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# Epidemic dynamics of a vector-borne disease on a villages-and-city star network with commuters



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## HIGHLIGHTS

- The basic reproductive number for an epidemic in a star network is explicitly derived.
- Control decisions are sensitive to vector densities and commuters; and favor villages.
- With more vectors in the city commuting can reduce the basic reproductive number  $R_0$ .
- Heterogeneous populations of vectors and hosts in villages raise the  $R_0$ .

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## ABSTRACT

We develop a star-network of connections between a central city and peripheral villages and analyze the epidemic dynamics of a vector-borne disease as influenced by daily commuters. We obtain an analytical solution for the global basic reproductive number  $R_0$  and investigate its dependence on key parameters for disease control. We find that in a star-network topology the central hub is not always the best place to focus disease intervention strategies. Disease control decisions are sensitive to the number of commuters from villages to the city as well as the relative densities of mosquitoes between villages and city. With more commuters it becomes important to focus on the surrounding villages. Commuting to the city paradoxically reduces the disease burden even when the bulk of infections are in the city because of the resulting diluting effects of transmissions with more commuters. This effect decreases with heterogeneity in host and vector population sizes in the villages due to the formation of peripheral epicenters of infection. We suggest that to ensure effective control of vector-borne diseases in star networks of villages and cities it is also important to focus on the commuters and where they come from.

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## 1. Introduction

The role of host mobility in the epidemic dynamics of vector-borne diseases was not taken into consideration during the malaria eradication programs of the 1950s and 1960s. This was cited as one of the reasons for failure of that program (Bruce-Chwatt, 1968; Prothero, 1977). Since then there has been a substantial increase in the human population size, revolutions in transportation technologies and a sharp rise in urbanization. Poor levels of hygiene in most tropical cities has led to a rise in incidence of vector-borne diseases such as malaria and dengue (Knudsen and Slooff, 1992; Robert et al., 2003; Sharma, 1996).

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Concentration of most economic and social activities in cities has led to the formation of mobility patterns of hosts between these central hubs and the surrounding villages. When hosts move between the central city and peripheral villages they form a network structure of contact between themselves and the vector populations of the two spatial places. Since malarial vectors have short maximum flight distances, such as about 691 m per life time for *Anopheles funestus* and *Anopheles gambiae* (Midega et al., 2007), it is effectively the host movements and their contact with stationary vectors that determine epidemic dynamics between two spatially separate localities.

Commuters move back and forth between two subpopulations forming a connecting link that couples the epidemic dynamics of those subpopulations (Barrat et al., 2008; Colizza and Vespignani, 2008). This coupling forms a system of populations with semi-independent local dynamics, called meta-populations (Adams and Kapan, 2009). An infection event at one spatial point could trigger

a full-blown outbreak at another spatial point in this meta-population structure making the study of the role of connectivity important for disease control (Hanski and Gaggiotti, 2004; Hanski and Gilpin, 1997; Keeling et al., 2004).

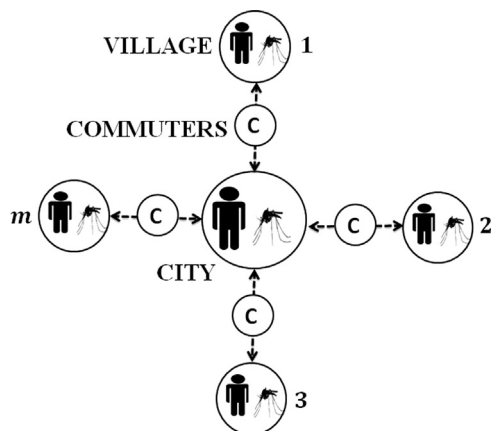
Theoretical studies on vector-borne disease dynamics in inter-connected populations have produced several useful results. For example, in meta-populations mobility leads to disease occurrence among connected patches and speeds up the time for disease to reach equilibrium in the system (Cosner et al., 2009; Hsieh et al., 2007; Torres-Sorando and Rodri'guez, 1997). Besides, for heterogeneous vector densities among patches the disease burden is determined by the patch with the largest vector subpopulation and decreased with a greater degree of mixing of hosts (Adams and Kapan, 2009). While most studies do not elicit specific network structure, we believe that geographical relationships between villages and cities are approximately structured as a star-network in most tropical cities (Briggs and Mwamfupe, 2000) and that host commute patterns are not random (Gonzalez et al., 2008). We construct a simple star-network in which daily commuters connect an arbitrary number of villages to a central city, and incorporate a vector-borne disease transmission epidemic model to understand the influence of meta-population parameters on the epidemic dynamics.

The most important parameter in epidemiology is the basic reproductive number, defined as the total number of secondary infections resulting from a single infectious agent after its introduction into a totally susceptible population throughout the agent's infectious period (Anderson and May, 1992; Arino and Van Den Driessche, 2003; Diekmann et al., 1990; Dietz, 1993; Shao, 1999). Because of the importance of the basic reproductive number in understanding infectious diseases epidemiology and guiding their public health interventions (Ferguson et al., 2003, 2005, 2006), we derive this quantity explicitly and investigate how it can inform disease control decisions about behavior of the epidemic.

## 2. Model

### 2.1. Epidemiological dynamics in a homogeneous star network

Network structure of the host population assumed here is a star with daily commuters between the central node (city) and each of  $m$  peripheral nodes (or villages) (Fig. 1).



**Fig. 1.** A star-network with a central city and  $m$  peripheral villages. Mobility patterns in the homogeneous assumption is such that daily commuters (shown by C in the figure) from surrounding villages connect the infection dynamics of all populations of villages with each other as well as with the city. Mosquitoes do not move between city and village or between villages.

For mathematical simplicity we assume that all peripheral populations have identical numbers of residents, mosquitoes and commuters to the city. This assumption is relaxed later. We also assume that infection dynamics of all peripheral populations are synchronized. The rate of movement of hosts is not affected by their disease statuses.

We adopt frequency-dependent transmission in a susceptible-infectious-susceptible (SIS) epidemic model for hosts (Anderson and May, 1992; Macdonald, 1956; Ross, 1911). We adopt a susceptible-infectious (SI) epidemic model for mosquito vectors because once infected they do not recover from infection. There is no vertical transmission within the mosquito population; that is, newborns do not acquire infection from their parents. Susceptible mosquitoes are supplied by newborns. In this construction an infection of a susceptible host occurs through a bite by an infected mosquito, and an infection of a susceptible mosquito occurs through its bite of an infected host. There is no direct transmission between hosts or between mosquitoes.

The variables describing epidemic dynamics of the SIS model among hosts and the SI model among mosquitoes are as follows (see also Table 1). The number of susceptible and infected mosquitoes is denoted respectively by  $x_u$  and  $y_u$  in the central city (or urban area, and hence the subscript  $u$ ), and by  $x_r$  and  $y_r$  in a peripheral village (or rural area, and hence the subscript  $r$ ). On the other hand, the number of susceptible and infected hosts is denoted respectively by  $X_u$  and  $Y_u$  in the central city; by  $X_c$  and  $Y_c$  in those hosts commuting (and hence the subscript  $c$ ) from a peripheral village to the central city everyday and staying in the city only during daytime; and by  $X_r$  and  $Y_r$  for resident hosts who stay in a peripheral village for the whole day.

During daytime in the city, there are  $X_u + mX_c$  susceptible hosts and  $Y_u + mY_c$  infected hosts (where  $m$  stands for the number of peripheral villages as noted before), and  $x_u$  susceptible mosquitoes and  $y_u$  infected mosquitoes. During nighttime,  $m(X_c + Y_c)$  people go back to their own villages, leaving only  $X_u + Y_u$  in the city.

In a frequency-dependent transmission we assume that mosquitoes bite hosts at a constant rate. Transmission is therefore sensitive to the number of hosts available to receive the bites. Infection dynamics are separated into daytime and nighttime dynamics. The people who commute to the city can be infected when being bitten by an infected mosquito in the city during daytime and when being bitten by an infected mosquito in the village during nighttime. Writing only dynamics for infected components (see Electronic Supplementary material (ESM) for full ODEs) we have the following expressions for dynamics at any arbitrary point in daytime (time is measured in units of days)  $k \leq t < k + 0.5$  ( $k = 0, 1, 2, \dots$ ):

$$\frac{dY_u}{dt} = \frac{b_d \tau X_u}{N_u + mN_c} y_u - \gamma Y_u \tag{1}$$

$$\frac{dy_u}{dt} = \frac{b_d \tau' (Y_u + mY_c)}{N_u + mN_c} x_u - D y_u, \tag{2}$$

$$\frac{dY_c}{dt} = \frac{b_d \tau X_c}{N_u + mN_c} y_u - \gamma Y_c, \tag{3}$$

$$\frac{dy_r}{dt} = \frac{b_d \tau' Y_r}{N_r} x_r - D y_r, \tag{4}$$

$$\frac{dY_r}{dt} = \frac{b_d \tau X_r}{N_r} y_r - \gamma Y_r, \tag{5}$$

where  $b_d$  is the rate at which a mosquito bites a host in daytime,  $\tau$  is the per bite probability that the disease is transmitted from an infected mosquito to a susceptible host and  $\tau'$  is the per bite probability that the disease is transmitted from an infected host to a susceptible mosquito.  $\gamma$  is the rate at which an infected host

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