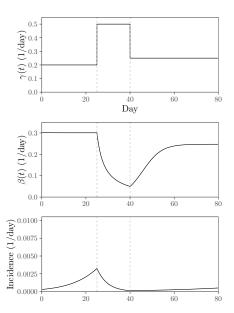
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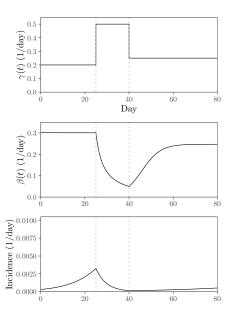
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Unidentifiability



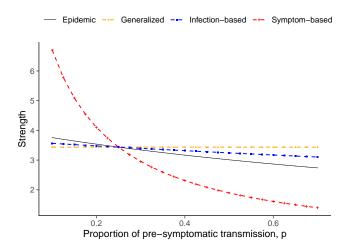
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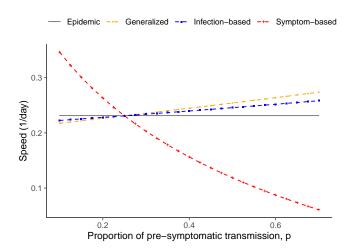


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