



# Generation intervals in space

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

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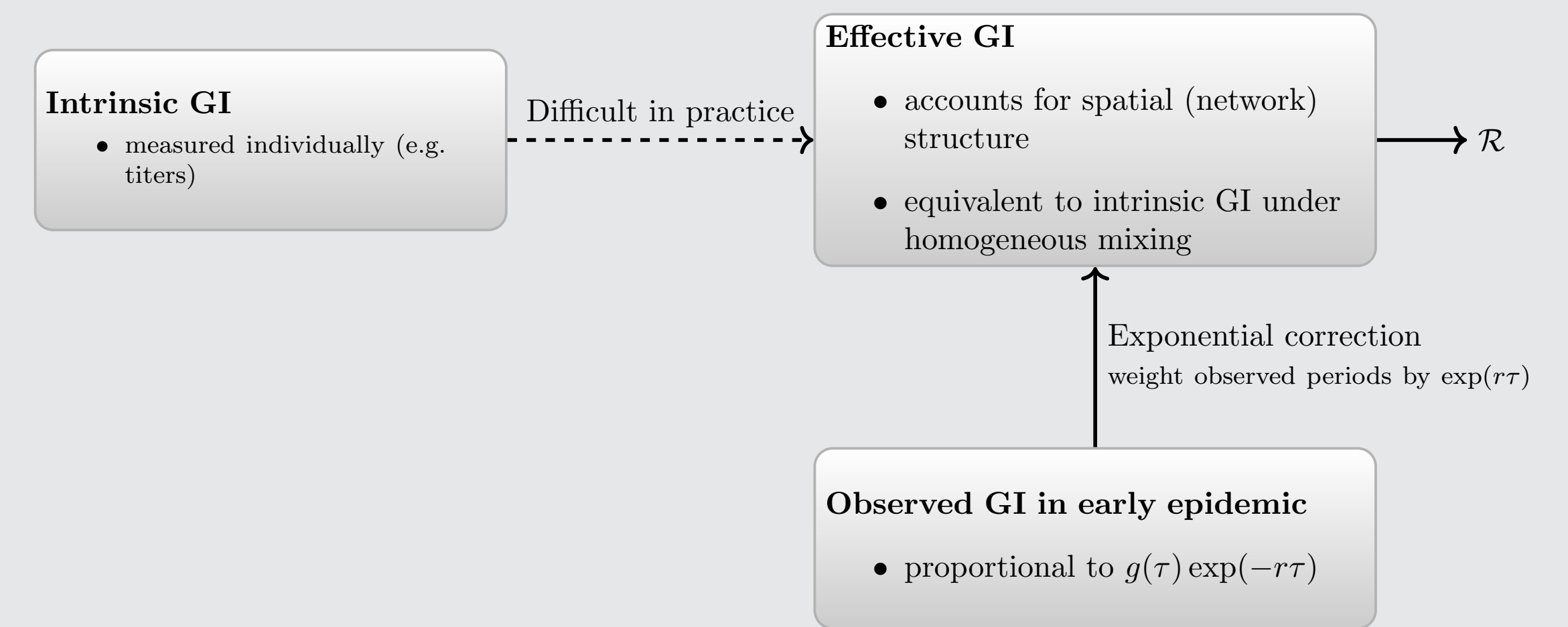
## Background

- ▶ 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]:

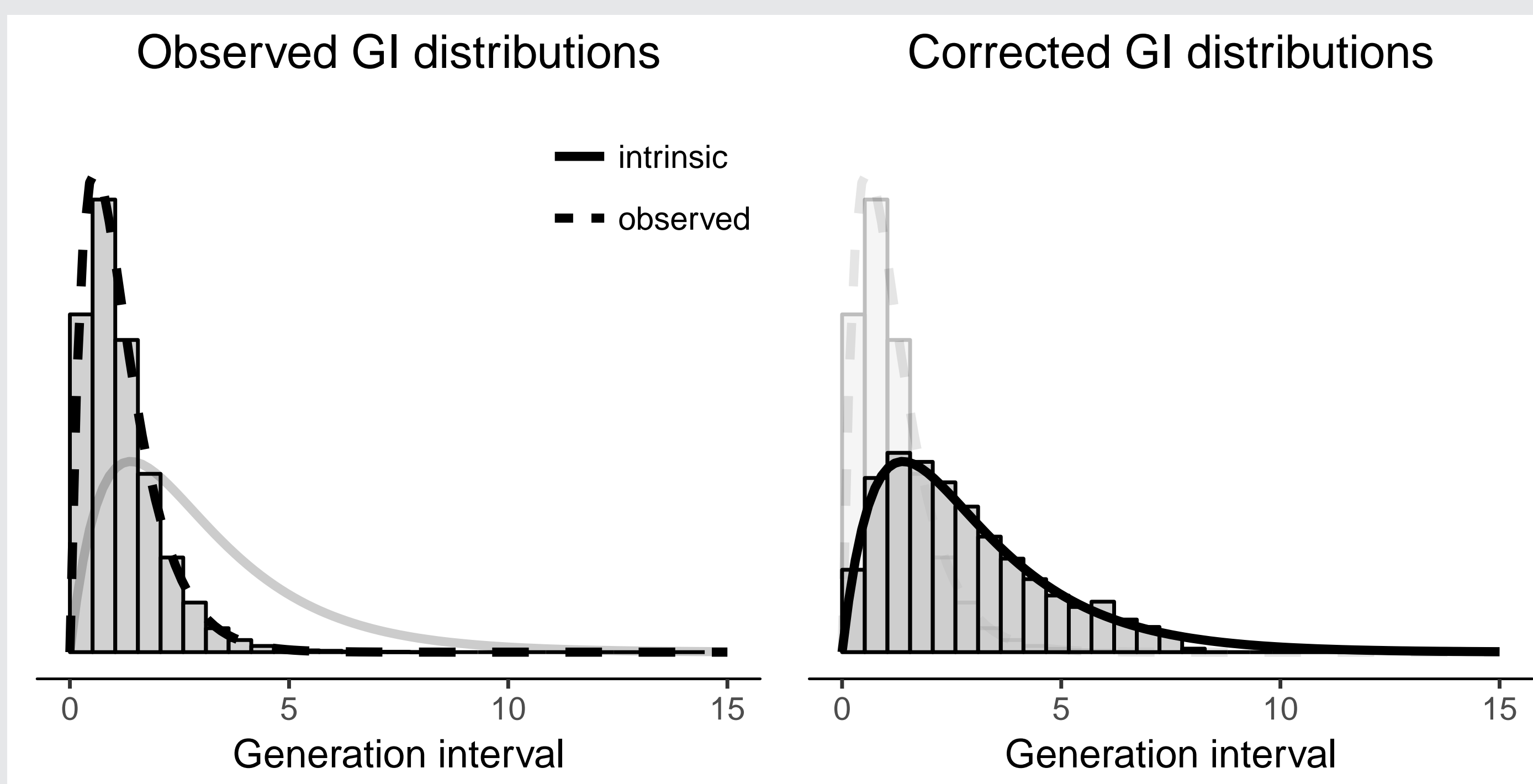
$$1/\mathcal{R} = \int g(\tau) \exp(-r\tau) d\tau$$

- ▶ 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

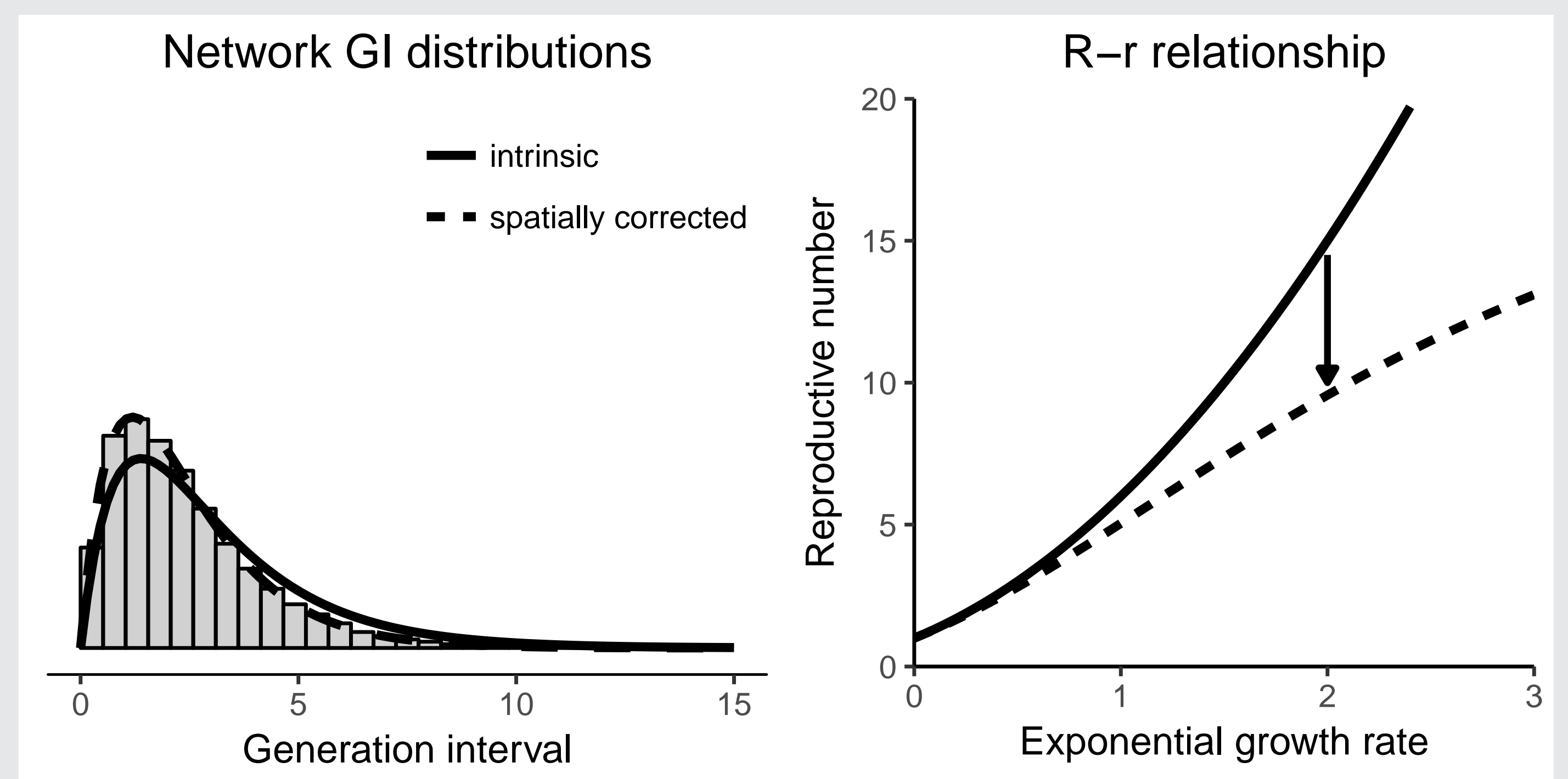


## Temporal correction on a homogeneous network



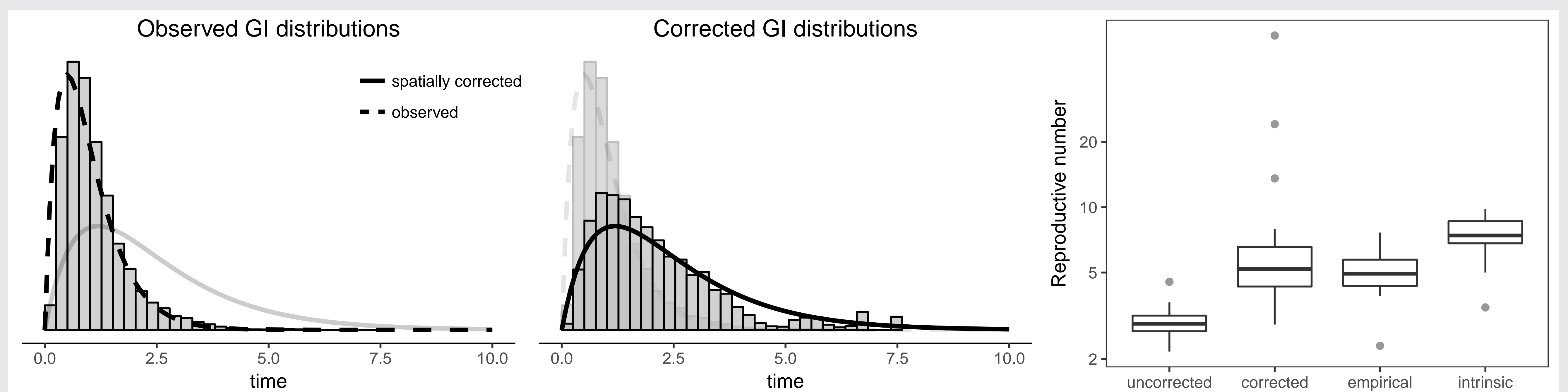
The intrinsic GI distribution can be recovered from an observed GI distribution during an outbreak by appropriately weighting the observed distribution. Solid line: intrinsic GI distribution. Dashed line: GI distribution expected to observed during exponential growth phase. Histogram: (left) observed 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.

## 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 intrinsic 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.