

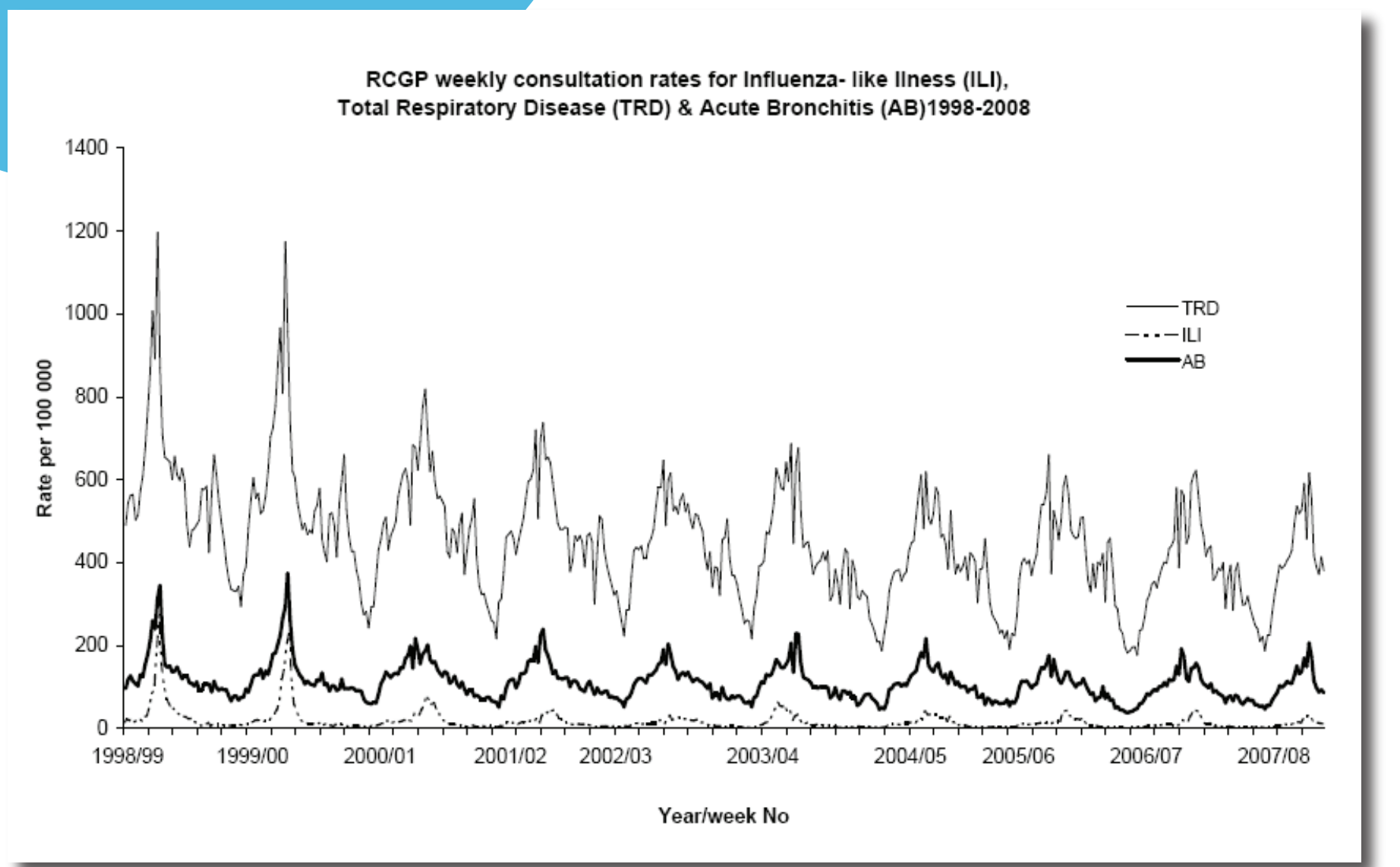
Contact Network Modeling of Flu Epidemics

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Epidemic spreading is an intricate biological and sociological process which involves multiscale events from the molecular level of virus-cell interaction to the physical behavioral patterns in a population. Using actual census, family and age structure, land-use and population-mobility data, we have developed a model and related software to study disease propagation. In particular, we address age dependency in epidemic spreading, in which we look into age-dependent locations, contact networks, infection propensities as well as vaccination techniques. As a case study we study influenza epidemics in the UK. The results indicate the relative merits of different vaccination strategies combined with early detection without resorting to mass vaccination of a population.

Influenza

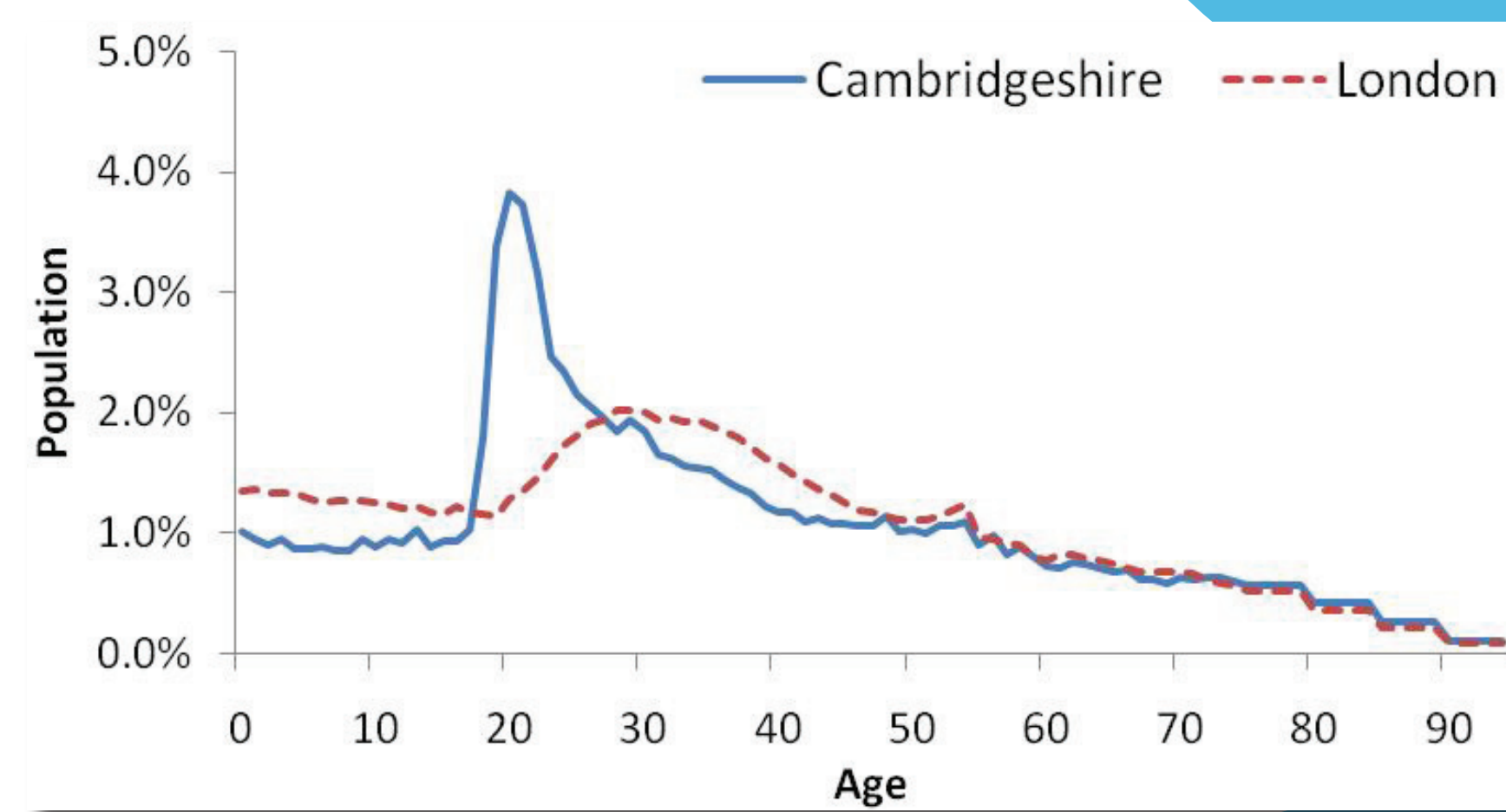
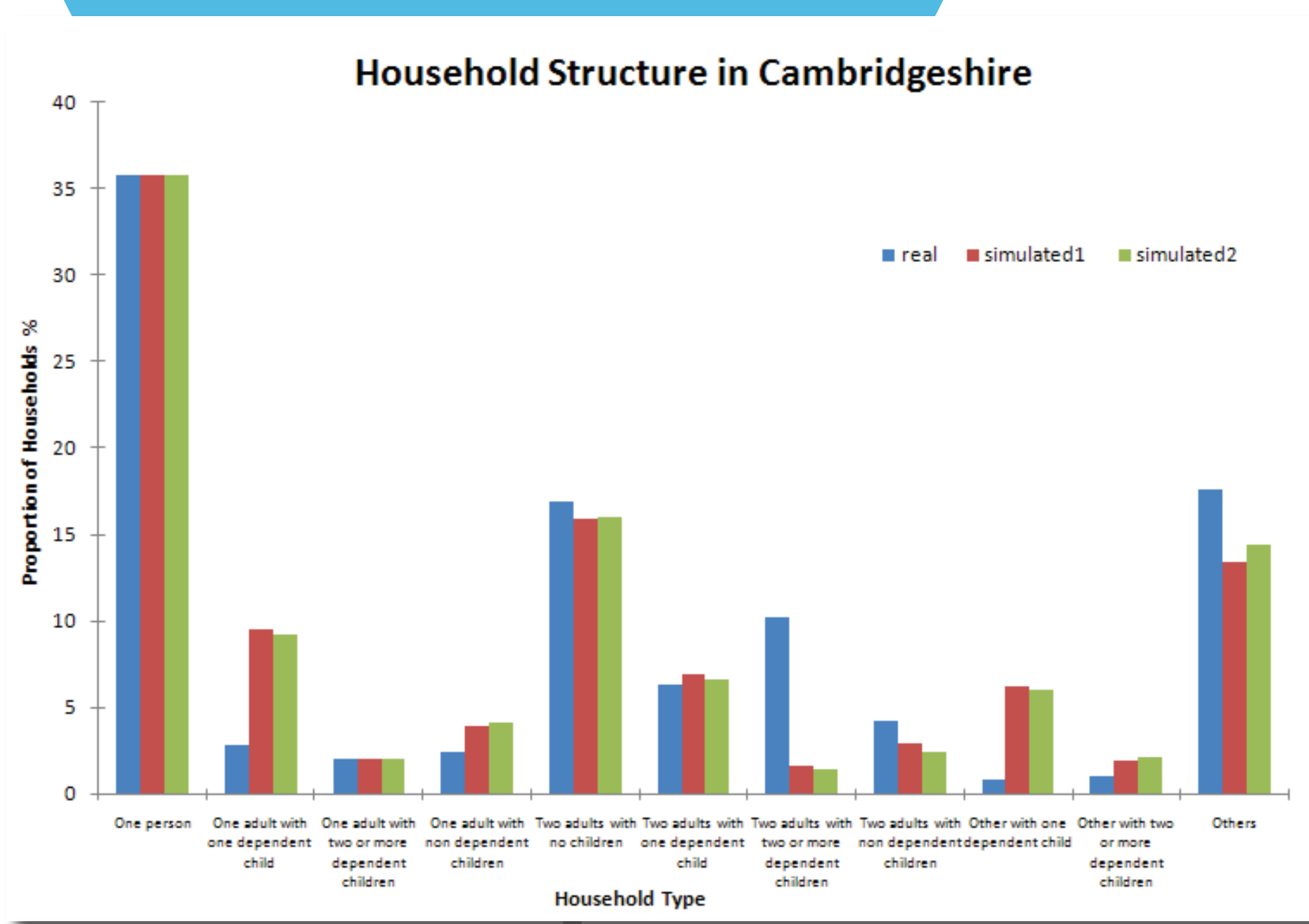
Influenza (commonly flu), known for its high prevalence, contagiousness and mutability, is the subject of investigation. Here we employ dynamic bipartite graphs to model the physical contact patterns that result from movements of individuals between specific locations. In particular, we address age dependency and obtain the contact networks through the analysis of location co-presence.



*Health Protection Agency UK National Influenza Season summary (<http://www.hpa.gov.uk>) (2007)

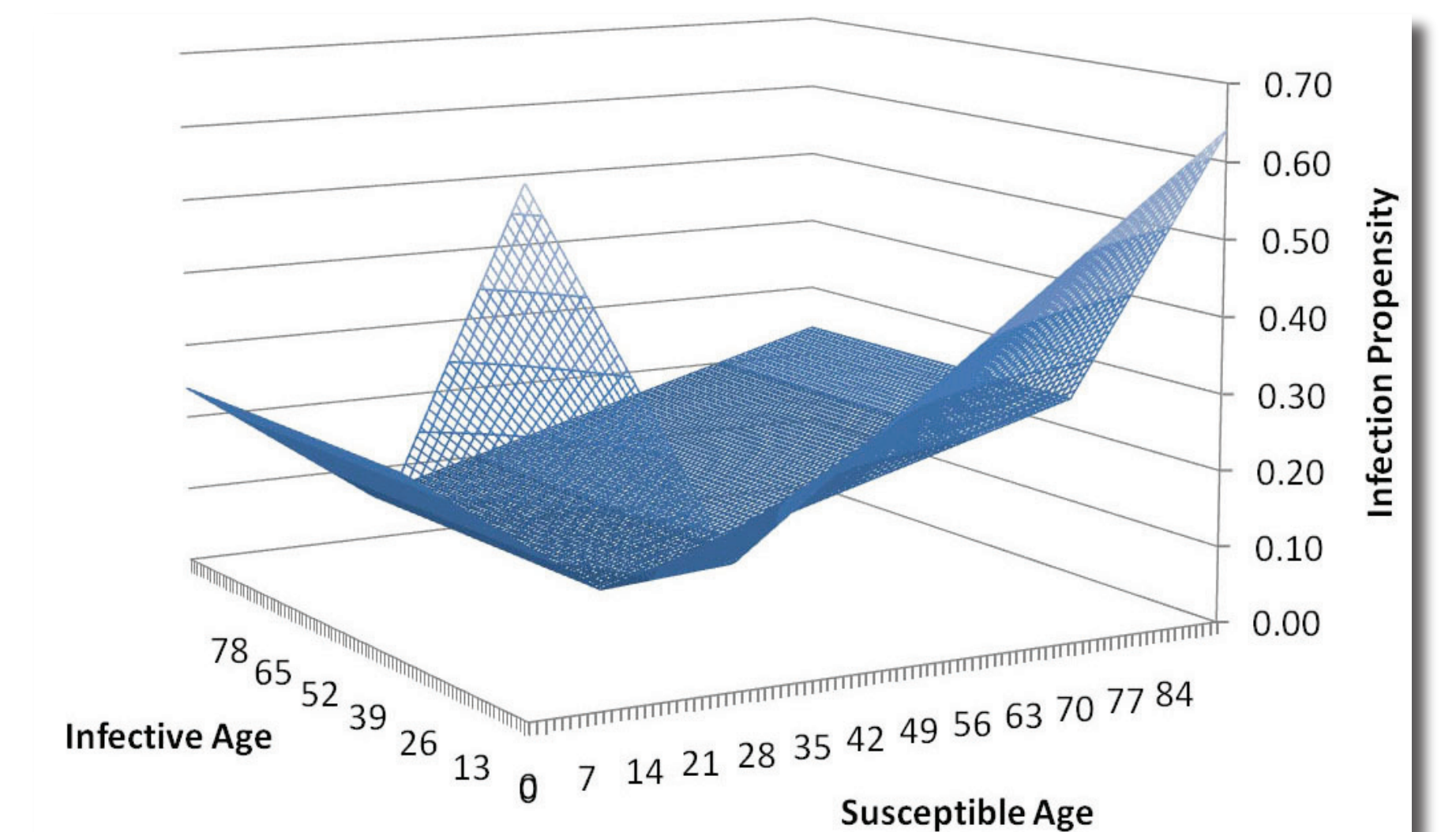
Demographics

Our model utilises large-scale demographic and mobility data based on actual census and land-use. These data dictates the mobility characteristics of nodes in the model. The simulated age distribution of the population structure corresponds to actual statistics from the UK Census 2001 (<http://www.statistics.gov.uk>).



Age Dependency

Brownstein (2005) showed that influenza spread firstly in children aged 3-4 years old. Following these findings and data from HPA, our model considers that flu season begins with preschoolers. We also take into account age dependency in disease infectivity, susceptibility, locations, social contact networks, etc.

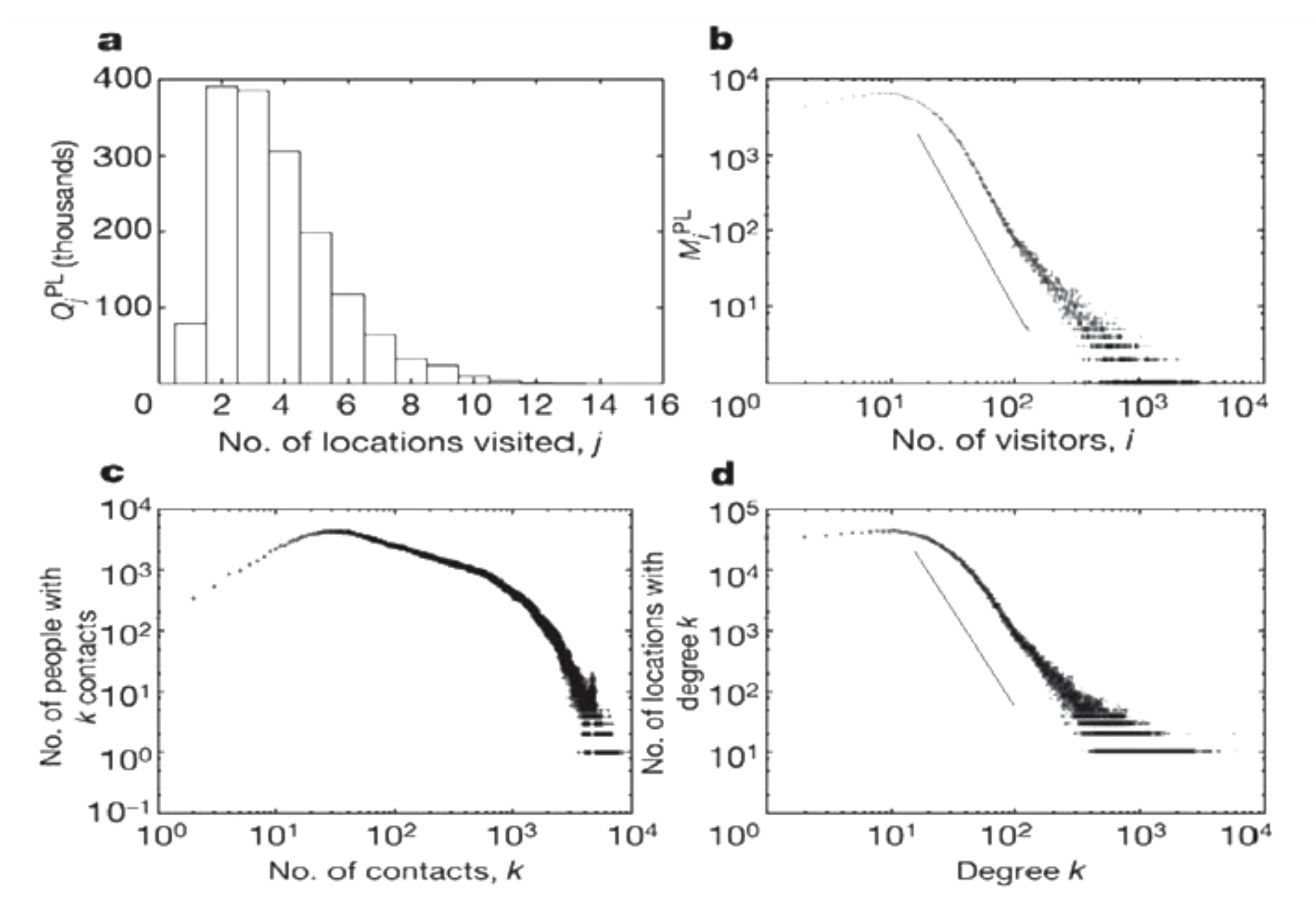


Social Networks

We employ here a cellular automata model of epidemics on an effective social network that is constructed by considering the actual interactions as the time average of the persistence of individuals being in the same location. One of the main points of our study is to construct the people-people social contact network J_{ij} using locations, ages, residential and work places, and considering the time that two people spend together, in average, in such places. In principle, J_{ij} should be considered a weighted matrix. Noticeably, if person i goes to location k , an edge T_{ik} is drawn. We could also extend this definition by weighing the link with the time spent in the location, and considering time coincidence. The effective social contact network J_{ij} is then obtained as:

$$J_{ij}(k) = T_{ik} T_{jk}$$

*Eubank, S., et al. (2004) Modelling disease outbreaks in realistic urban social networks. Nature 429.6988:180-4.



Conclusion

We discussed the parameters of the model and tested three vaccination strategies. We found that targeted vaccination, albeit unrealistic, is a better strategy under normal circumstances but given less constraint on the provision of vaccines, age-prioritised vaccination prevails. Both epidemic spreading and vaccination strategies are highly intricate and stochastic. Our model has shown how one infected individual is sufficient in causing a small scale infection that involved only a few people in a few days to a half a year region-wide epidemic. The ultimate aim of any kind of epidemic modeling is to bolster the development of better efficient countermeasure strategies and this will require further insights into social networks, vaccination and virus-specific pathogenesis.

