# **Epidemics on Dynamic, Empirical Networks**

Carl A. B. Pearson & Thomas J. Hladish Emerging Pathogens Institute, University of Florida



### Introduction

Contact networks are **intrinsically temporal**, but often analyzed as **time-aggregated** to simplify analysis and simulation. Simulation on empirical networks, however, may skip this aggregation with minimal additional complexity.

We consider such simulation on  $P\approx 10^6$  nodes, interacting via  $N\approx 10^6$  edges, over 5-years of geo-temporal co-location data, derived from municipal WiFi access at businesses. We start with a review of network measures for different aggregation windows on that data, and conclude comparing simulated infections on these dynamic networks.

# **Materials**

Network analysis and epidemic simulation used EpiFire[1]. Visualization and poster prepared with Rweave, source @ github.com/pearsonca/epidemics4-talk.

## Methods

Network measures computed in the standard way, after edges are determined on a per-time-period basis. An edge exists between individuals if their access periods at a location overlap during a time period.

The epidemic is simulated given three parameters:

- ightharpoonup transmission probability along a contact per simulation time, ho,
- ightharpoonup latent period,  $\lambda_L$ , and
- lacktriangle infectious period,  $\lambda_I$

We selected the  $\lambda$ s from literature estimates for influenza. We fit  $\rho$  for each binning scale to reproduce mean final size literature estimates for influenza. The simulation proceeds as typical for a static contact network, however as time passes one of the binning boundaries, edges are added and removed accordingly.

# **Mathematical Section**

Probably not relevant. Maybe restate the network measures? Diagram SIR flow?

# Conclusion

The aggregation of empirical observations has important implications for simulation results.

# References

Thomas Hladish, Eugene Melamud, Luis Barrera, Alison Galvani, and Lauren Meyers. Epifire: An open source c++ library and application for contact network epidemiology. *BMC Bioinformatics*, 13(1):76, 2012.

### Results

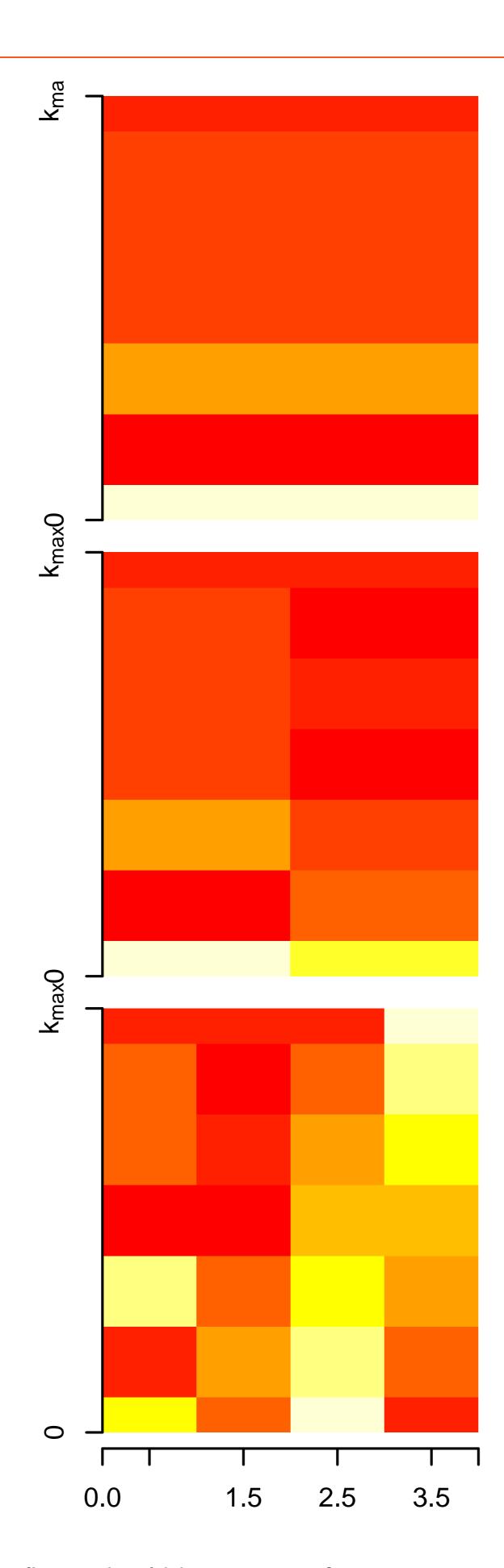


Figure: The first figure should be a series of comparisons of network measures (e.g., degree distribution) for the totally aggregated network vs averaged values of the network aggregated at different time periods - 1 year, 1 month, 1 week, 1 day. May also want to do some heat charts of those measures through time, since the averages might hide neat insights like seasonality. I also think we could use some plots of something approximating edge weights — like the distribution of edge duration proportion (time edge exists as fraction of interval).

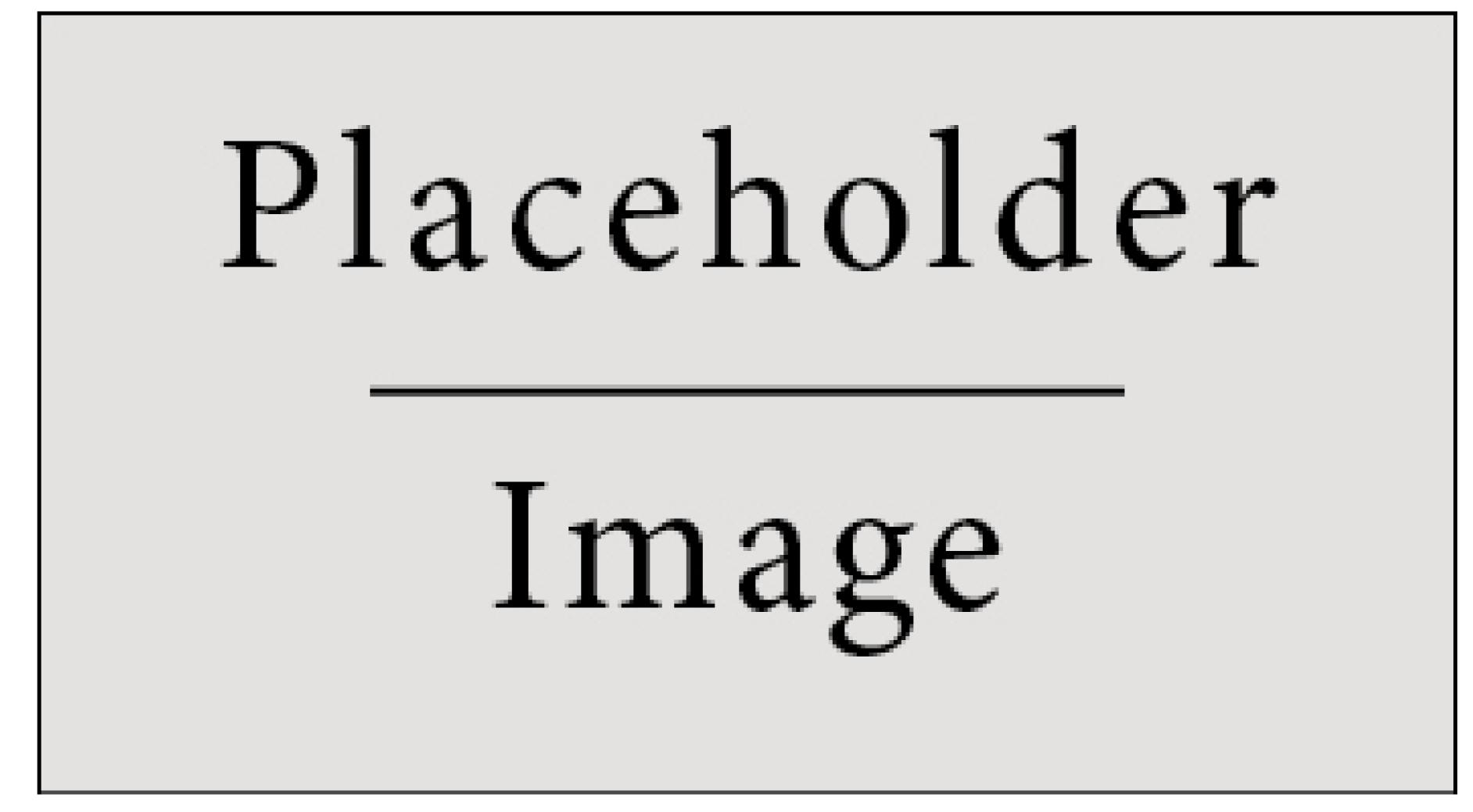


Figure: This should be the figure showing the simulation results for aggregation on whole network vs having day-by-day networks. Probably should be two figures, one for final sizes and one for trajectories. If we have time, multiples of these for some parameter variation.