Hotspot model shows how location-based superspreading accelerates and reshapes epidemics

Please accept our manuscript "Hotspot model shows how location-based superspreading accelerates and reshapes epidemics" for consideration as a Research Article in the *Proceedings of the National Academy of Sciences*.

During outbreak of a disease, it's common for 80% of infections to trace back to as few as 20% of infected people. It's crucial to understand how this phenomenon – "superspreading" – occurs, and the ways in which it changes disease dynamics.

Our work begins with a simple and plausible premise. A disease spreads more easily at certain "hotspot" locations, such bars or churches; and across the population, some people are more or less likely to visit and spend time at these locations. We set out to establish a theoretical understanding how of outbreak of such a disease – one with location-based superspreading – differs from outbreak of a disease that spreads homogeneously. Location-based superspreading was of great importance in the COVID-19 pandemic and previous airborne pandemics, and will certainly play a role in future airborne disease outbreaks. Yet despite its obvious applicability and relevance, location-based superspreading is surprisingly challenging to model in a simple way and its effects are therefore not well described on a basic theoretical level.

In our manuscript, we introduce an agent-based model that captures the essential features of location-based superspreading. Our model is simple, in the spirit of compartment or network models. Compartment and network models have been used to great effect to understand heterogeneities due to individual variation in infectiousness or social connectedness, but are ill suited for the temoporal and spatial dynamics we study here. Our results agree with established understanding of superspreading in the assessment of the probability of large outbreaks taking place, but we predict key differences in the overall size and rate of development of an outbreak driven by location-based superspreading.

Our model stands alongside efforts to quantify the effects of human mobility and location-specific factors on disease outbreak, but we believe it is foundational in its perspicacity and novel analytical results and will be of broad interest to readers of *PNAS*.