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An agent-based model driven by tropical rainfall to understand the spatio-temporal heterogeneity of a chikungunya outbreak

Vector-borne diseases, such as dengue, malaria and chikungunya, are increasing across their traditional ranges and continuing to infiltrate new, previously unaffected, regions. The spatio-temporal evolution of these diseases is determined by the interaction of the host and vector, which is strongly dependent on local social structures and mobility patterns. We develop an agent-based model, in which each individual is explicitly represented and vector populations are linked to local host and precipitation estimates in a tropical setting. The model is implemented as a scale-free network. The spatio-temporal transmission of chikungunya fever is demonstrated on this network and the presence of asymptomatic silent spreaders within the population is investigated in the context of implementing travel restrictions during an outbreak. Preventing the movement of symptomatic individuals is found to be an insufficient mechanism to halt the spread of the disease, which can be readily carried to neighbouring nodes via sub-clinically infected individuals. Public health interventions should attempt to identify such asymptomatic infected individuals to help control the spread of a chikungunya epidemic.