

# Epidemics on Dynamic, Empirical Networks

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## 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  **$P \approx 2 \times 10^6$  nodes**, interacting via  **$N \approx 2 \times 10^6$  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

Data preparation with R and Scala. Network analysis and epidemic simulation with EpiFire[1] (new features to be formally documented in future publication, development code now available). Visualization and poster with R and Rweave. Source @ [github.com/pearsonca/epidemics4-talk](https://github.com/pearsonca/epidemics4-talk).

## Methods

The raw data have three issues: some logouts before logins, missing logout times, and overlapping logins for a single user at a location. The first issue was resolved by swapping the times; this affected  $\approx 10$  rows, and the swapped durations were consistent with other durations for those users. For the missing logout times, we set them to their login times; this still allows those visits to intersect with other users. Finally, we union all login periods to address to the overlapping periods. The network measures for reference are the maximum component size and maximum degree, computed according to the standard definition for the edge configuration in each time period. An edge exists between individuals if their access at a location overlaps during a time period. The epidemic is an  $S \rightarrow E \rightarrow I \rightarrow R \rightarrow S$  model. simulated given three parameters:

- transmission probability along a contact per simulation time,  $\rho$ ,
- latent period,  $\lambda_L$ , and
- 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?

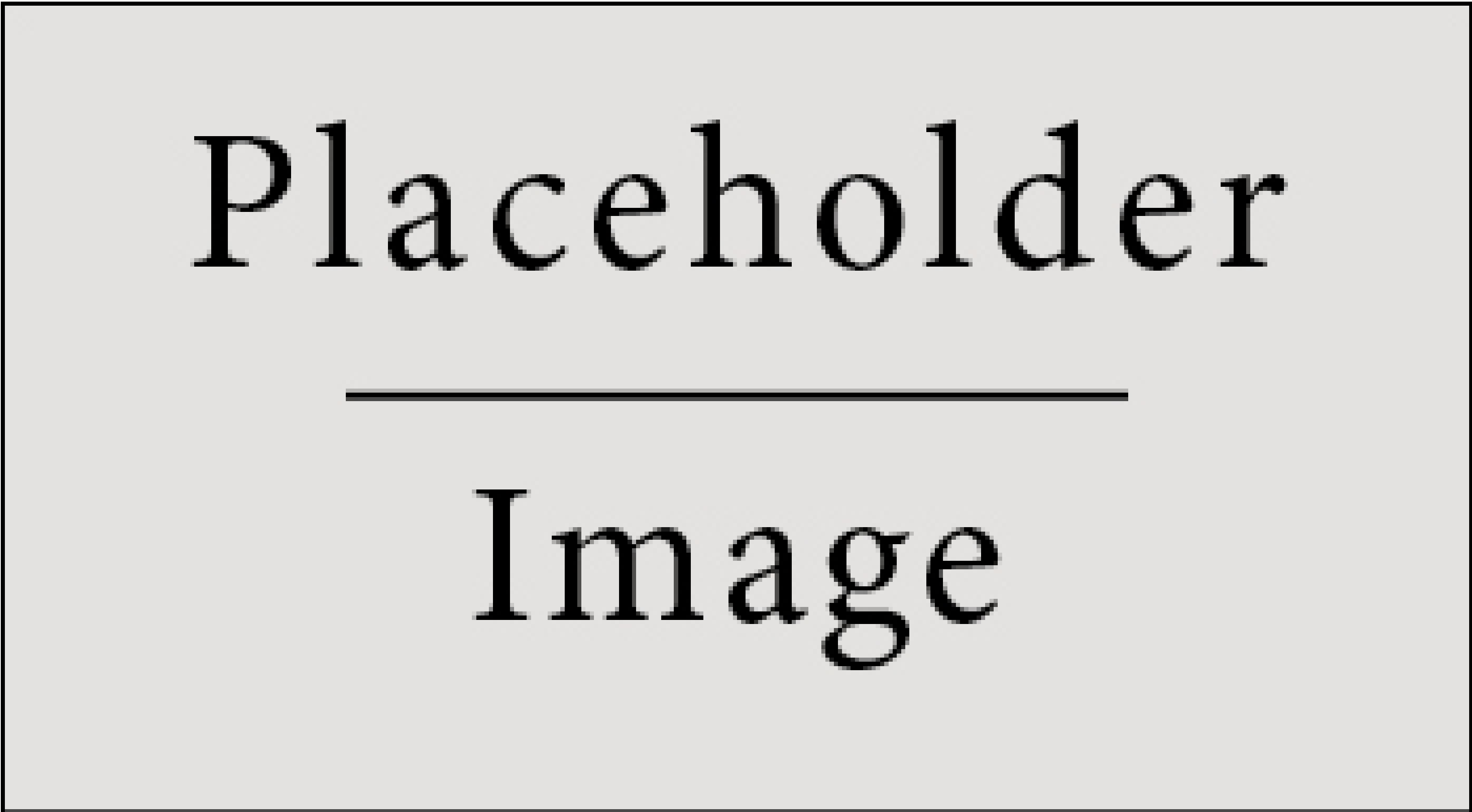
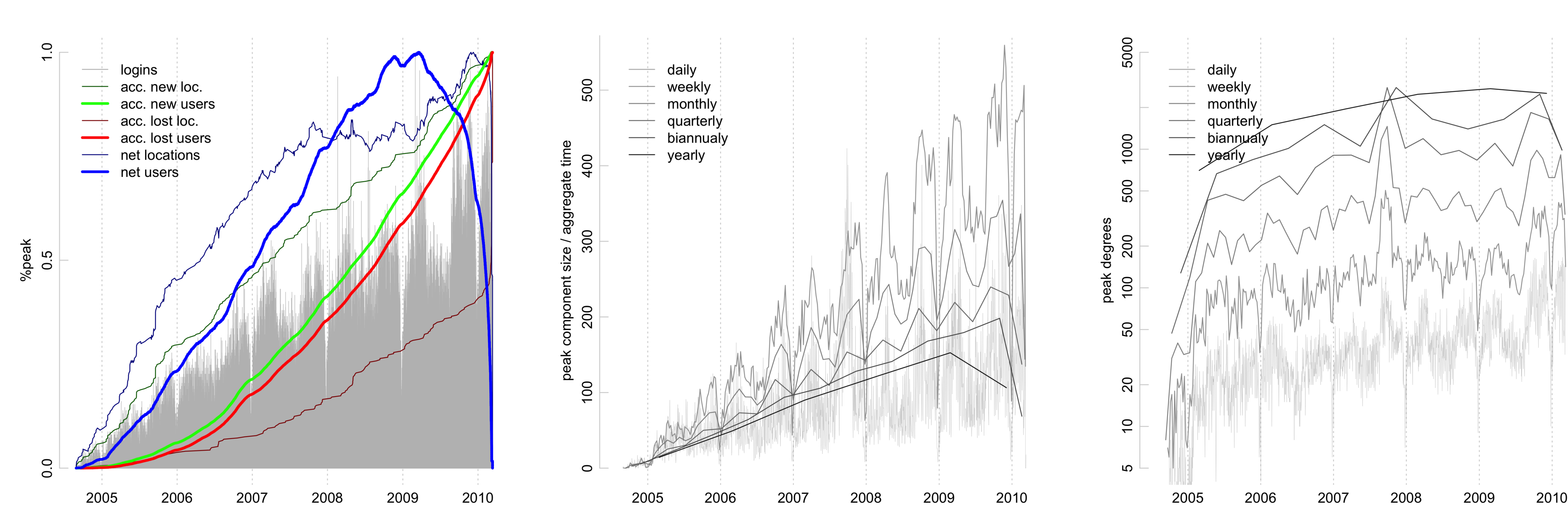
## Conclusion

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.

## Source Data Overview



**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.