



Generation intervals in space

Understanding the effects of spatial and network structure on links between generation interval and growth rate

Jonathan Dushoff¹, Sang Woo Park¹, and David Champredon²

¹McMaster University, Hamilton, Ontario, Canada; ²York University, Toronto, Ontario, Canada

Introduction

- ▶ Generation interval (GI) measures time between when a person is infected and when that person infects another person
- ▶ GI distribution, $g(\tau)$, plays an important role in linking exponential growth rate, r , and reproductive number, \mathcal{R} , of an epidemic [1]:

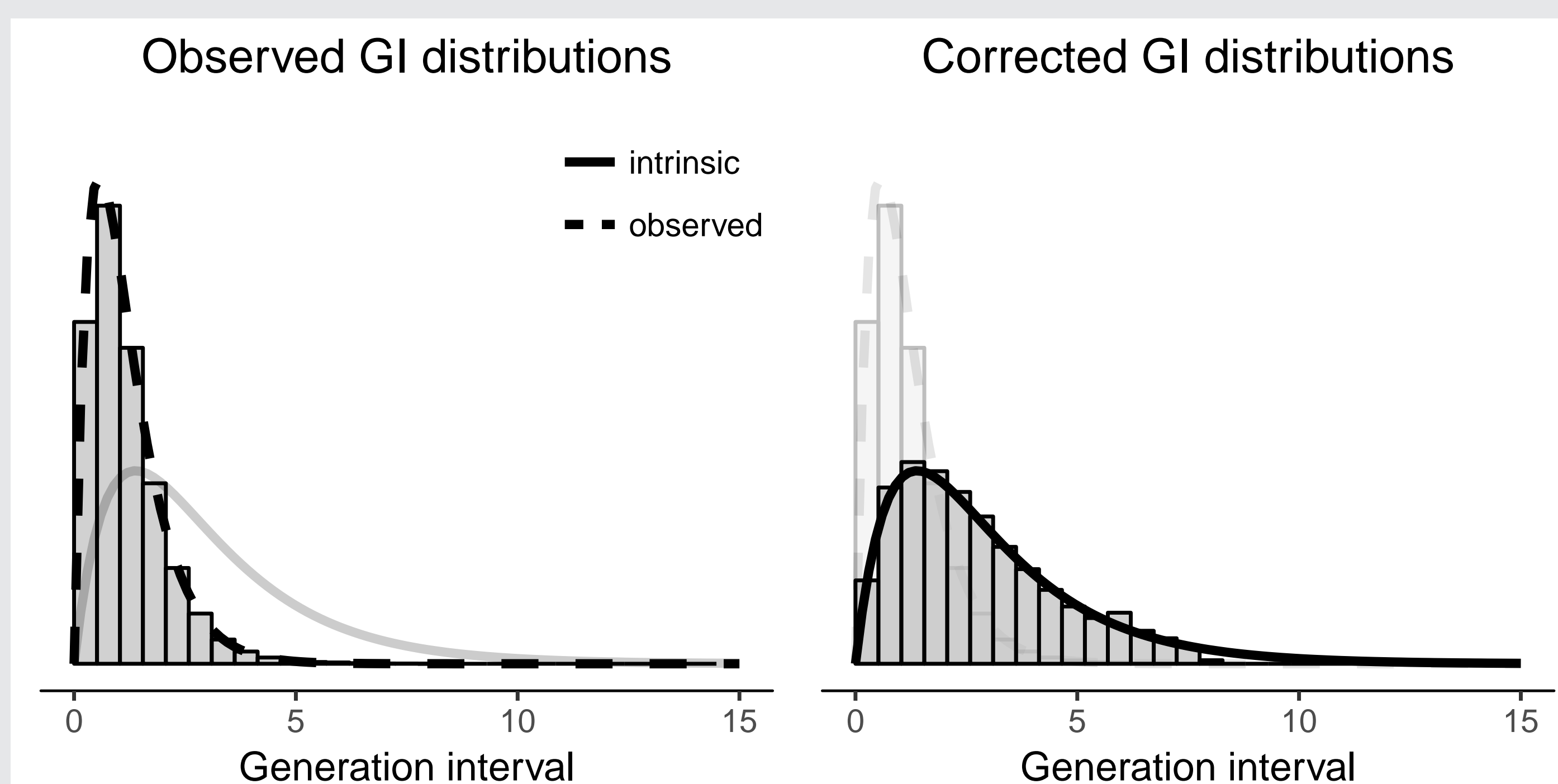
$$1/\mathcal{R} = \int g(\tau) \exp(-r\tau) d\tau$$

- ▶ Previous work showed that measuring GI through contact tracing data can introduce bias [2]
- ▶ Trapman *et al.* [3] demonstrated that network structure can affect \mathcal{R} ; ultimately, it changes GI distribution and $r - \mathcal{R}$ relationship

Different types of generation intervals

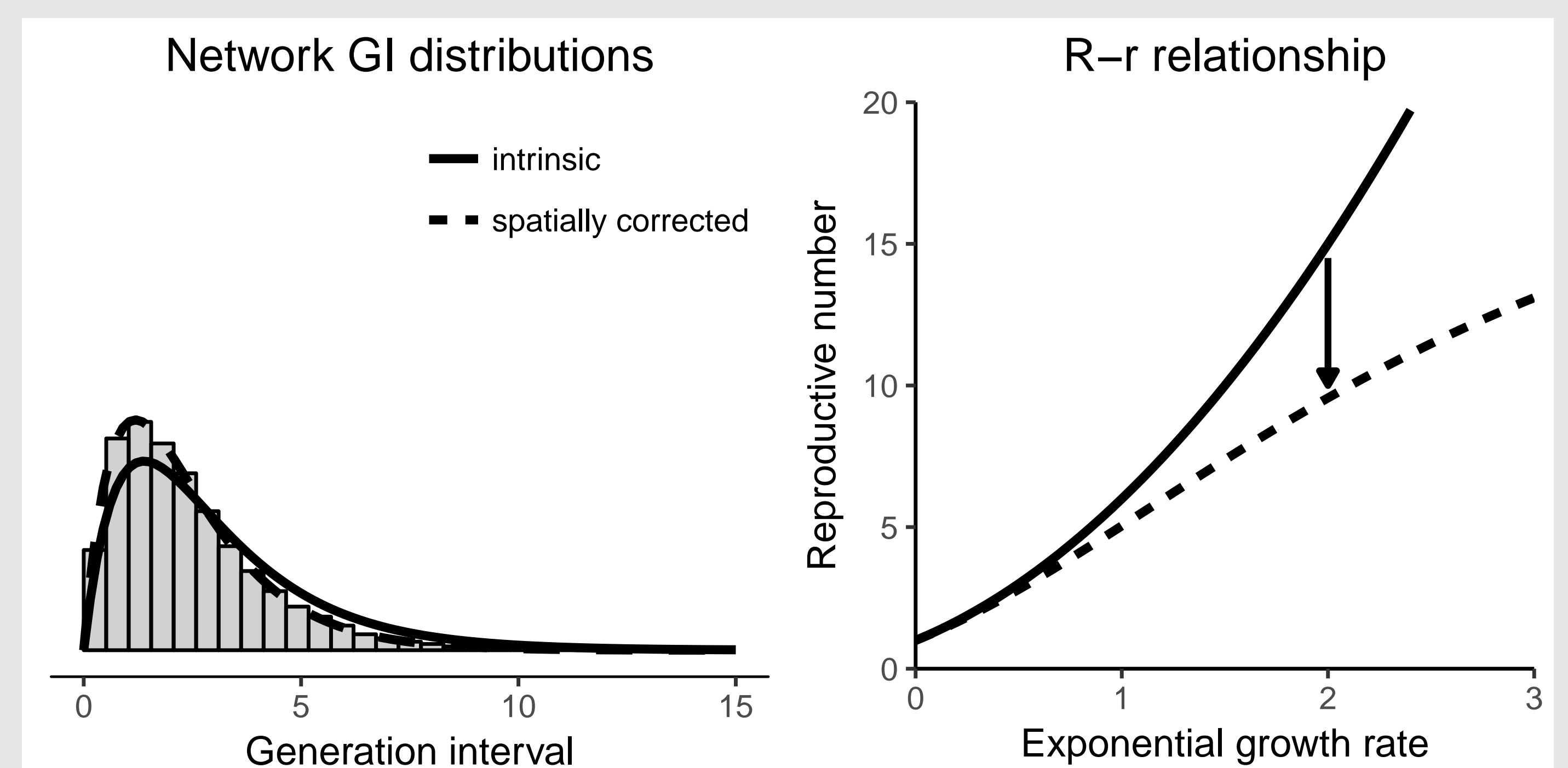
	Homogeneous	Spatially structured
Equilibrium	<ul style="list-style-type: none"> • intrinsic generation interval • can be measured using titer 	<ul style="list-style-type: none"> • shorter than intrinsic • can be approximated locally
Early	<ul style="list-style-type: none"> • observed during exponential phase • proportional to $g(\tau) \exp(-r\tau)$ 	<ul style="list-style-type: none"> • observed during outbreaks • measured through contact tracing

Temporal correction on a homogeneous network



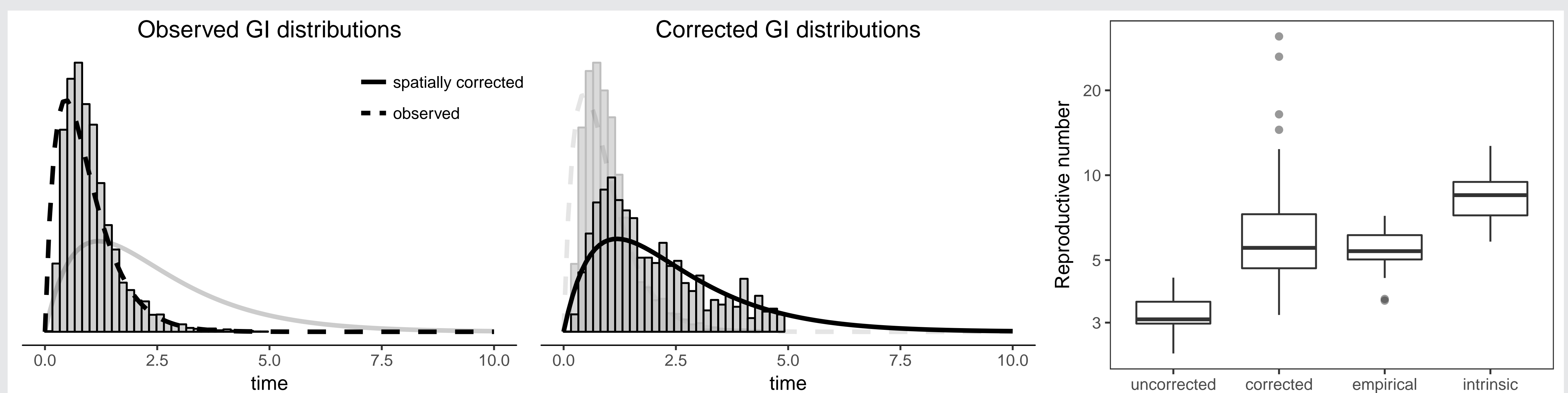
The intrinsic GI distribution can be recovered from an observed GI distribution during an outbreak by appropriately weighting the observed distribution. Solid line: intrinsic GI distribution. Dotted line: GI distribution expected to be observed during exponential growth phase. Histogram: (left) observed GI distribution simulated with a stochastic SEIR model on a homogeneous network (right) weighted histogram of observed GI distribution. Model parameters: $\mathcal{R} \approx 6$, population size at 60000, mean latent and infectious periods equal to 1 and 2 time units, respectively.

Local approximation to spatial effect



Local approximation predicts shorter mean GI and predicts saturating $r - \mathcal{R}$ relationship. (Left) Solid line: intrinsic GI distribution. Dotted line: intrinsic GI distribution accounting for spatial effect when $\mathcal{R} \approx 6$. Histogram: simulated GI distribution using local networks (Right) Solid line: expected $r - \mathcal{R}$ relationship using intrinsic GI distribution. Dotted line: expected $r - \mathcal{R}$ relationship accounting for spatial effect and degree distribution.

Simulation on an empirical network



Reproductive number predicted by using the corrected GI distributions matches empirical estimate of the reproductive number. Write something here????

Summary and future direction

- ▶ spatiotemporal effects makes GI shorter
- ▶ correcting an observed GI distribution is crucial to estimating \mathcal{R}
- ▶ temporal correction is sensitive to long infections and \mathcal{R} can be overestimated by a large factor
- ▶ ??

Bibliography

- [1] Jacco Wallinga and Marc Lipsitch. How generation intervals shape the relationship between growth rates and reproductive numbers. *Proceedings of the Royal Society of London B: Biological Sciences*, 274(1609):599–604, 2007.
- [2] David Champredon and Jonathan Dushoff. Intrinsic and realized generation intervals in infectious-disease transmission. In *Proc. R. Soc. B*, volume 282, page 20152026. The Royal Society, 2015.
- [3] Pieter Trapman, Frank Ball, Jean-Stéphane Dherin, Viet Chi Tran, Jacco Wallinga, and Tom Britton. Inferring r_0 in emerging epidemics: the effect of common population structure is small. *Journal of the Royal Society Interface*, 13(121):20160288, 2016.