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Reducing mosquito-borne disease outbreak size: The relative importance of contact and transmissibility in a network model

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ABSTRACT

The complex biological and environmental factors involved in the transmission of mosquito-borne diseases in humans have made their control elusive in many instances. Conceptual models contribute to gain insight and help to reduce the risk of taking poor managerial decisions. The focus of this paper is to compare, using a contact network model, the impact that perturbation of the number infectious contacts and of transmissibility have on the size of an outbreak. We illustrate the analysis on a contact network parametrized with data that associates humans and the mosquito *Culex quinquefasciatus*, a vector for lymphatic filariasis. The model suggests that, if the values corresponding to transmissibility and number of infectious contacts is relatively large, variations in the size of an outbreak are significantly in favor of control measures to reduce infectious contacts.

1. Introduction

Mosquito-borne diseases, like malaria, dengue or filariasis, continue to cause extensive mortality and morbidity around the world, despite huge efforts to control them. Assessing the impact of vector control, medication, management of clinical illness and vaccines leading to the eradication of these diseases is a difficult task due to biological, geographical and temporal variations that are expected to influence the transmission dynamics. As pointed out in [1], the development and extension of simulation and analytical models to establish threshold levels and entomological end points for optimal vector control and disease prevention is a top priority.

The aim in this note is to show how to obtain a better assessment of the impact that changes in transmissibility or infectious contacts values have on the mean size of outbreaks in mosquito-borne diseases. We model the process of transmission with a well known network approach. If the situation is that we are in a region of parameters where an outbreak would appear then intervention measures are required in order to “move” in the direction towards smaller size outbreaks. To anticipate outbreak size responses to control measures and deciding which are more efficient is necessary to support public health decisions, specially under scarse distribution of resources.

Examples of measures to control infectious contacts and transmissibility are, respectively, the use of bednets and the implementation of transmission-blocking vaccines that target the pathogen development within the vector, blocking its transmission to humans [2].

In Section 2 of the paper we review the probability generating functions formalism for bipartite graphs in the context of vectors (mosquitoes) and hosts (humans). Using this tool, in Section 3 we analyse a specific example, using published data, of contact between humans and *Culex quinquefasciatus*, and determine, employing sensitivities of minor outbreak sizes with respect to the parameters, under which circumstances it is better to reduce the number or contacts or to reduce transmissibility.

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2. Materials and methods

2.1. Newman's formalism for mosquito-borne diseases

In contrast with homogeneous mixing, assumed in compartmental mean field models, heterogeneity plays a key role at the beginning stages of an epidemic development [3], which are better described using percolation ideas initially proposed by Newman in [4,5]. Intended to improve the understanding of contact phenomena, the mathematical formalism presented in [4,5], and subsequently refined and extended in [6–8,3,9], is briefly described in this section for bipartite graphs. In our network both hosts (humans, animals or plants) and vectors (insect hosts) are vertices. Edges in the network stand for the contact between hosts and vectors. A main assumption in this model is that the disease spreads within the network in a tree-like fashion where loops are excluded. This assumption is approximately valid for large populations, [4,5].

2.1.1. The contact network

We define the contact between a host and a vector when the vector bites on the host at least once. Let r_k and g_k be the probabilities that a randomly chosen host is contacted by k different vectors, and that a randomly chosen vector contacts k different hosts, respectively. Thus, $(r_k)_{k=0}^{\infty}$ and $(g_k)_{k=0}^{\infty}$ define the probability distributions of the number of contacts received by a host and given by a vector. The corresponding probability generating functions are

$$G_{h0}(z) = \sum_{k=0}^{\infty} r_k z^k \quad \text{and} \quad G_{m0}(z) = \sum_{k=0}^{\infty} g_k z^k. \tag{1}$$

The mean number of contacted hosts by a single vector is

$$\sum_{k=1}^{\infty} k g_k = G'_{m0}(1). \tag{2}$$

Consider an edge that starts at a vector. If we follow this edge to a vertex (host), the *excess degree* of this vertex is the degree minus one. The excess degree is used because the disease is not transmitted back along the edge from which it came. The probability that the selected edge ends in a vector with excess degree $k-1$ is proportional to kg_k and the generating function corresponding to the excess degree distribution of the vector is

$$G_{m1}(z) = \frac{1}{G'_{m0}(1)} \sum_{k=1}^{\infty} k g_k z^{k-1} = \frac{G'_{m0}(z)}{G'_{m0}(1)}. \tag{3}$$

Similarly, the distribution of the excess degree of a host at which we arrived through a randomly chosen edge that starts at a vector is determined by

$$G_{h1}(z) = \frac{G'_{h0}(z)}{G'_{h0}(1)}. \tag{4}$$

The contacted vector will produce a mean number of new contacts given by

$$\frac{1}{G'_{m0}(1)} \sum_{k=1}^{\infty} (k-1) k g_k = G'_{m1}(1). \tag{5}$$

Then, the generating function for the probability distribution of the number of secondary contacted hosts is

$$\sum_{k=0}^{\infty} r_k [G_{m1}]^k = G_{h0}(G_{m1}(z)) \tag{6}$$

and, using (4), the generating function for the probabilities of the secondary host contacts starting at a host vertex reached through a randomly chosen edge is given by

$$\hat{G}(z) = \frac{\sum_{k=1}^{\infty} k r_k [G_{m1}(z)]^{k-1}}{G'_{h0}(1)} = \frac{G'_{h0}(G_{m1}(z))}{G'_{h0}(1)}. \tag{7}$$

2.1.2. Transmissibility

A measure of transmissibility is the probability that the disease is successfully transmitted, given a contact. It appears in the contact network model, as we will see, because not all the contacts made may transmit the disease, [5]. Let T_{hm} and T_{mh} be the transmissibility from host to vector and vector to host, respectively. The probability that an infectious host vertex, with degree k in the network, transmits the disease to m vectors is

$$P(\text{number of new infected vectors from a host} = m | \text{host degree} = k) = \binom{k}{m} T_{hm}^{m} (1 - T_{hm})^{k-m}.$$