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Reciprocal movements drive heterogeneity in pathogen transmission

Human movement strongly influences pathogen transmission. In directly transmitted diseases such as influenza, human movement has been shown to play a significant role at both a global scale and extremely fine scales (e.g. a single school). For sexually transmitted diseases, description of individual contact networks continues to be a popular method of identifying risk. Understanding where people go, how long they spend there, and what level of risk they are accruing during each visit is key to modeling and understanding the spread of pathogens in space and time as well as constructing optimal control strategies.

Unlike directly transmitted diseases, vector-borne diseases like malaria and dengue do not require two individuals to be at the same location in the same time period. In fact, given the intermediate vector step in the transmission cycle, sharing the same space at the same time as an infected individual confers no risk to susceptible individuals. However, an infective individual can expose multiple vectors. Once the pathogen has completed its incubation period within the vectors (assuming they survive long enough), identifying a single secondary infection could lead to finding other individuals who were also infected, provided one can identify who else was at the infested location at the point in the past when the infective vectors were active. Assuming people travel to the same places consistently through time, the movement patterns of an infective individual should contain the house they were infected in; one may expect to find other infective individuals in that single home. Though the movement patterns of an infective person can be a good indication of multiple locations where risk will be elevated in the future, one would not expect many of the houses an infective person visits to currently contain other infective individuals.

A recent study in Iquitos, Peru showed that not only are contact networks important indicators of risk for the vector-borne disease dengue, but also found patterns that indicate there may be further important structures of human movement. There were significantly more homes with at least one infective individual in the contact network of an infective individual than that of a non-infective individual. This difference strongly suggests reciprocal movement, where the contact networks of multiple individuals overlap.

In an attempt to show reciprocal movement can recreate the observed patterns, as well as get a crude understanding of the amount of overlap necessary, we created an agent-based model of dengue that explicitly defined movements of every individual. We varied the level of overlap and found that, in these simulations, only when there was a considerable level of overlap could we achieve results similar to those from the study. Future efforts will include using these models as a guide to inform the design of new studies to investigate the actual level of overlap in real cities, as well as understand the implications of various control efforts in light of extensive reciprocal movement. Preliminary work shows that when contact networks guide the locations of spraying, the presence or absence of reciprocal movement greatly changes the effect of the effort.