

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, can incorporate temporal changes with minimal additional complexity. We consider such simulation on $\approx 2 \times 10^6$ **nodes**, interacting via $\approx 2 \times 10^6$ **edges**, over **5-years** of geo-temporal co-location data, derived from municipal WiFi access at businesses in Montreal[1]. 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[2] (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.

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 ≈ 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 each user’s login periods to address concurrent use from multiple devices. The network measures for reference are the maximum component size and maximum degree, computed using the edge configuration in each time period. An edge exists between individuals if their access at a location overlaps in time. The epidemic is an $\mathbf{S} \rightarrow \mathbf{E} \rightarrow \mathbf{I} \rightarrow \mathbf{R} \rightarrow \mathbf{S}$ model, simulated given four parameters:

- ▶ contact rate, $\beta = 2.0 \text{ contacts/day}$,
- ▶ latent period, $\mu = 1.2 \text{ days}$,
- ▶ infectious period, $\gamma = 4.1 \text{ days}$
- ▶ resistant period, $\omega = 365 \text{ days}$

We selected μ , γ , and ω from literature estimates for influenza. The resistant (immune) duration is the same for all individuals; other state durations are exponentially distributed. As each individual is infected, contact and state transition times are generated. As time passes, edges are added and removed when binning boundaries are reached. At contact times, a contact is chosen from the edges that exist at that moment.

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

■ Anne Gatewood Hoen, Thomas J. Hladish, Rosalind M. Eggo, Michael Lenczner, Alison P. Galvani, John S. Brownstein, and Lauren Ancel Meyers.
Epidemic wave dynamics attributable to urban community structure.
TBD, in review.

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

Source Data Overview

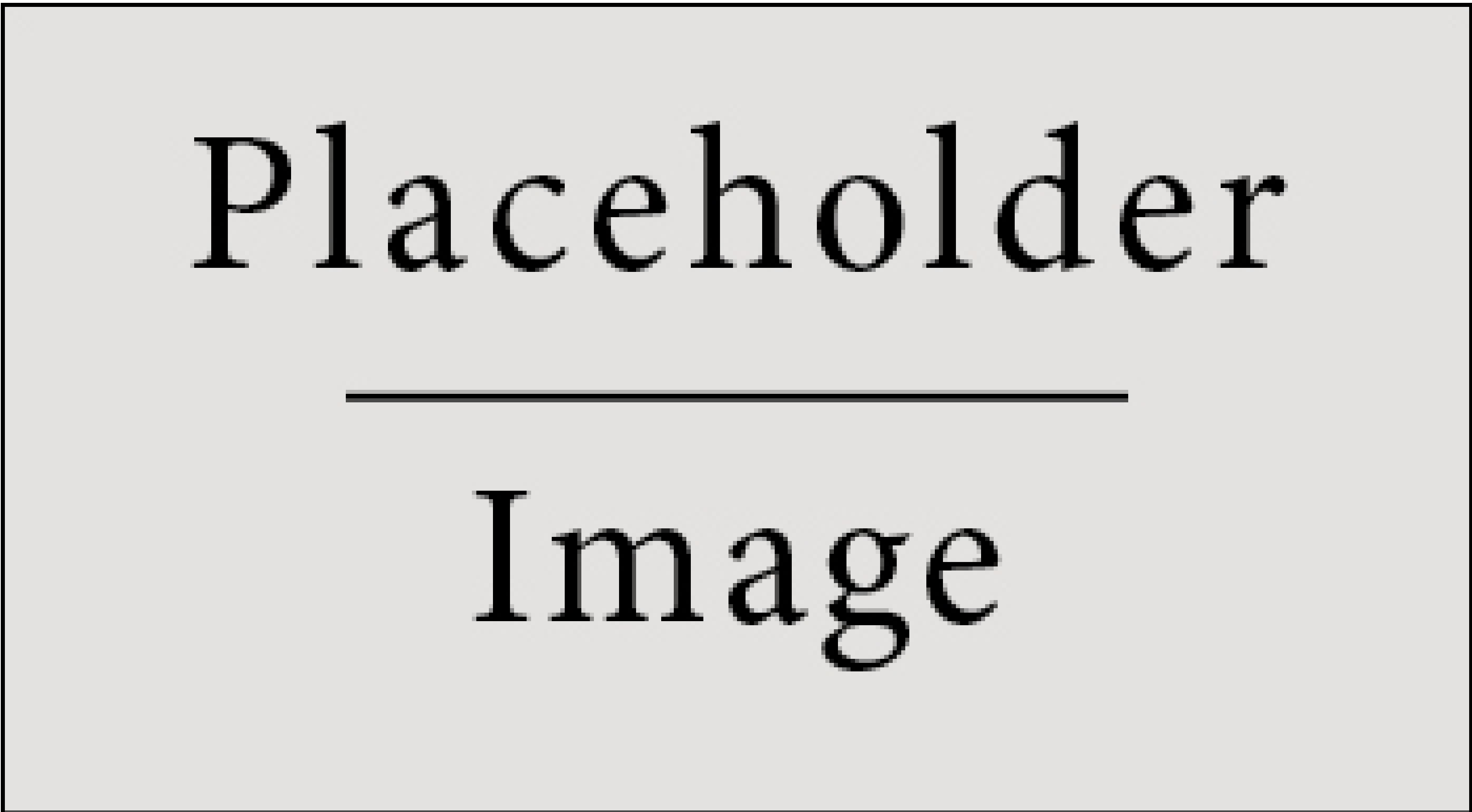
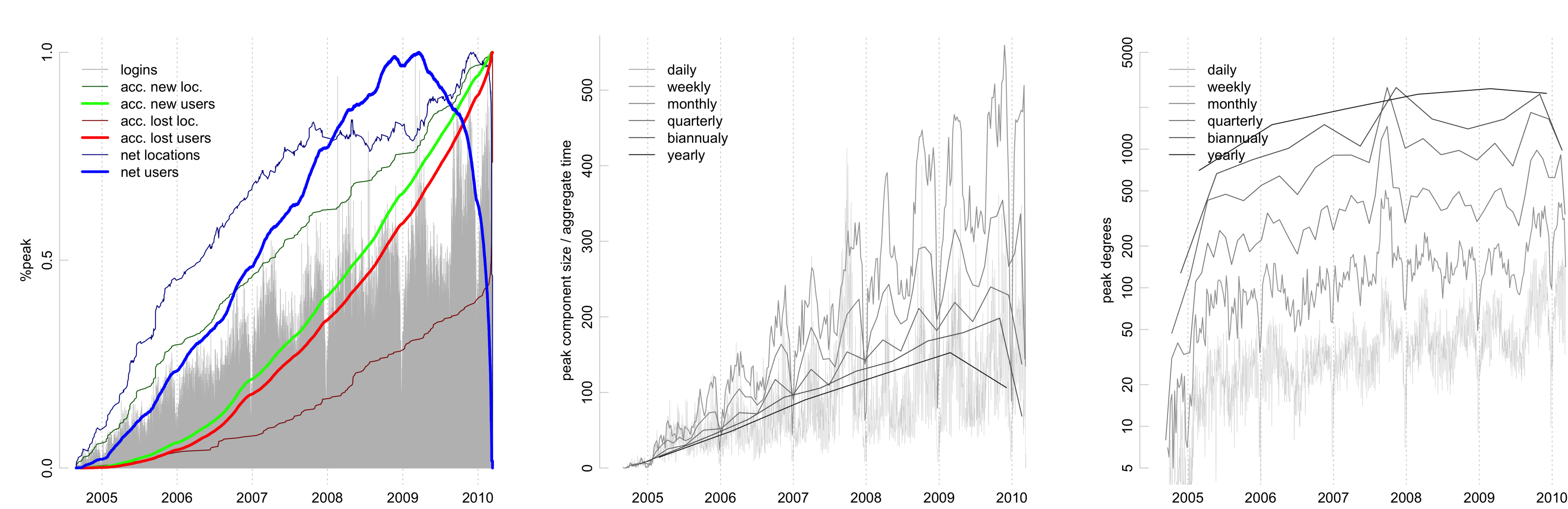


Figure: This should be the figure showing the simulation results for aggregation on whole network vs having day-by-day networks. Probably should be two figures, one for final sizes and one for trajectories. If we have time, multiples of these for some parameter variation.