



# Generation intervals in space

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

Jonathan Dushoff, Sang Woo Park, and David Champredon  
McMaster University, Hamilton, Ontario, Canada

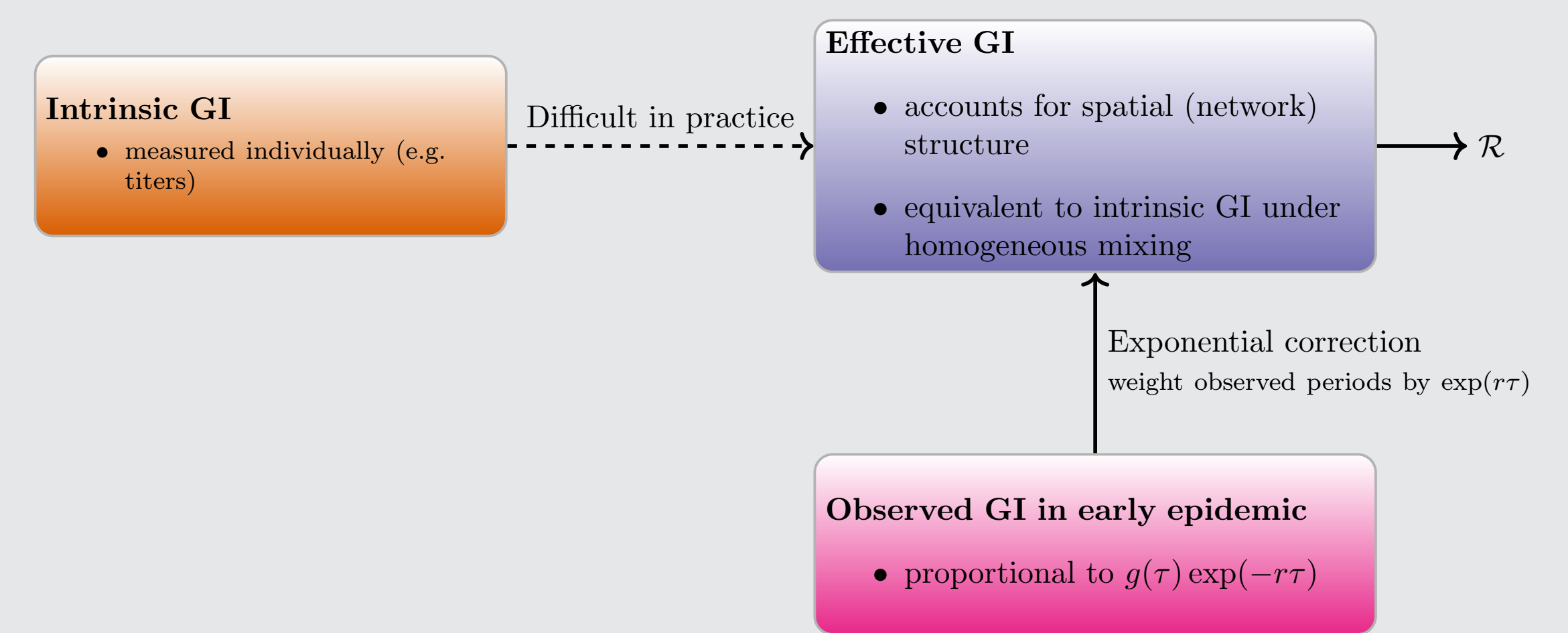
## Background

- ▶ 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]:

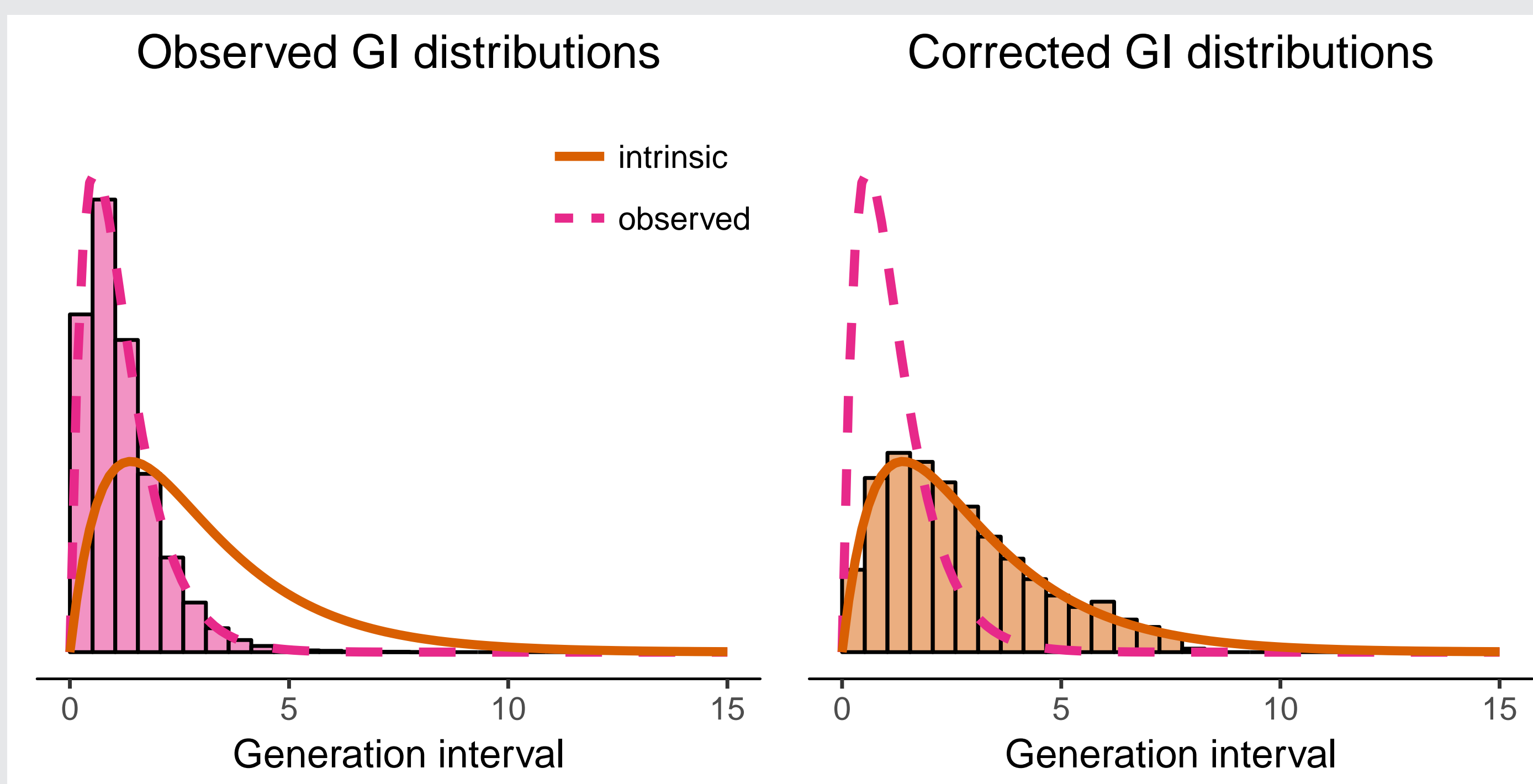
$$1/\mathcal{R} = \int g(\tau) \exp(-r\tau) d\tau$$

- ▶ 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

## Summary

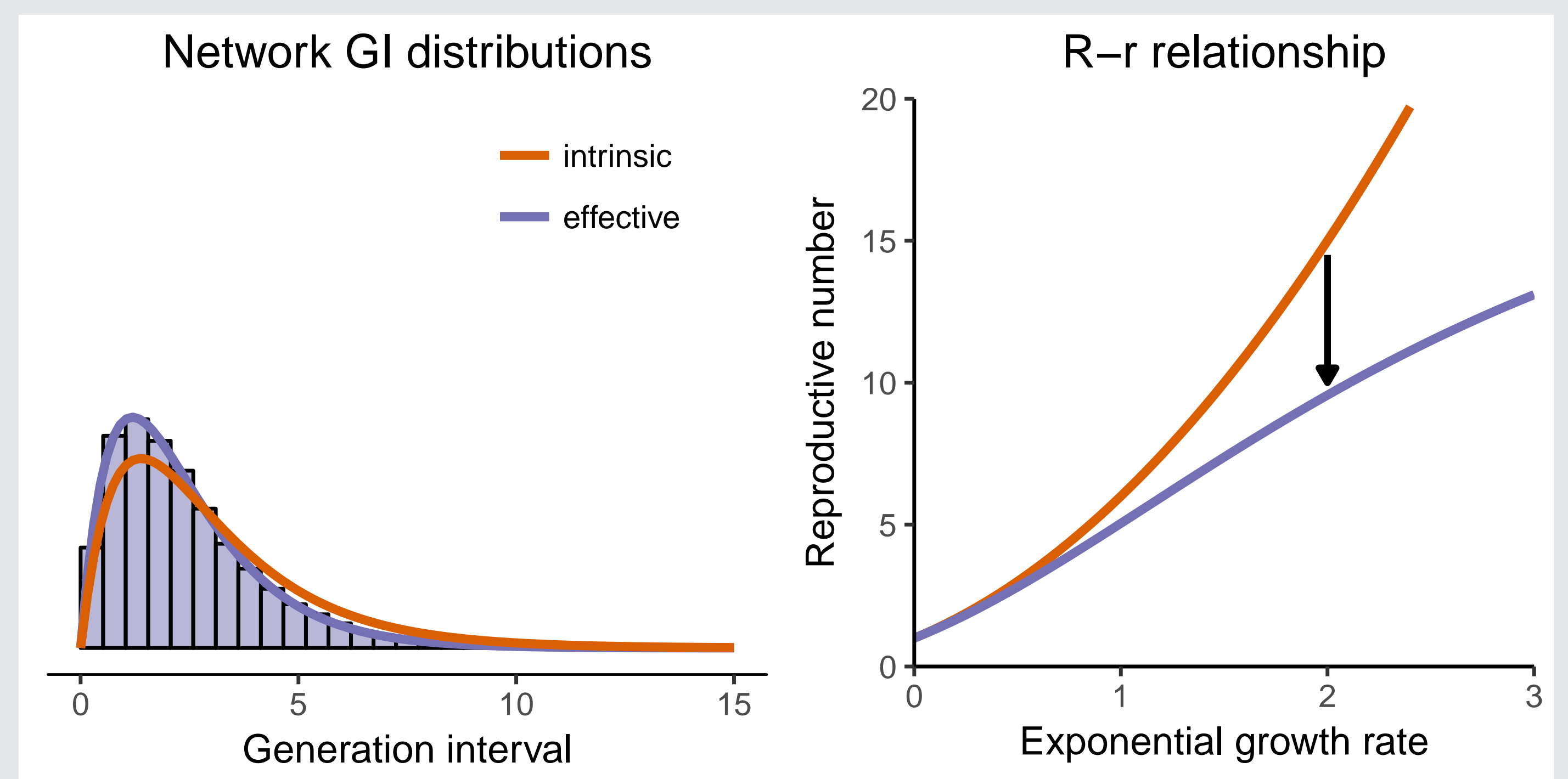


## Temporal correction on a homogeneous network



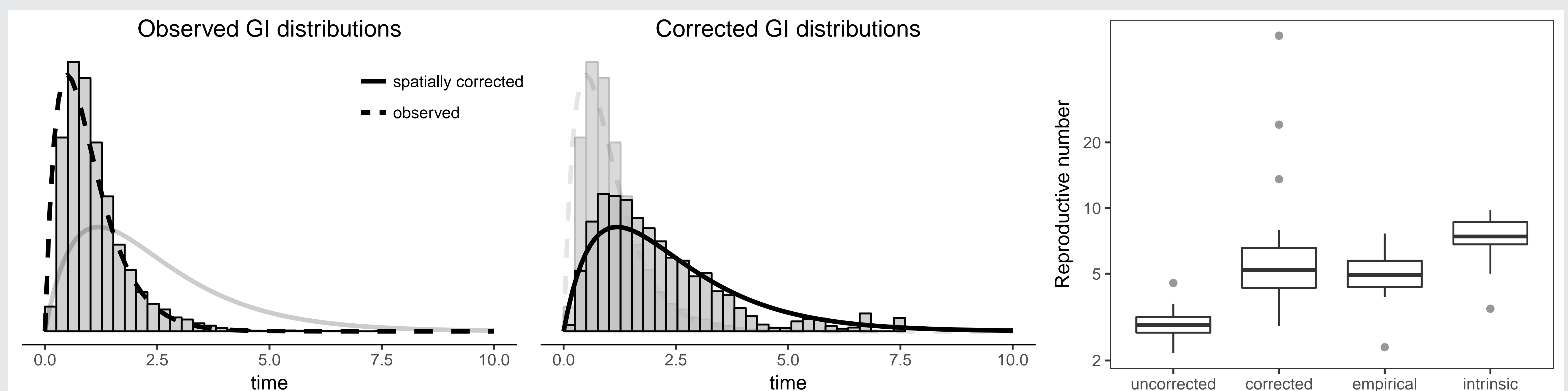
The intrinsic GI distribution can be recovered from an observed GI distribution during an outbreak by appropriately weighting the observed distribution. Solid line: intrinsic GI distribution. Dashed line: GI distribution expected to observed during exponential growth phase. Histogram: (left) observed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

## Local effect of spatial structure on GI distributions



Accounting for limited contacts in space shortens generation interval and predicts saturating  $r - \mathcal{R}$  relationship. (Left) Solid line: intrinsic GI distribution. Dashed line: effective GI distribution when  $\mathcal{R} \approx 6$  and mean excess degree  $\approx 21$ . Histogram: simulated GI distribution using local networks (a tree network with a single infected parent node). (Right) Solid line: expected  $r - \mathcal{R}$  relationship using intrinsic GI distribution. Dashed line: expected  $r - \mathcal{R}$  using effective GI 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.