Dynamical biases in epidemic inference

Sang Woo Park

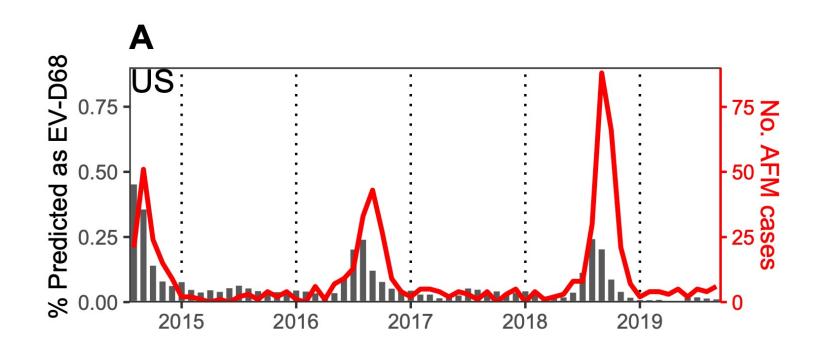
Princeton University

Introduction

 3rd year PhD candidate at Princeton University

Advisor: Bryan Grenfell

 Dynamics of childhood diseases, especially acute flaccid myelitis and enterovirus D68



Reconciling early-outbreak estimates of the basic reproductive number and its uncertainty: framework and applications to the novel coronavirus (SARS-CoV-2) outbreak

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The time scale of asymptomatic transmission affects estimates of epidemic potential in the COVID-19 outbreak

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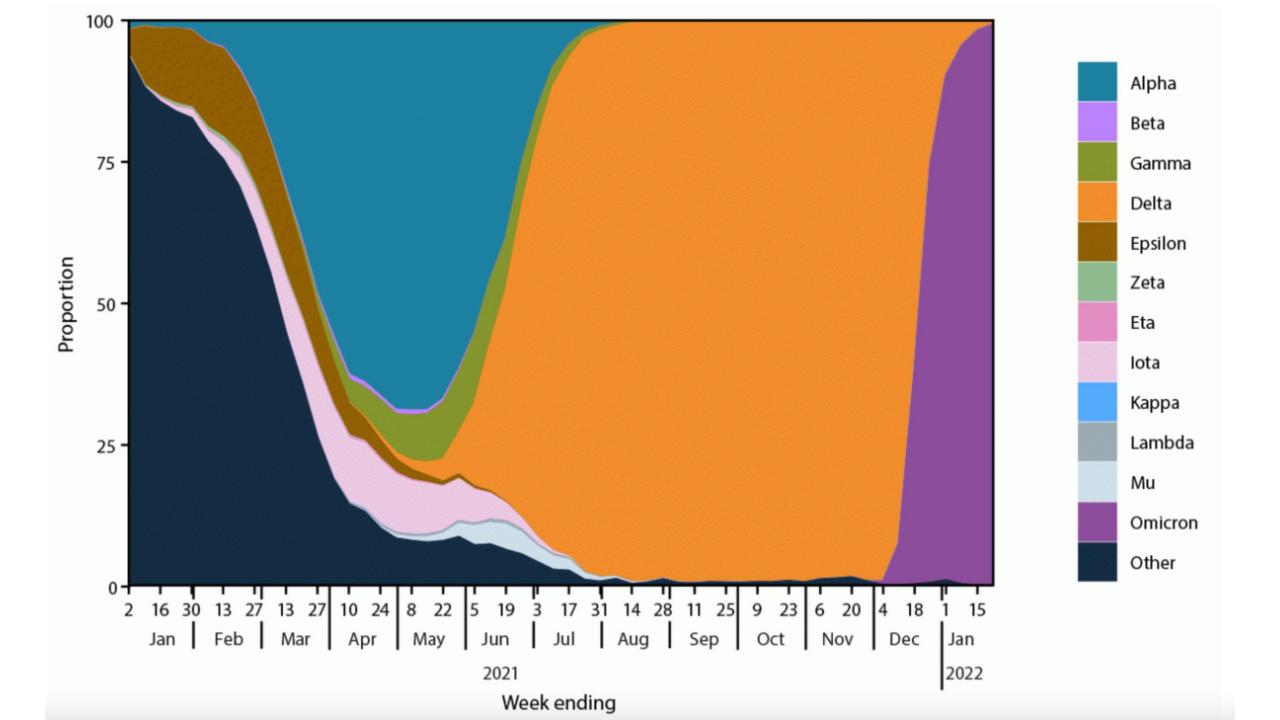
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Roles of generation-interval distributions in shaping relative epidemic strength, speed, and control of new SARS-CoV-2 variants

Sang Woo Park^{1,*} Benjamin M. Bolker^{2,3,4} Sebastian Funk^{5,6} C. Jessica E. Metcalf^{1,7} Joshua S. Weitz^{8,9} Bryan T. Grenfell^{1,7,10} Jonathan Dushoff^{2,3,4}



Overview

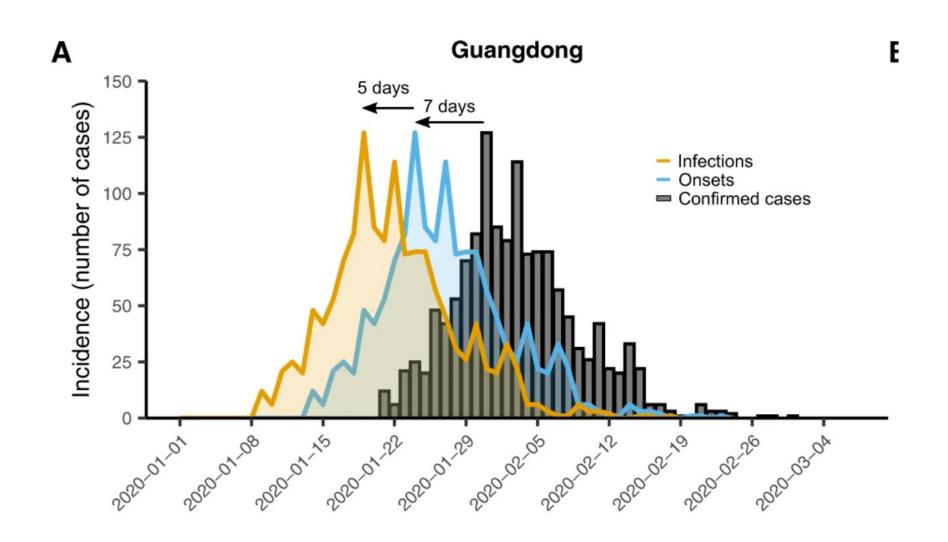
1. Introduction to dynamical biases

2. Dynamical biases in serial-interval distributions

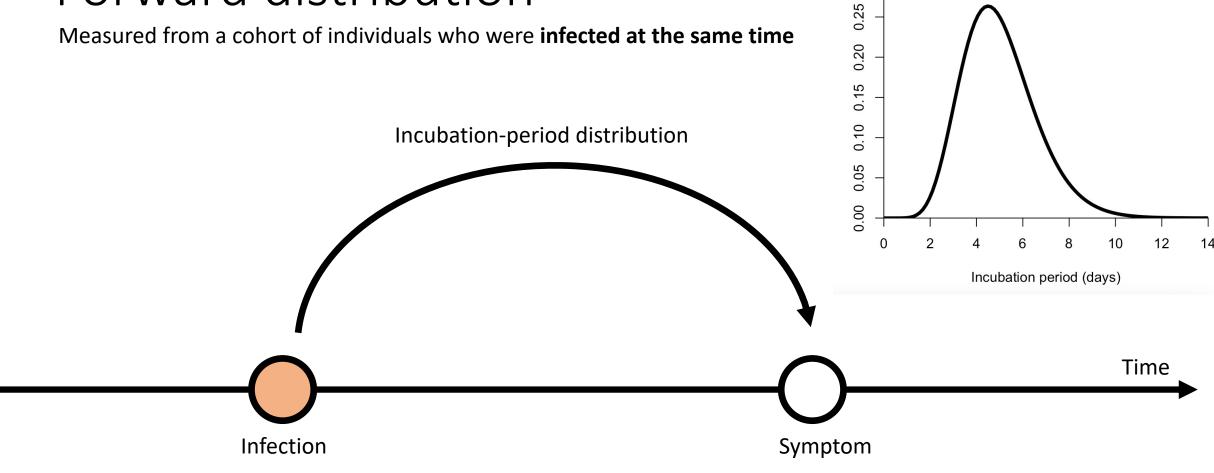
3. Application: incubation periods and generation intervals of the Omicron variant

Introduction to dynamical biases

Observed vs latent dynamics

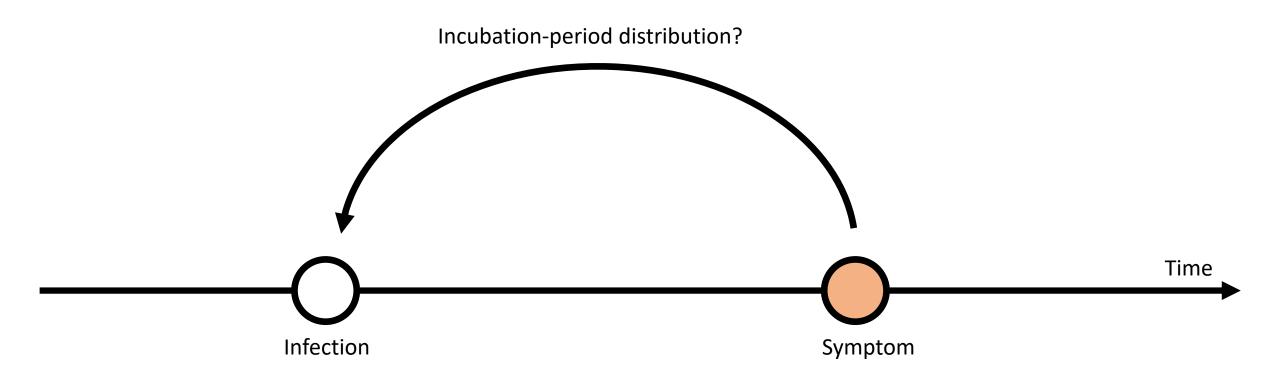


Forward distribution

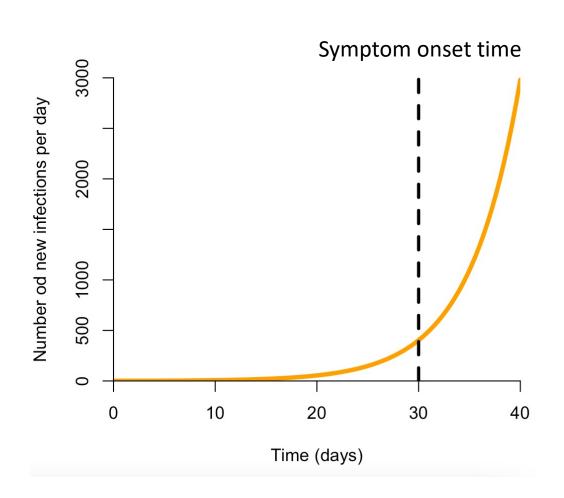


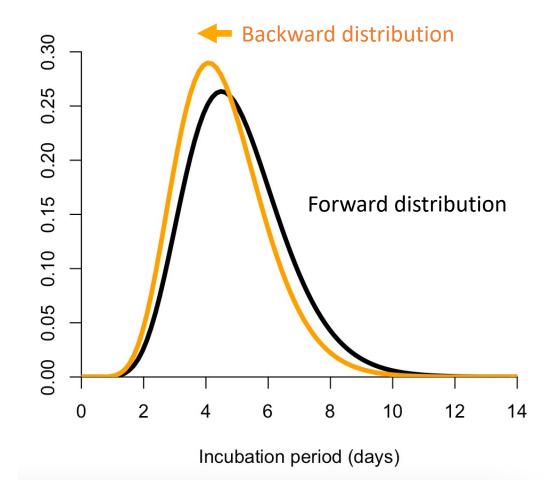
Backward distribution

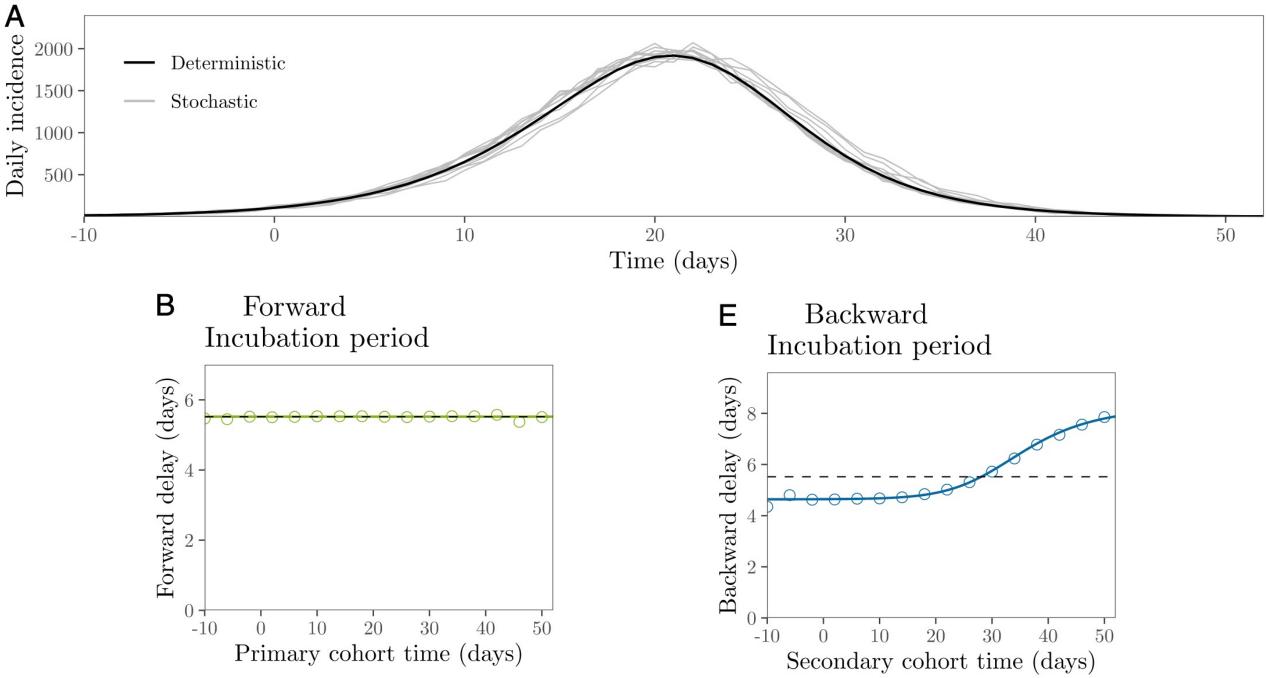
Measured from a cohort of individuals developed symptoms at the same time



Exponential growth & Dynamical bias



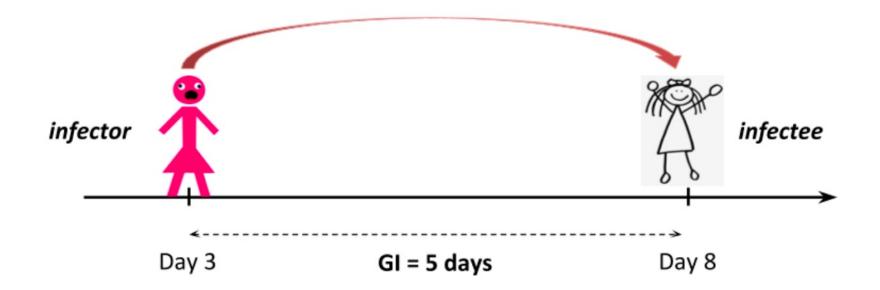




Dynamical biases in serialinterval distributions

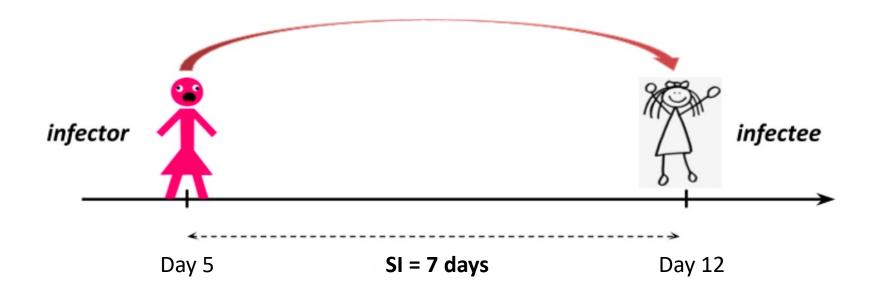
Generation interval

Time between when an individual (infector) becomes infected and when their infectee becomes infected

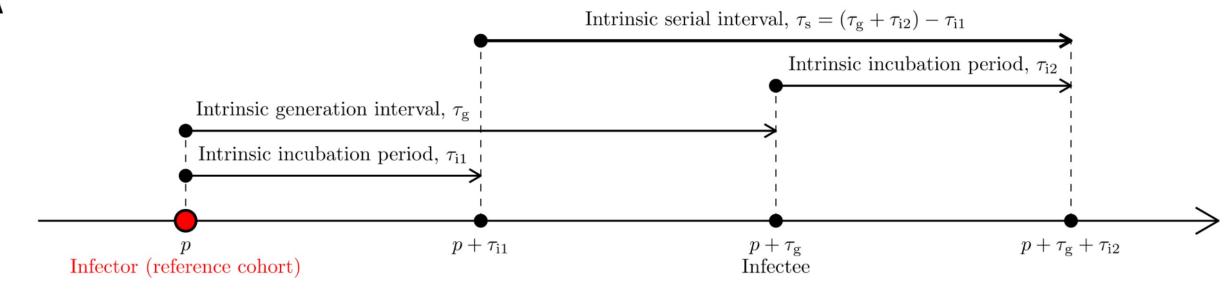


Serial interval

Time between when an individual (infector) develops symptoms and when their infectee develops symptoms



▲ Intrinsic serial interval

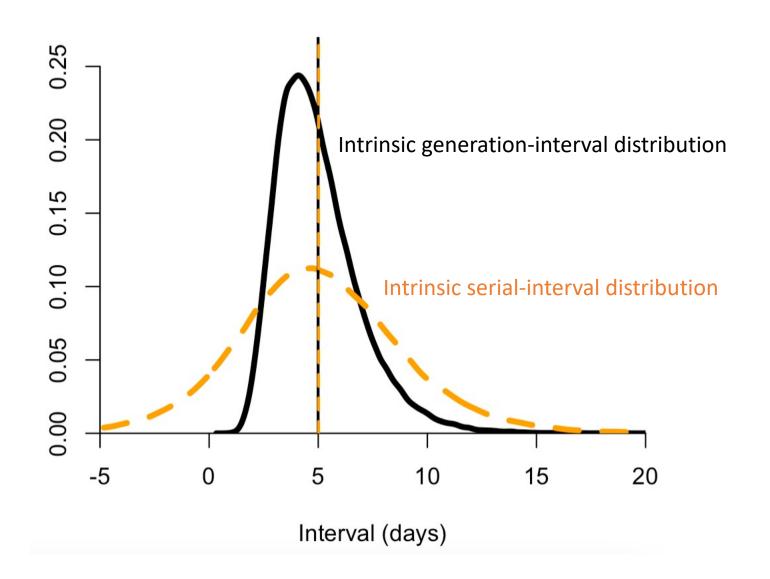


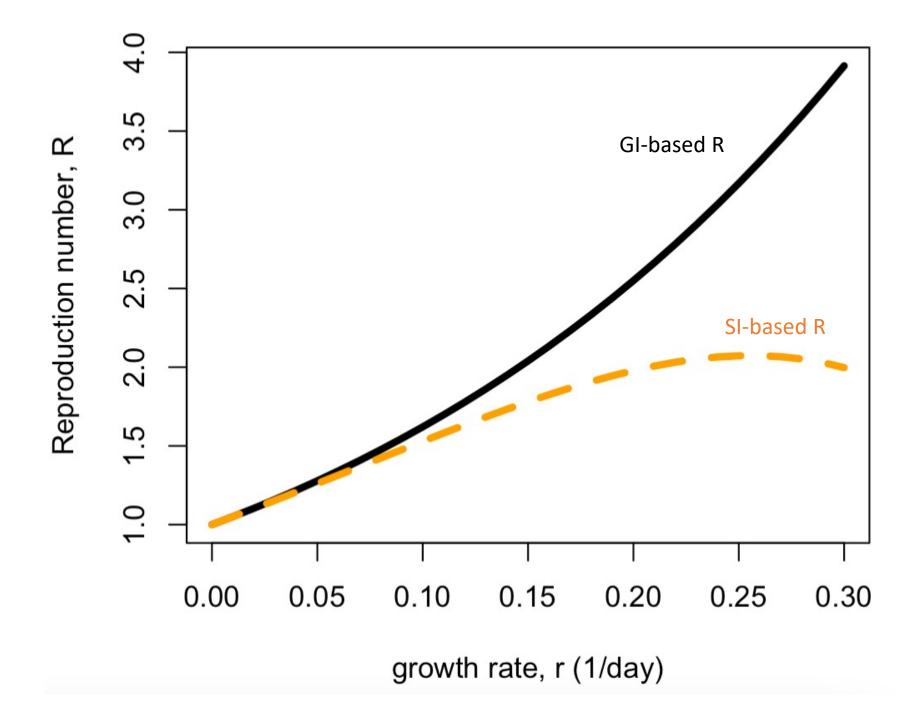
Intrinsic serial interval = -(intrinsic incubation period of the infector) +

(intrinsic generation interval) +

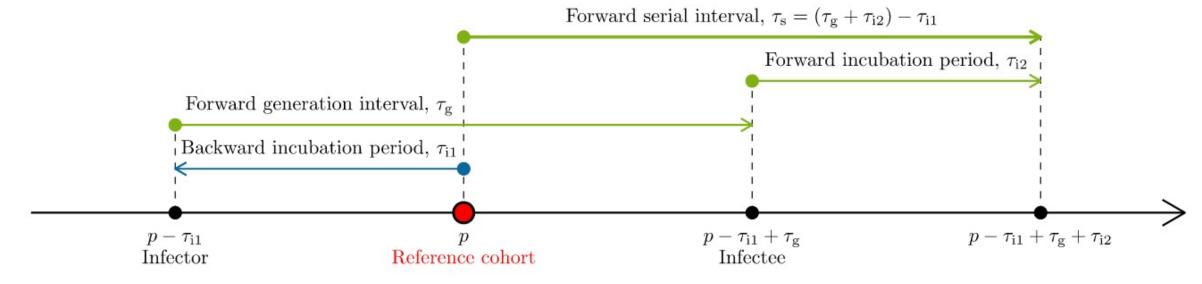
(intrinsic incubation period of the infectee)

Mean Intrinsic serial interval = Mean intrinsic generation interval





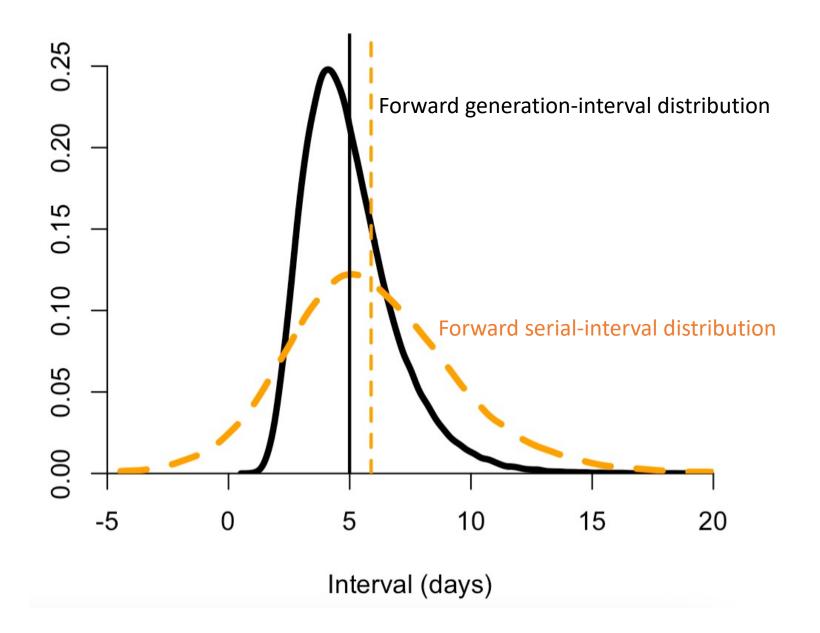
B Forward serial interval

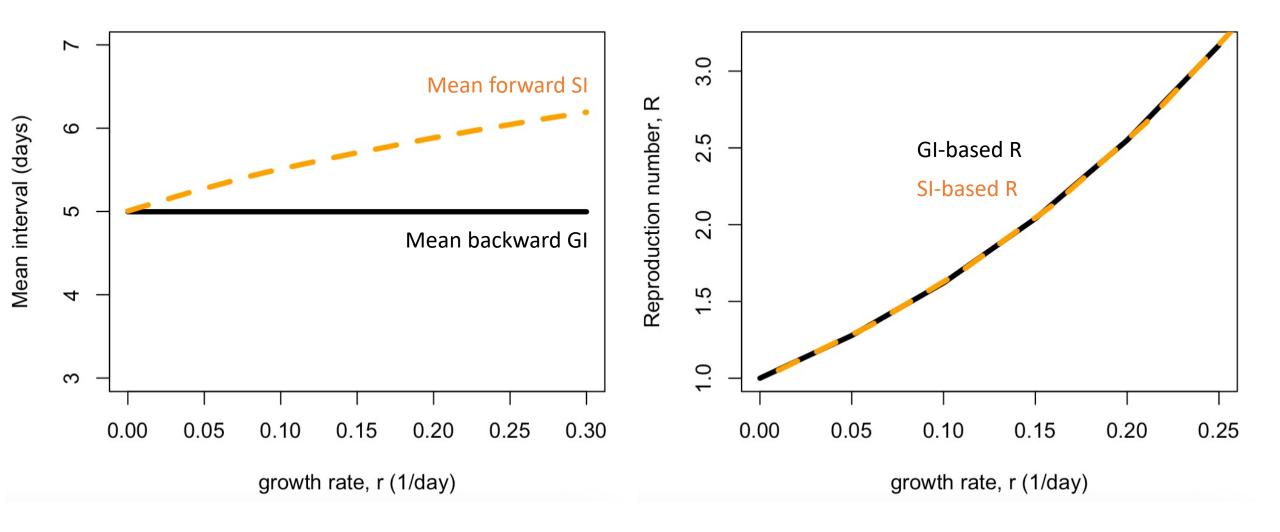


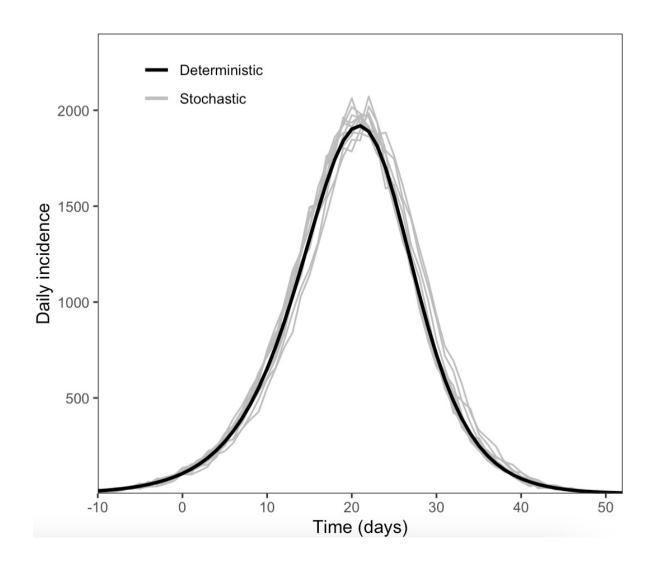
Forward serial interval = -(backward incubation period of the infector) +

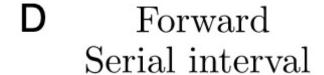
(forward generation interval) +

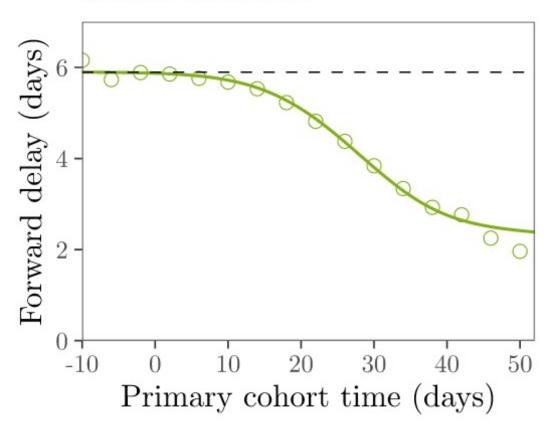
(forward incubation period of the infectee)

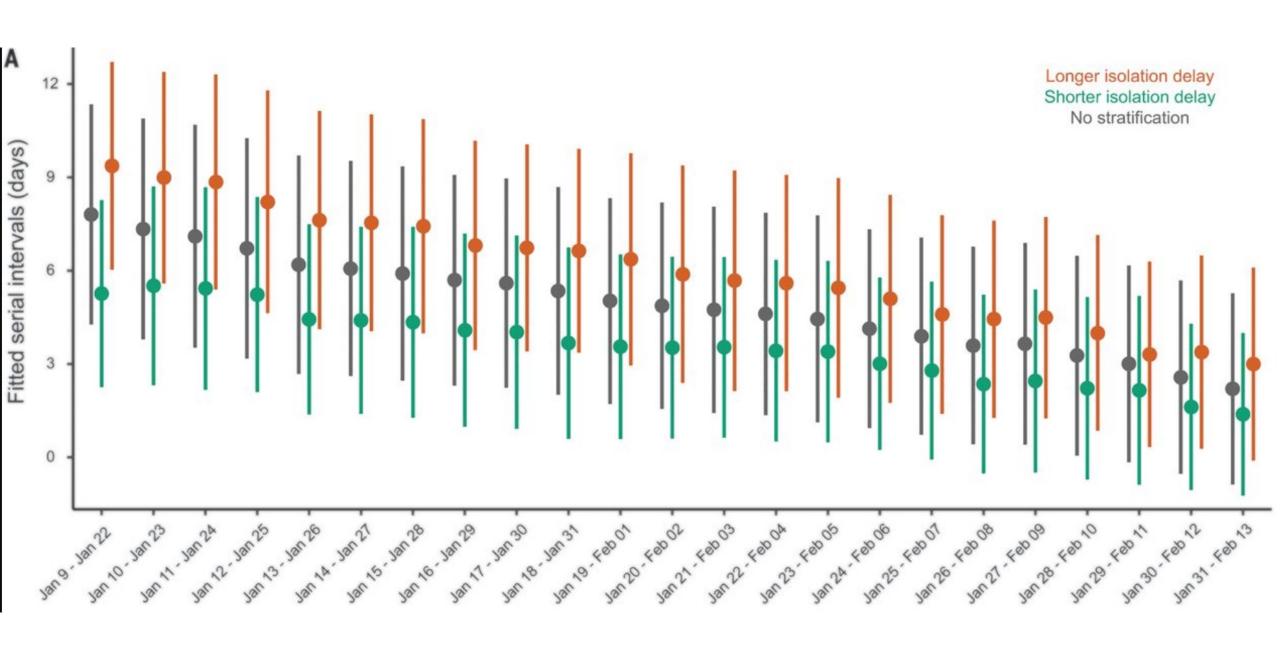






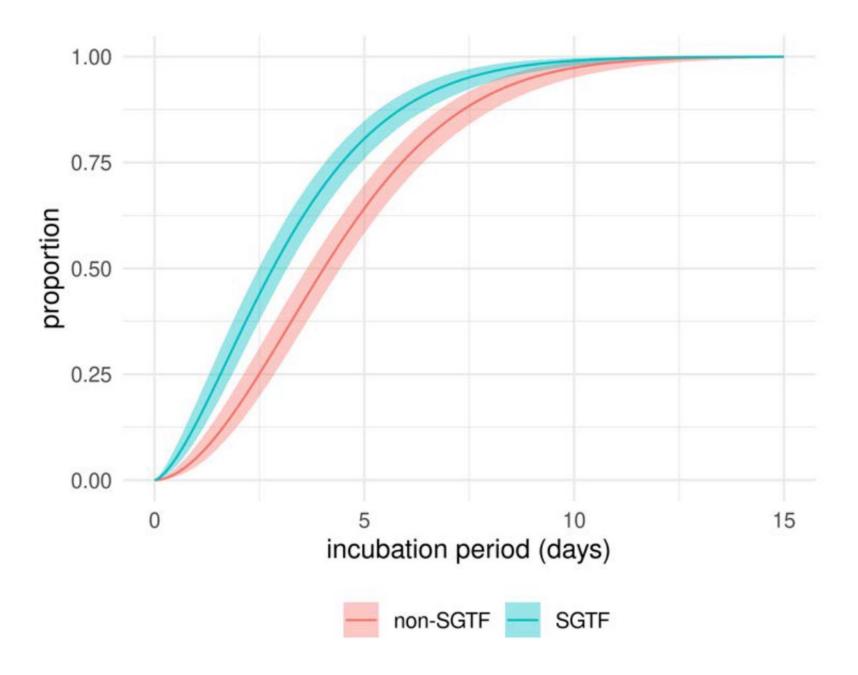


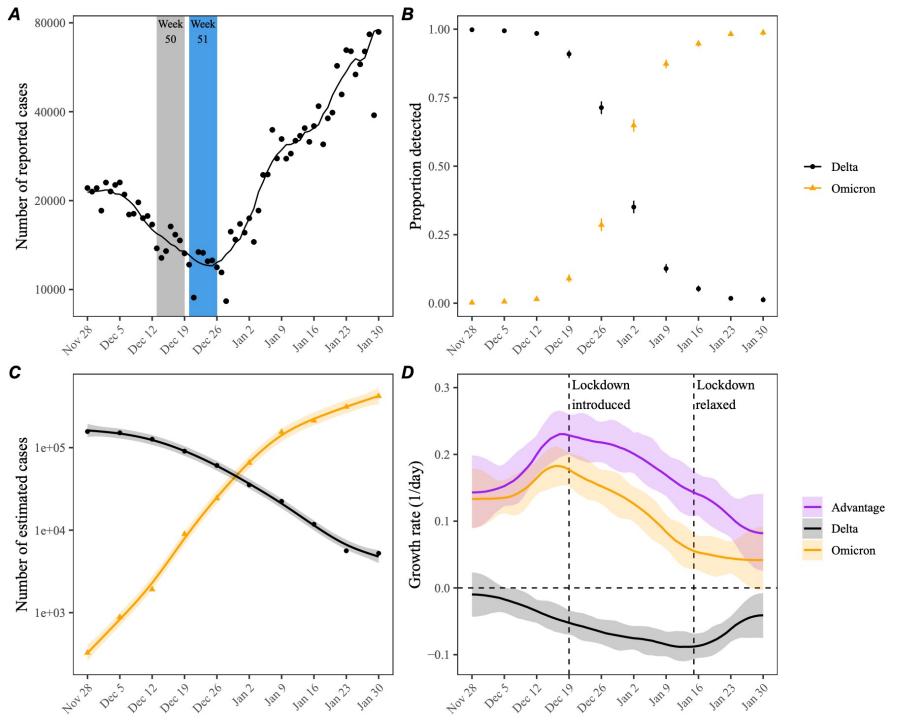




Application: incubation periods and generation intervals of the Omicron variant

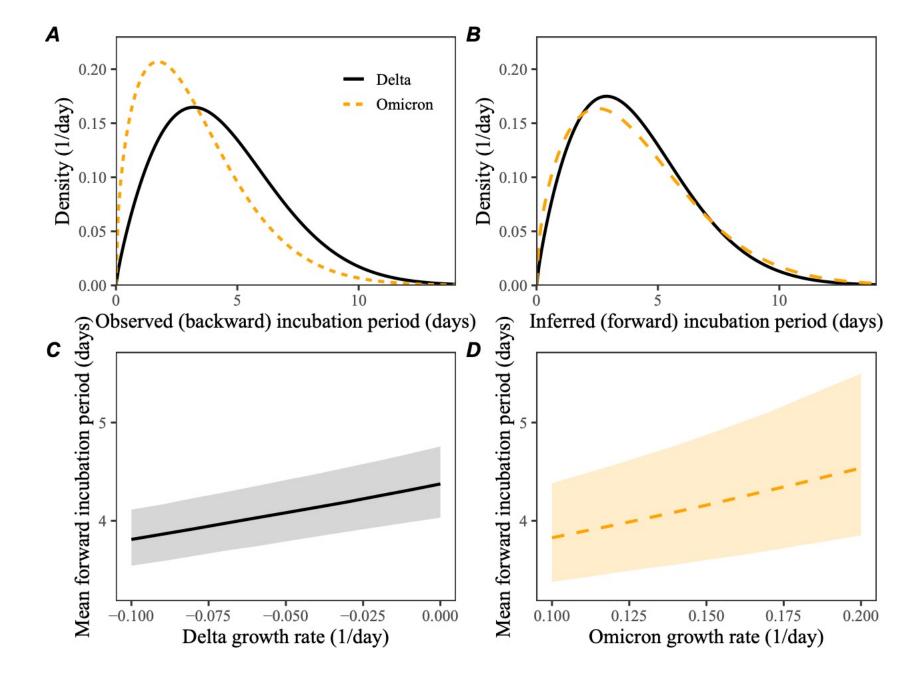
Does the Omicron variant have shorter incubation periods and generation intervals than the Delta variant?

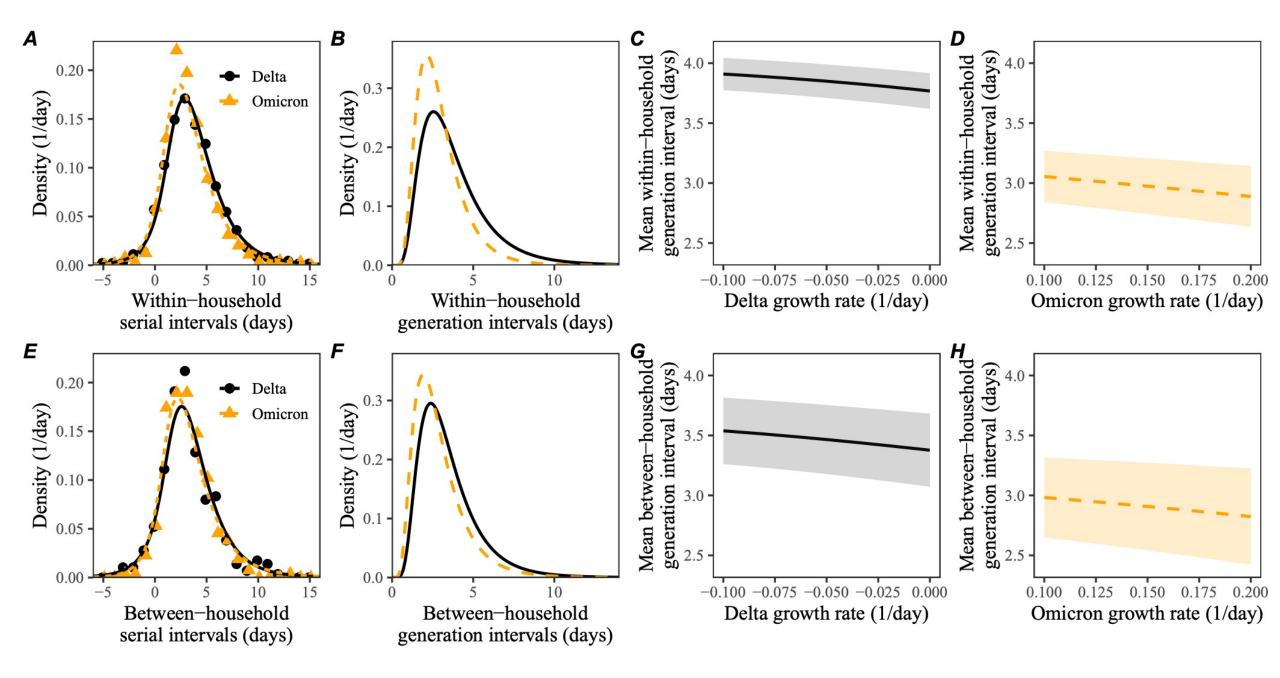


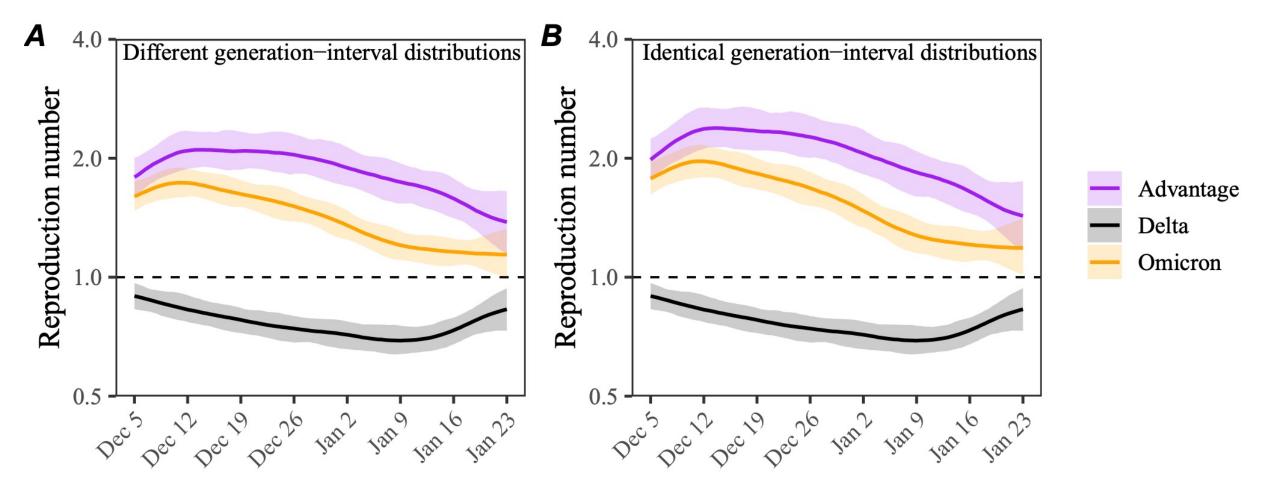


 Epidemic growth: shorter incubation periods for the Omicron variant

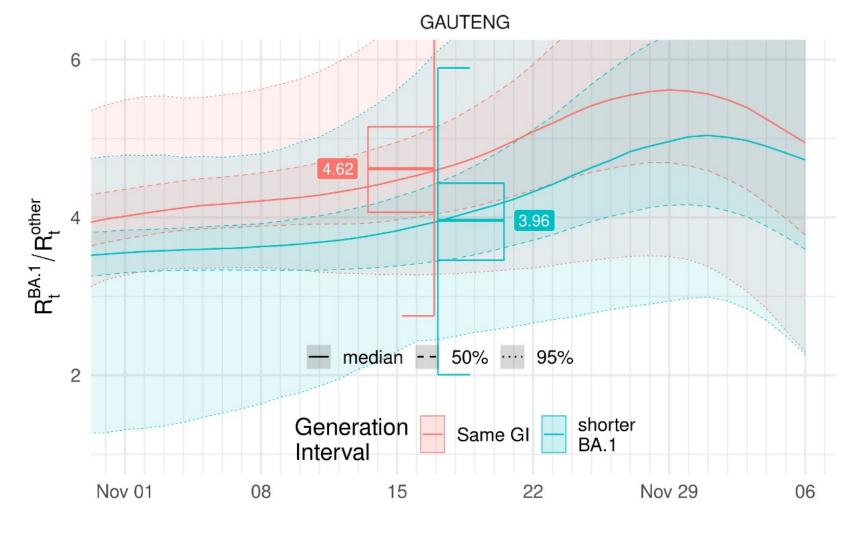
 Epidemic decay: longer incubation periods for the decay variant







~10% bias



- Previous estimate:
 >4 fold
 reproduction
 advantage
- Revised estimate based on our GI estimates: 2.6 fold reproduction advantage

Summary

- Accounting for dynamical biases are important for accurately estimating epidemiological delay distributions, especially when comparing variants with different growth rates
- Dynamical biases allow us to resolve the paradox between serial and generation intervals
- Neglecting uncertainties in variant generation intervals can lead to 10-50% difference in estimates of the Omicron transmission advantage

Acknowledgements

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- Jonathan Dushoff
- Bryan Grenfell
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Questions?