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# A final size relation for epidemic models of vector-transmitted diseases

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ABSTRACT

We formulate and analyze an age of infection model for epidemics of diseases transmitted by a vector, including the possibility of direct transmission as well. We show how to determine a basic reproduction number. While there is no explicit final size relation as for diseases transmitted directly, we are able to obtain estimates for the final size of the epidemic.



## 1. Introduction

Diseases transmitted by vectors have been of importance and interest almost since the beginning of modern epidemiological modeling. The demonstration in 1897 by Dr. R.A. Ross that malaria is transmitted from person to person through a vector, the Anopheles mosquito, was a real landmark in the early history of mathematical epidemiology. Malaria remains a cause of hundreds of thousands of death annually, mostly children less than five years old. Ninety per cent of malaria cases are in Sub-Saharan Africa.

Recently, other diseases transmitted by vectors have become serious public health problems. There have been frequent outbreaks of dengue fever and chikungunya, and the number of reported cases has been increasing rapidly recently. According to the World Health Organization, approximately 50,000,000 people worldwide are infected with dengue. Symptoms may include fever, headaches, joint and muscle pain, and nausea, but many cases are very mild. There is no cure for dengue fever, but most patients recover with rest and fluids. There are at least four different strains of dengue fever, and there is some cross-immunity between strains. Dengue fever is transmitted by the mosquito *Aedes aegypti*, and most control strategies are aimed at mosquito control. Another disease transmitted by vectors, in fact the same *Aedes aegypti* mosquito that transmits dengue, is the Zika virus. The Zika virus was first observed about 1952, but initially cases were rare. In 2007 a major epidemic occurred in Yap Island, Micronesia. Since April 2015 there has been a large continuing outbreak of Zika virus that started in Brazil and has spread to much of South and Central America. It has become a major concern because it is now established that there is some correlation with microcephaly and other very serious birth defects in babies born to infected mothers (Schuler-Faccini, 2016). A new feature of the Zika virus that has been identified is that infection may be transmitted directly by blood transfusions and sexual contact (Musso et al., 2015) as well as through vectors.

In the past, models for vector-transmitted diseases have been of *SIR*/*SI* or *SEIR*/*SEI* type, assuming that vectors do not recover from infection but are infected for life. Our purpose here is to formulate and analyze models with infectivity

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depending on age of infection. This allows arbitrary periods of stay in each compartment and also the inclusion of control measures such as treatment, quarantine, or isolation. We will describe two models, beginning with a pure vector transmission model that may be considered as a prototype of a dengue fever model, and then proceeding to a model including both vector and direct transmission that may be considered as a prototype of a zika virus model.

In the modeling of epidemics of directly - transmitted diseases, a final size relation connecting the basic reproduction number and the size of the epidemic has been an essential tool for the description of the course of the epidemic. While epidemics of vector - transmitted diseases also have a final size, there is no explicit final size relation. However, we are able to establish an estimate with an upper bound for the final size of the epidemic. The result applies also to diseases that can be transmitted directly as well as through a vector. There is also a lower bound, but it is too small to be useful. The establishment of a sharper lower bound is an important open question.

## 2. An age of infection epidemic model

We describe an epidemic model for a vector-transmitted disease that includes the possibility of direct transmission of disease as well. We are thinking of mosquitoes as vectors, and because a mosquito lifetime is much shorter than that of the human hosts we must include demographics in the vector population.

We consider a constant total population size $N$ of hosts (humans) with $S$ susceptibles and total infectivity $\varphi(t)$. Typically the total infectivity is the sum of the number of members of infected classes multiplied by the relative infectivity of the class.

We assume an average mosquito makes $a$ bites in unit time. Thus the total number of mosquito bites in unit time is $aN_v$ and the number of bites received by an average host in unit time is $aN_v/N_h$. A host makes an average of $\beta_h$ contacts sufficient to receive infection in unit time from vectors. The contact rate $\beta_h$ is a product of two factors, namely the number of bites received in unit time by an average human and the probability $f_{vh}$ that a bite transmits infection from vector to human,

$$\beta_h = a f_{vh} \frac{N_v}{N_h}.$$

The total number of contacts by humans sufficient to transmit infection is $\beta_h N$.

The number of vectors (mosquitoes) is $N_v$ including $S_v$ susceptibles. Each vector makes $\beta_v$ contacts sufficient to receive infection from human hosts in unit time. The contact rate $\beta_v$ is a product of two factors, namely the biting rate $a$ and the probability $f_{hv}$ that a bite transmits infection from human to vector,

$$\beta_v = a f_{hv}.$$

There is a constant birth rate $\mu N_v$ of vectors in unit time and a proportional vector death rate $\mu$ in each class, so that the total vector population size $N_v$ is constant. Infected vectors do not recover from infection. The total number of contacts by vectors sufficient to transmit infection is $\beta_v N_v$.

Elimination of $a$ from the expressions for $\beta_h$ and $\beta_v$ gives

$$f_{hv}\beta_h N_h = f_{vh}\beta_v N_v. \tag{1}$$

This balance relation must hold at every time $t$. We think of $N, N_v, a, f_{vh}$ and $f_{hv}$ as fixed. Thus $\beta_v$ is also fixed and the number of effective bites of a human in unit time is

$$\beta = \beta_v \frac{f_{vh}}{f_{hv}} \frac{N_v}{N}.$$

We are assuming that the population sizes $N$ and $N_v$ are constant, but it is important to remember that if one of the population sizes changes, for example because of a program to kill mosquitoes, a change in the value of $\beta$ would be a consequence.

A susceptible human receives $\beta_h$ effective mosquito bites in unit time, of which a fraction $\varphi_v/N_v$ is with an infective mosquito. Thus the number of new infective humans in unit time is

$$\beta_h S \frac{\varphi_v}{N_v}.$$

A similar argument shows that the number of new mosquito infections is

$$\beta_v S_v \frac{\varphi}{N}.$$

For the Zika virus, it has been established that in addition to vector transmission of infection there may also be direct transmission through sexual contact. The Zika virus is the first example of an infection that can be transferred both directly