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 $\mathbf{P} \approx 2 \times 10^6$ **nodes**, interacting via $\mathbf{N} \approx 2 \times 10^6$ **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

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:

- transmission probability along a contact per simulation time, $\boldsymbol{\rho}$,
- latent period, $\boldsymbol{\lambda_L}$, and
- infectious period, $\boldsymbol{\lambda_I}$

We selected the $\boldsymbol{\lambda}$s from literature estimates for influenza. We fit $\boldsymbol{\rho}$ 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?

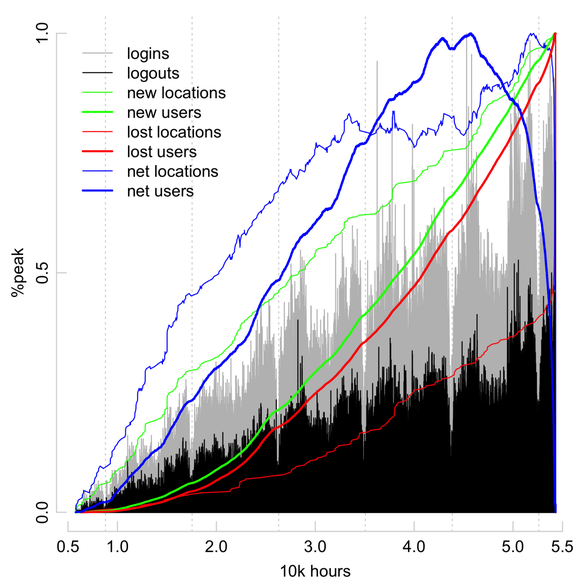
Conclusion

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



Placeholder

Image

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.