

Modeling vector-borne diseases

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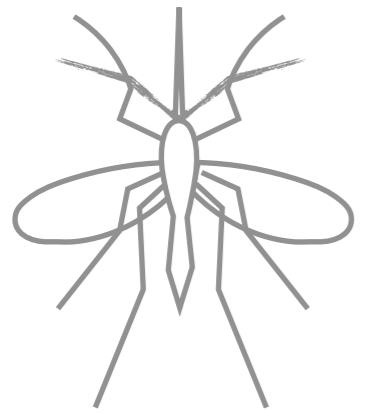
JOHNS HOPKINS

BLOOMBERG SCHOOL
of PUBLIC HEALTH

Learning objectives

- Understand the utility and development of mathematical models to study the transmission dynamics of vector-borne infectious diseases
Comprendre l'utilité et le développement de modèles mathématiques pour étudier la dynamique de transmission des maladies infectieuses à vecteur
- Compare and contrast epidemiological and life history features of vector-borne diseases versus directly-transmitted diseases
Comparer et comparer les caractéristiques épidémiologiques et biologiques des maladies à vecteur par rapport aux maladies directement transmises
- SIRS model structure
- Incorporate environmental variables into vector populations
Incorporer des variables environnementales dans les populations de vecteurs
- Understand the implications for disease elimination and control
Comprendre les implications pour l'élimination et le contrôle de la maladie





0. Introduction



Vector-borne diseases

maladie transmise par des vecteurs

Pathogens transmitted among hosts by an intermediate species, primarily arthropods such as mosquitos or ticks

Agents pathogènes transmis parmi les hôtes par une espèce intermédiaire, principalement des arthropodes tels que les moustiques ou les tiques

Examples: malaria, dengue, chikungunya, Crimean-Congo hemorrhagic fever, west nile virus, Japanese encephalitis paludisme, dengue, chikungunya, fièvre hémorragique de Crimée-Congo, virus du Nil occidental, encéphalite japonaise



What makes vector-borne diseases different to model and study than directly-transmitted diseases?

Two sets of population dynamics — demography, transmission, interactions, etc.

Environmental factors and abiotic conditions

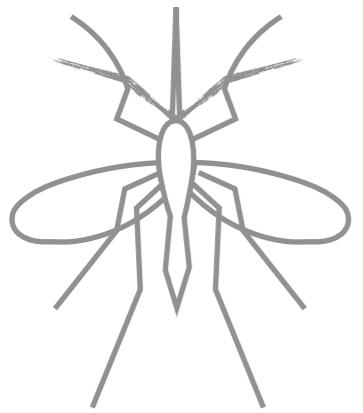
Transmission depends on both the human and vector compartments



Vector	Disease	Estimated or reported annual number of cases	Estimated annual number of deaths	Estimated annual disability-adjusted life years
Mosquitoes	Malaria ¹	212 000 000 (148 000 000–304 000 000) ¹	429 000 (235 000–639 000) ¹	NA
	Dengue	96 000 000 (67 000 000–136 000 000) ²	9 110 (5630–10 842) ³	1 892 200 (1 266 700–2 925 500) ⁵
	Lymphatic filariasis	38 464 000 (31 328 000–46 783 000) ⁶	NA	2 075 000 (1 120 500–3 311 500) ⁵
	Chikungunya (Americas)	693 000 ⁷ suspected, 2015	NA	NA
	Zika virus disease (Americas)	500 000 ⁸ suspected, 2016	NA	NA
	Yellow fever (Africa)	130 000 (84 000–170 000) ⁹	500* (400–600) ³	31 000* (25 000–37 000) ³
	Japanese encephalitis	42 500* (35 000–50 000) ¹⁰	9 250* (3500–15 000) ¹⁰	431 552* (107 435–755 670) ¹⁰
	West Nile fever	2 588 ¹¹	111 ¹¹	NA

**~17% of all infectious diseases, more than 700k deaths
(WHO, 2017)**





I. The basic model



Compartmental models (Mechanistic Models)

Populations are divided into compartments

Les populations sont subdivisées en compartiments

Compartments and transition rates are
determined by biological systems

Les compartiments et les taux de transition sont déterminés par les
systèmes biologiques

Rates of transferring between compartments
are expressed mathematically

Taux de transition entre les compartiments sont exprimés
mathématiquement

Individuals within a compartment are homogeneously mixed

Les individus d'un compartiment sont mélangés de manière homogène



How are these different from statistical models?

En quoi sont-ils différents des modèles statistiques?

Make explicit hypotheses about biological mechanisms that drive dynamics (may not be realistic, but still explicit)

Faire des hypothèses explicites sur les mécanismes biologiques qui régissent la dynamique (peut ne pas être réaliste, mais toujours explicite)



The basic vector model

susceptible

infected

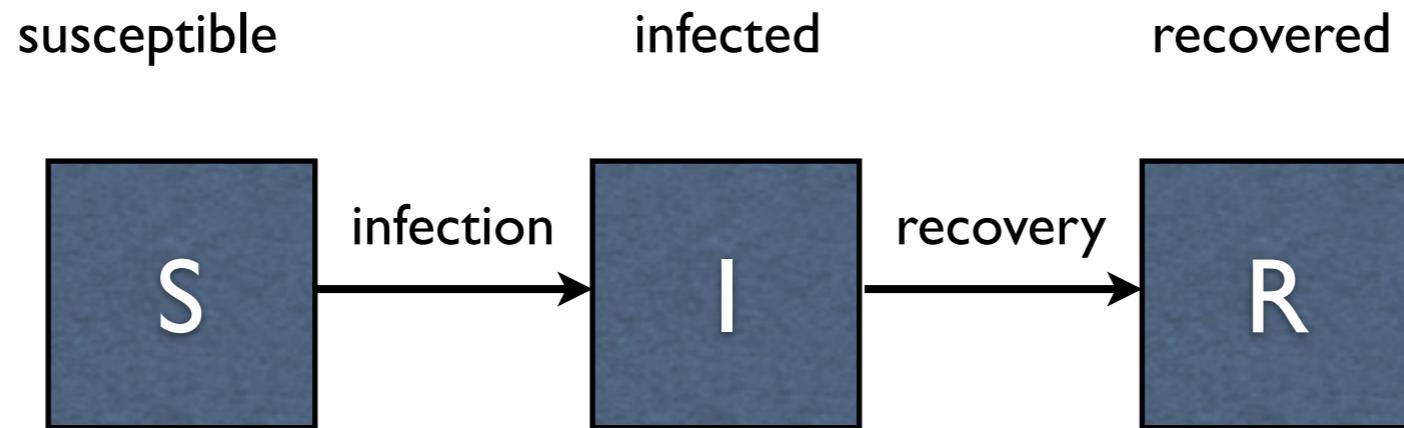
recovered

everyone is either:



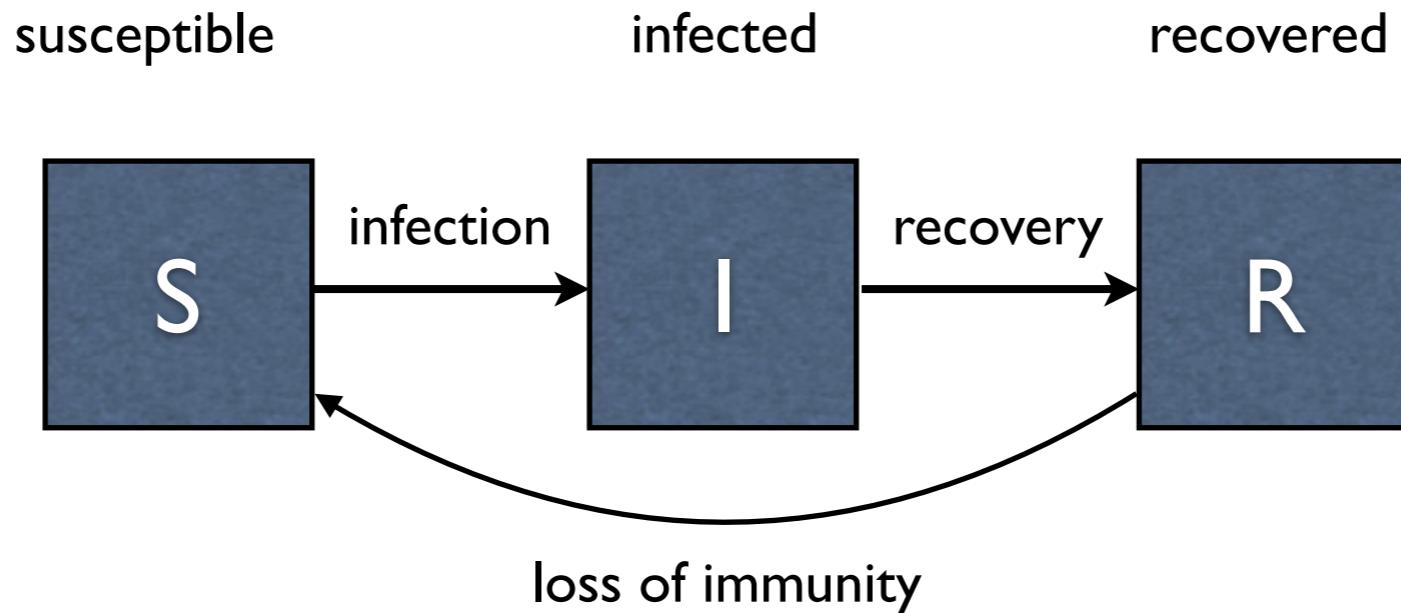
The basic vector model

everyone is either:



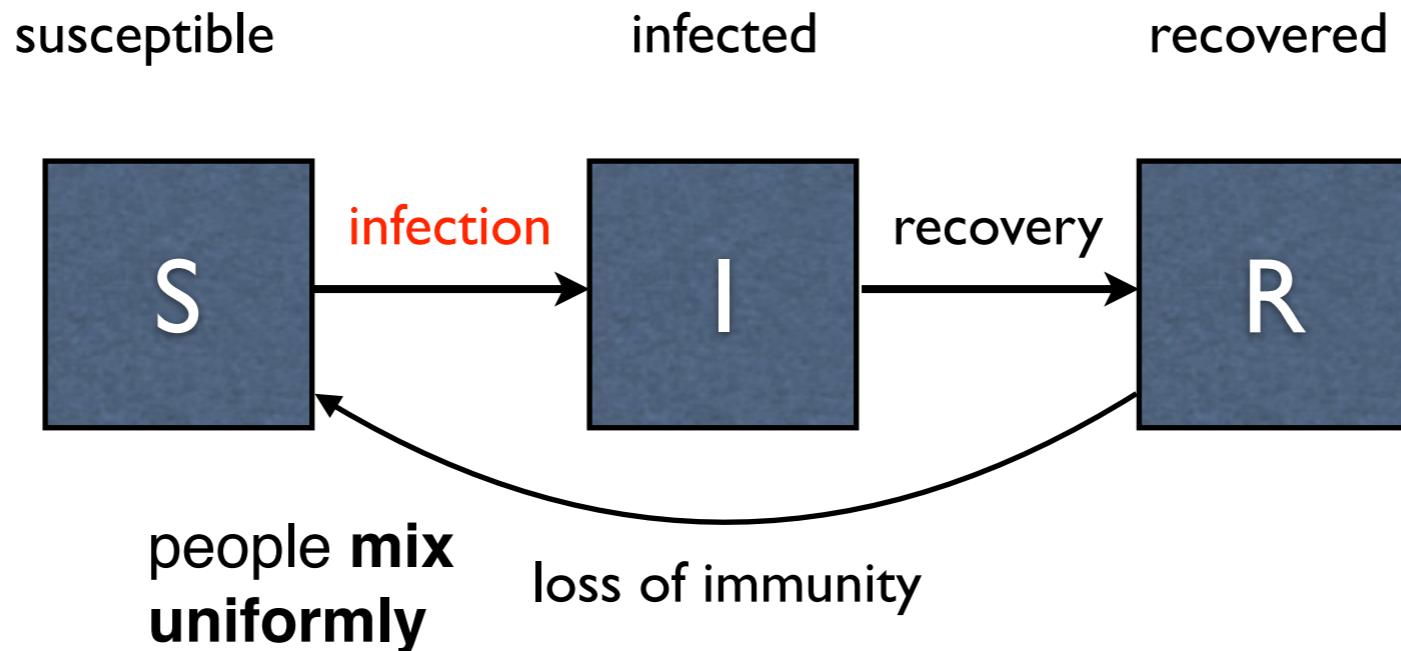
The basic vector model

everyone is either:



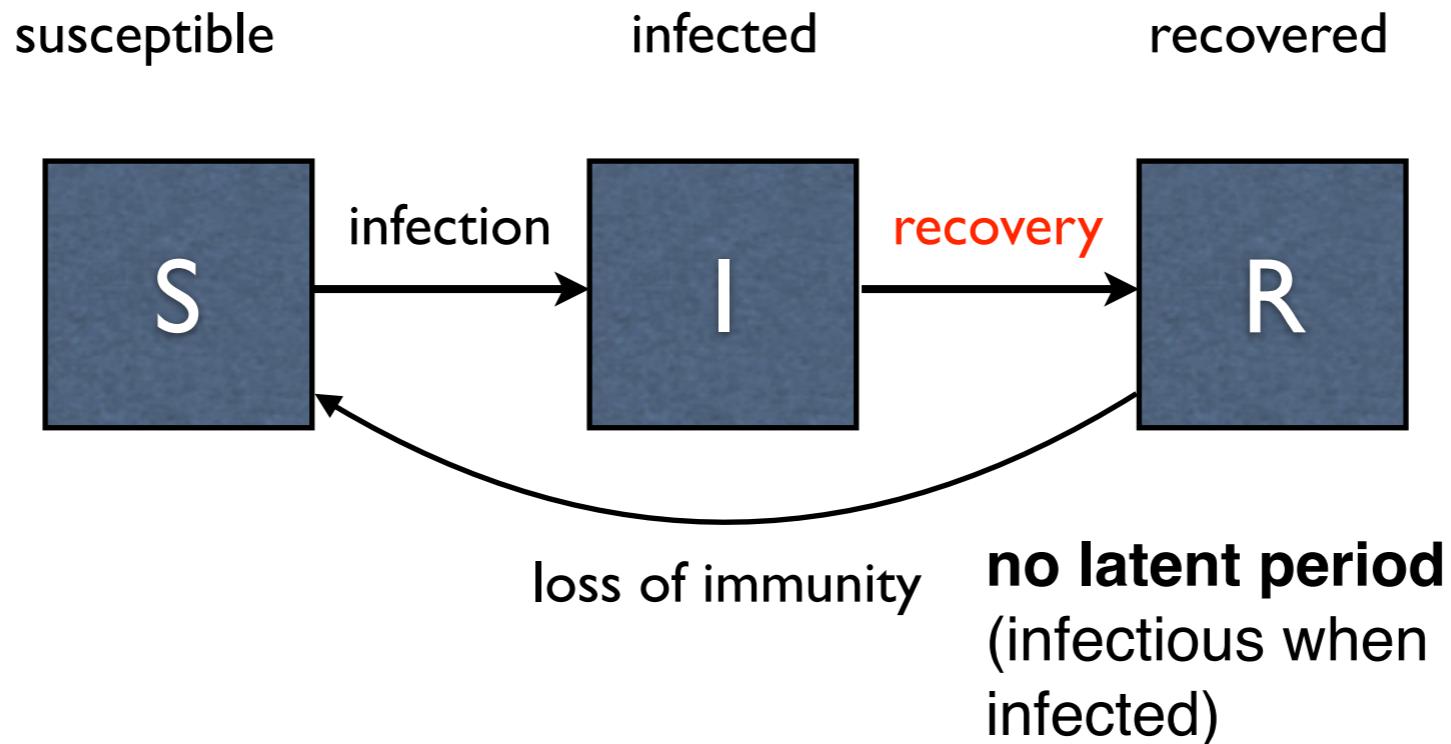
The basic vector model

everyone is either:



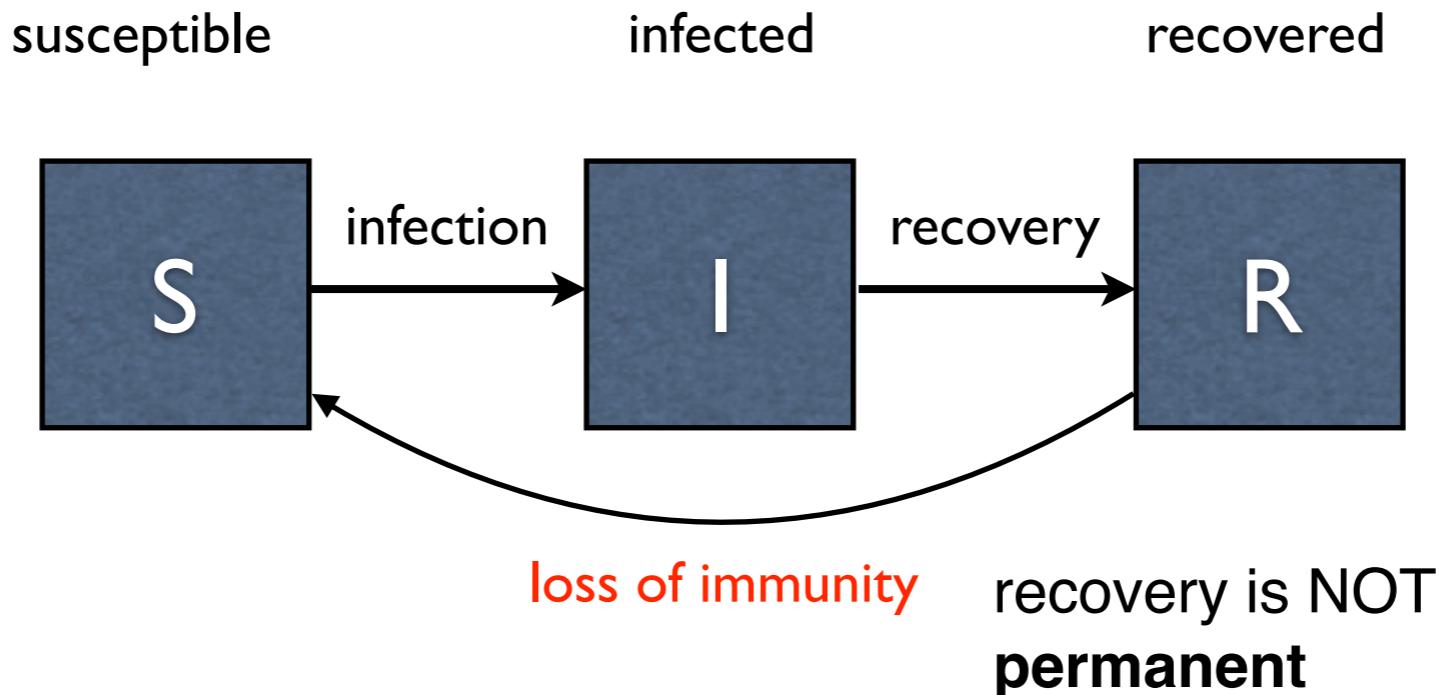
The basic vector model

everyone is either:



The basic vector model

everyone is either:



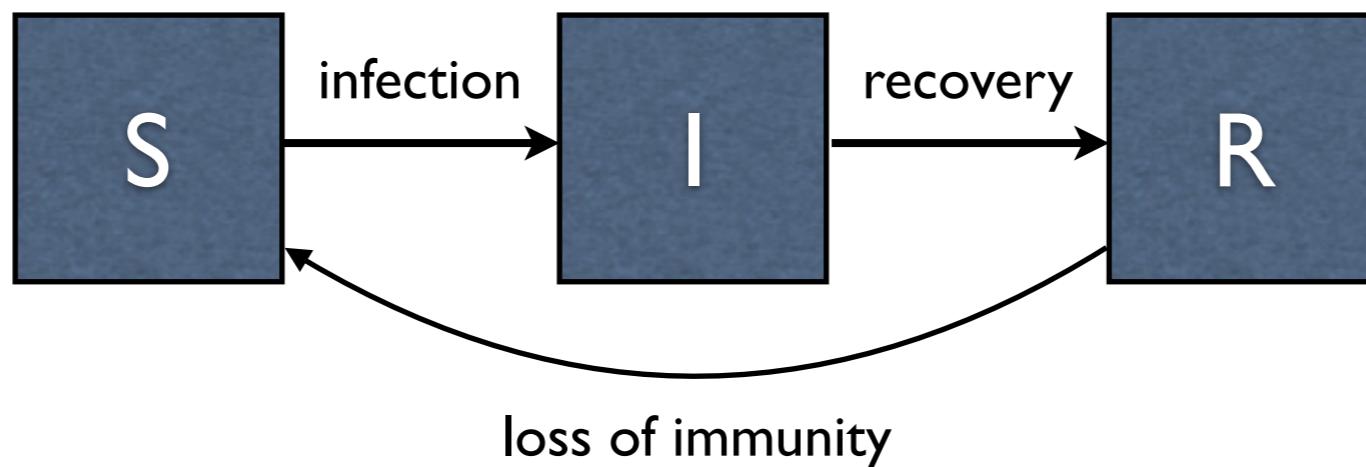
The basic vector model

susceptible

infected

recovered

everyone is either:

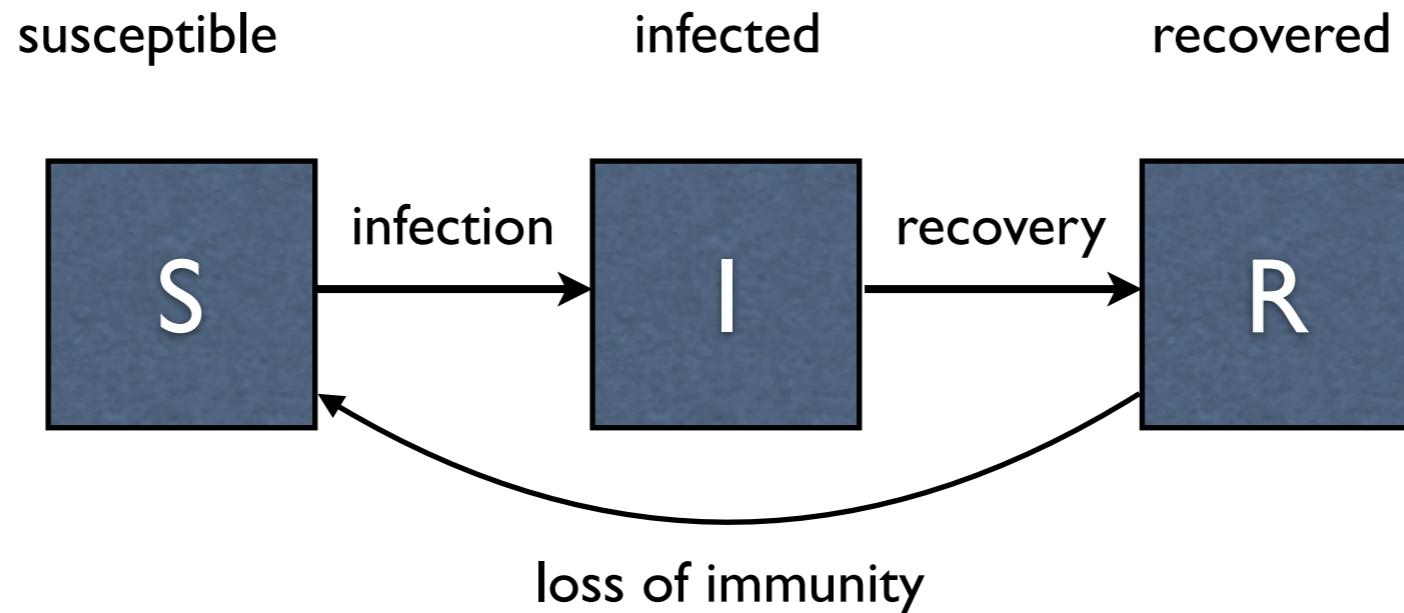


population size
constant - no births
or deaths, migration



The basic vector model

everyone is either:



Human compartments...

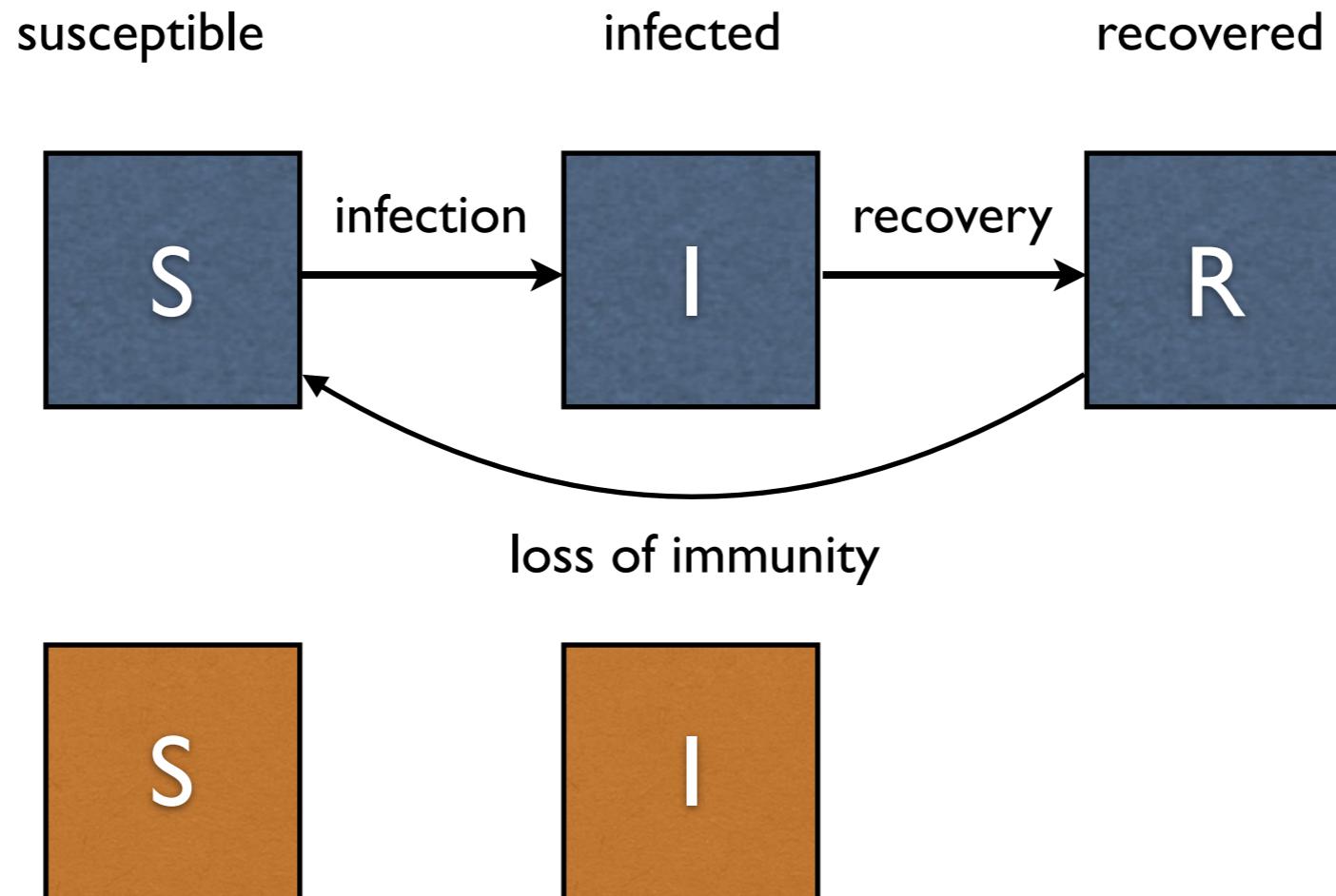
Individuals can be susceptible, infected, or recovered. After recovery they can then become susceptible here.

Similar to an SIR model, but now an SIRS model.

What is the assumption about immunity here?



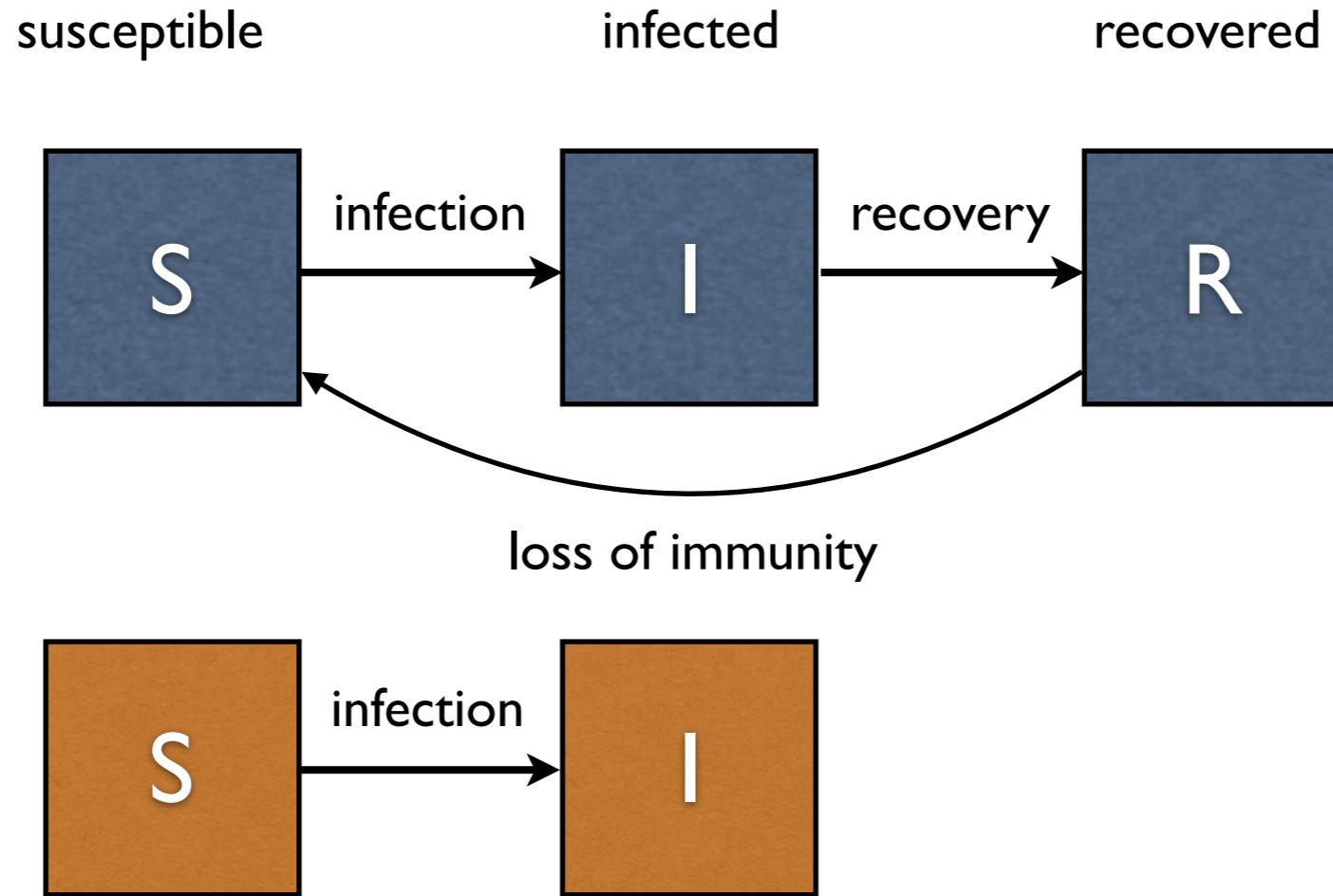
The basic vector model



Vector compartments...



The basic vector model

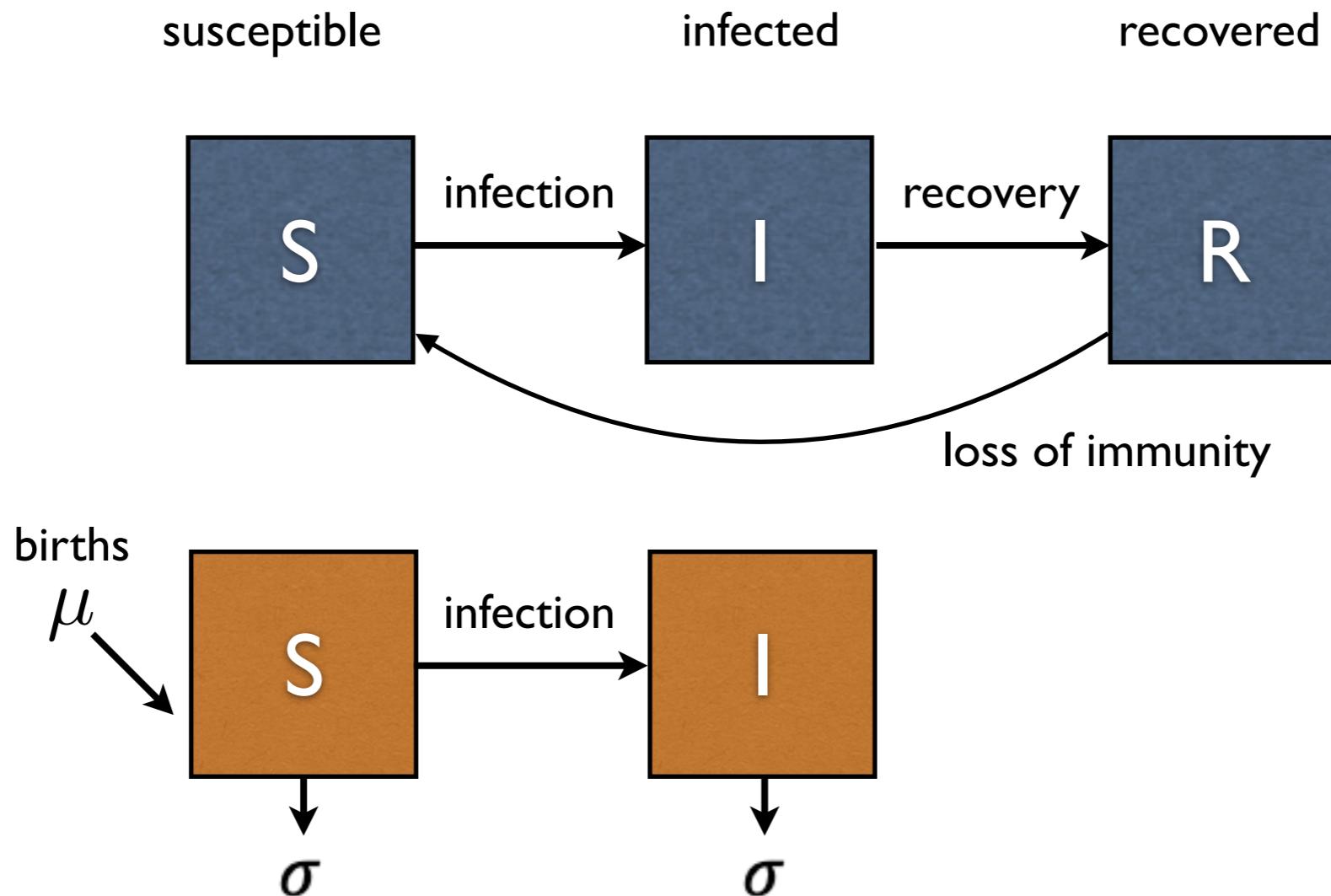


Vector compartments...

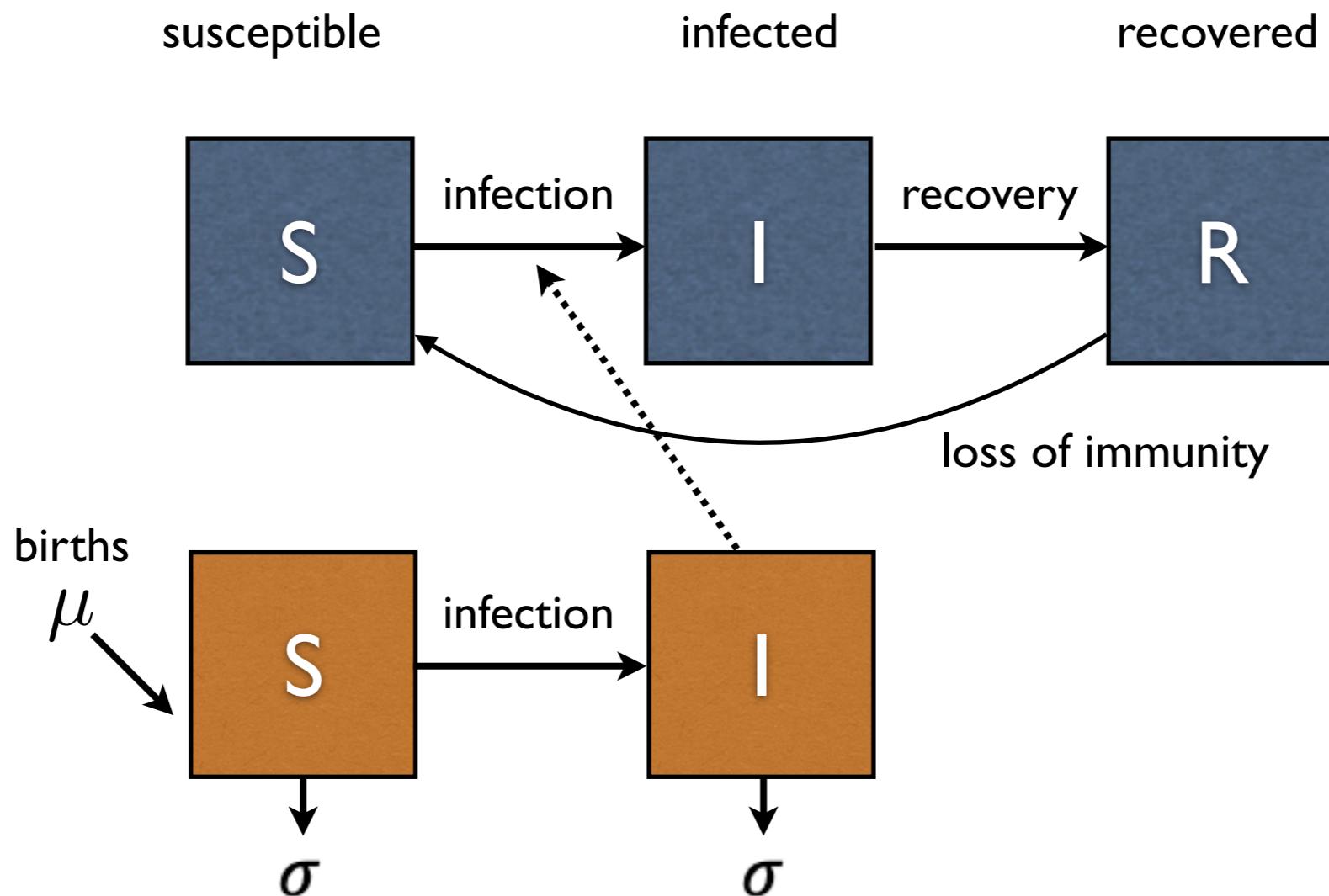
Vectors can either be susceptible or infected (assumes death after infection = no recovery).



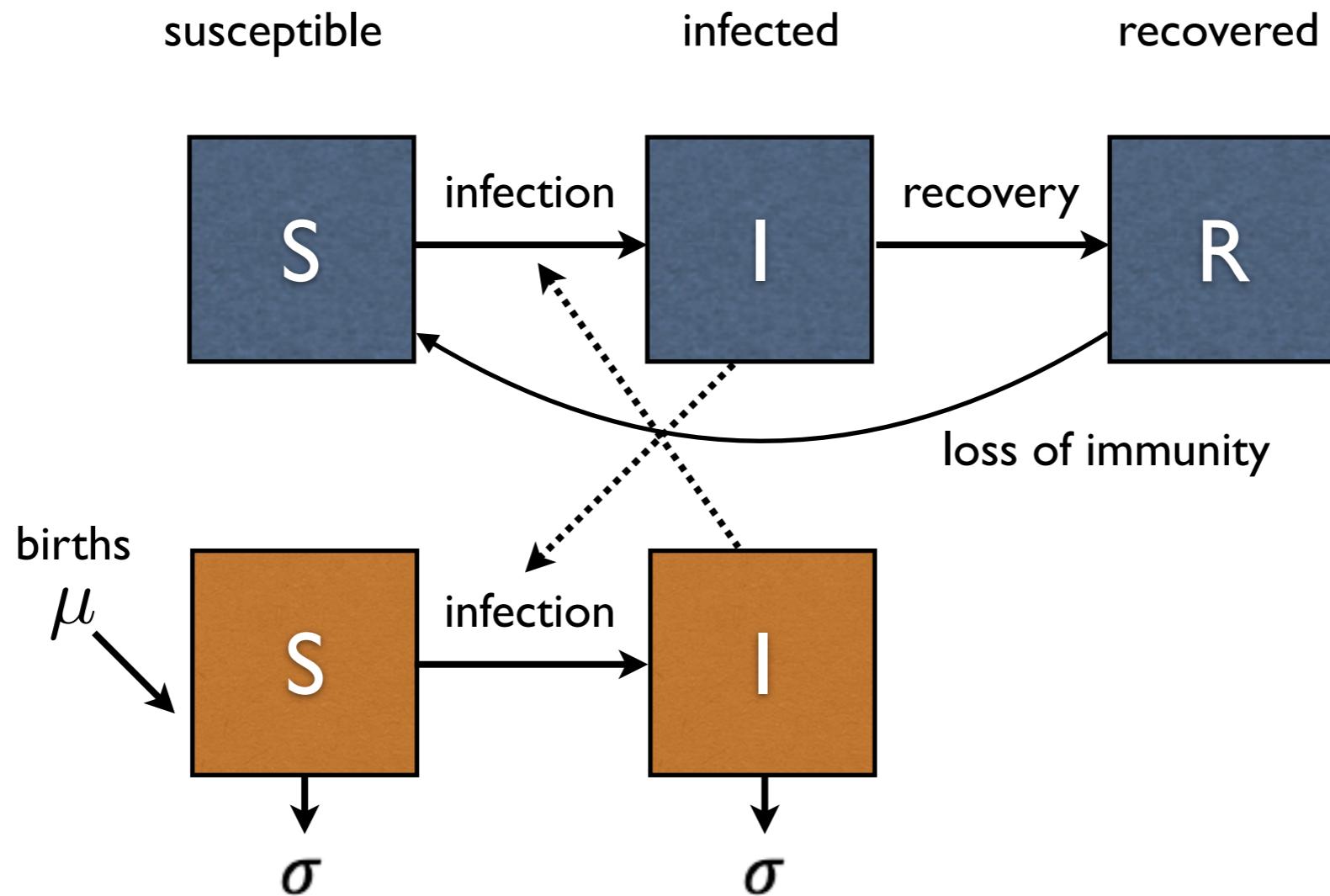
The basic vector model



The basic vector model



The basic vector model



**The infectious compartment of the humans impacts the transmission for vectors!
(and visa versa)**



The basic vector model

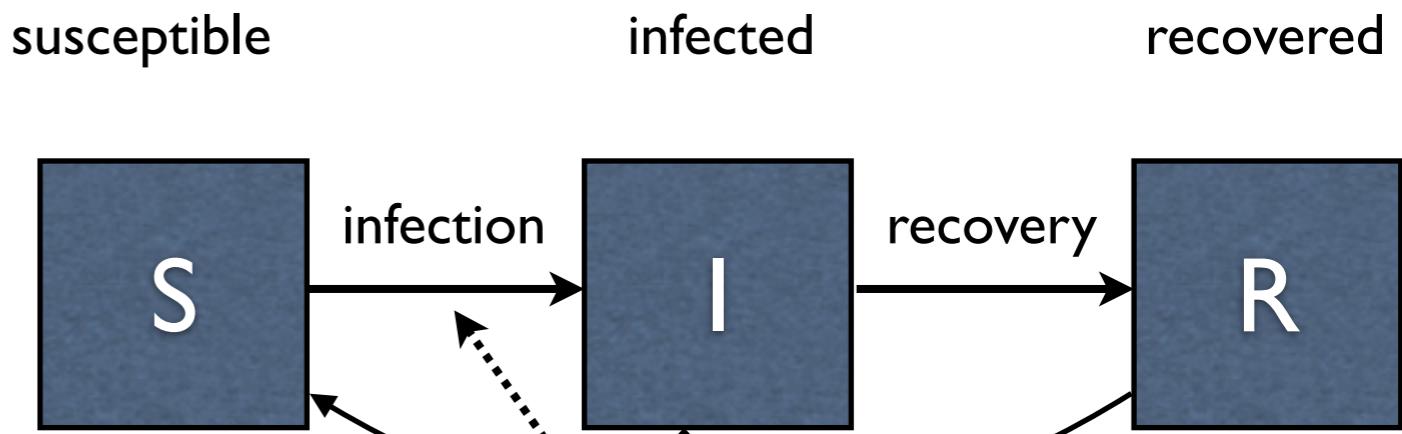
Parameters

β_H : transmission rate

γ : rate of recovery

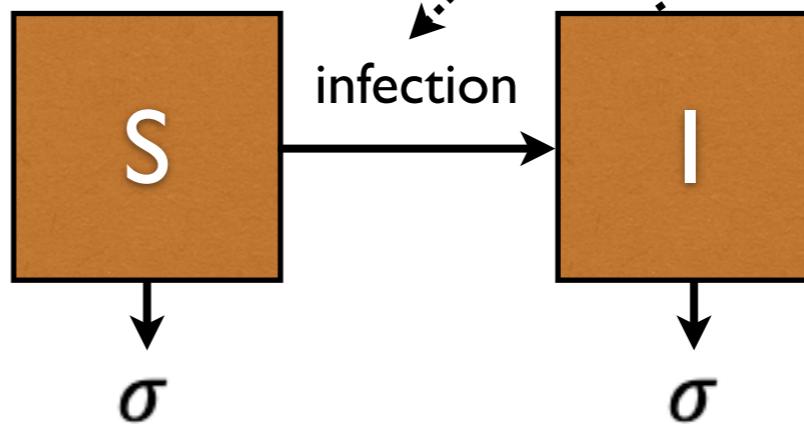
w : rate of loss of immunity

Humans



births

μ



Vectors



The basic vector model

Parameters

β_H : transmission rate

γ : rate of recovery

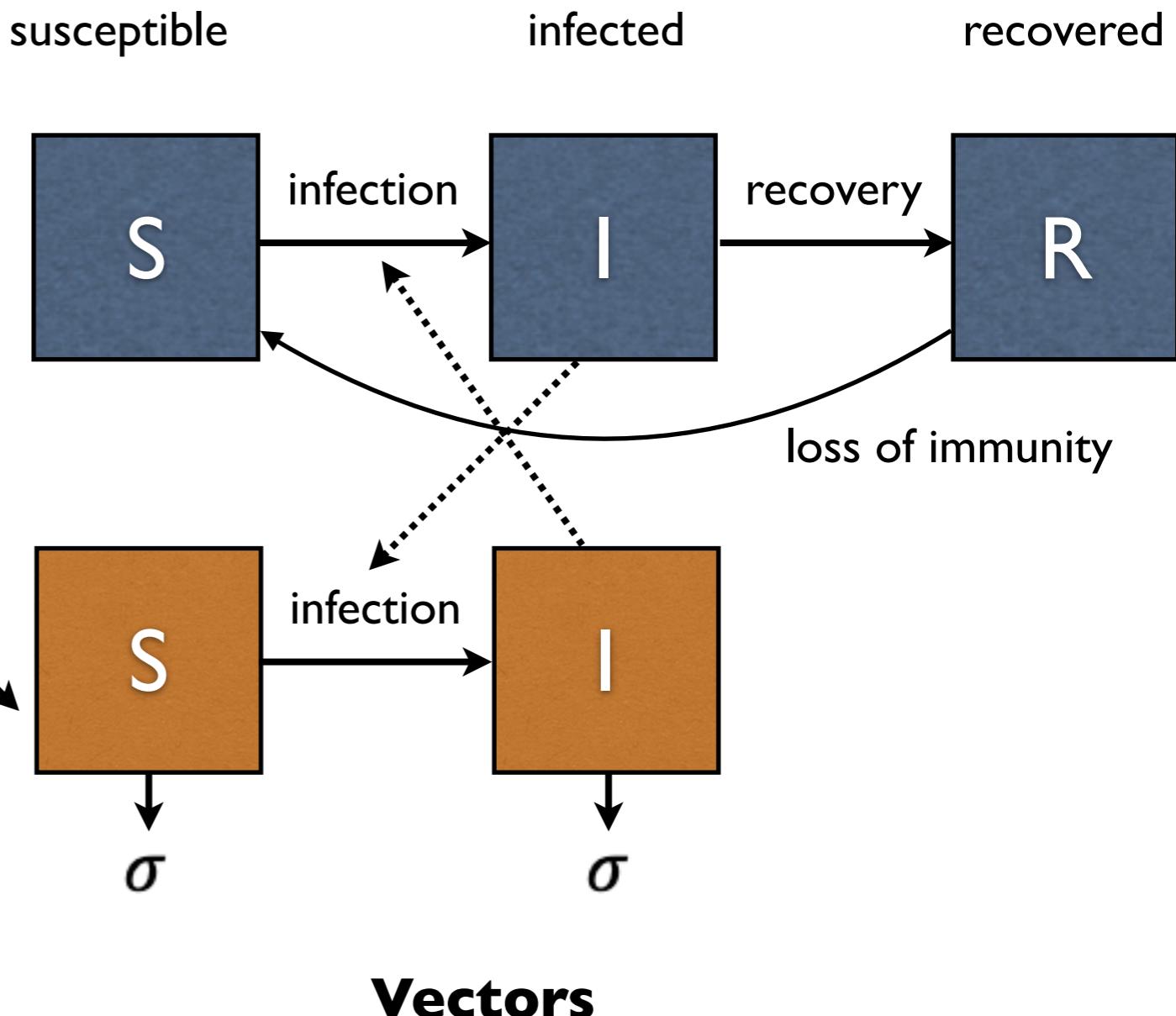
w : rate of loss of immunity

Humans

$$\frac{dS_H(t)}{dt} = -\beta_H S_H I_V + w R_H$$

$$\frac{dI_H(t)}{dt} = \beta_H S_H I_V - \gamma I_H$$

$$\frac{dR_H(t)}{dt} = \gamma I_H - w R_H$$



The basic vector model

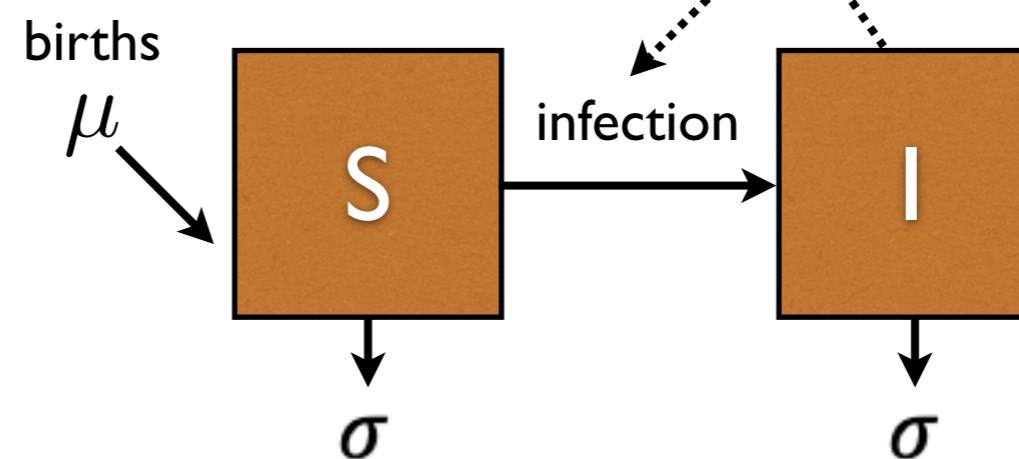
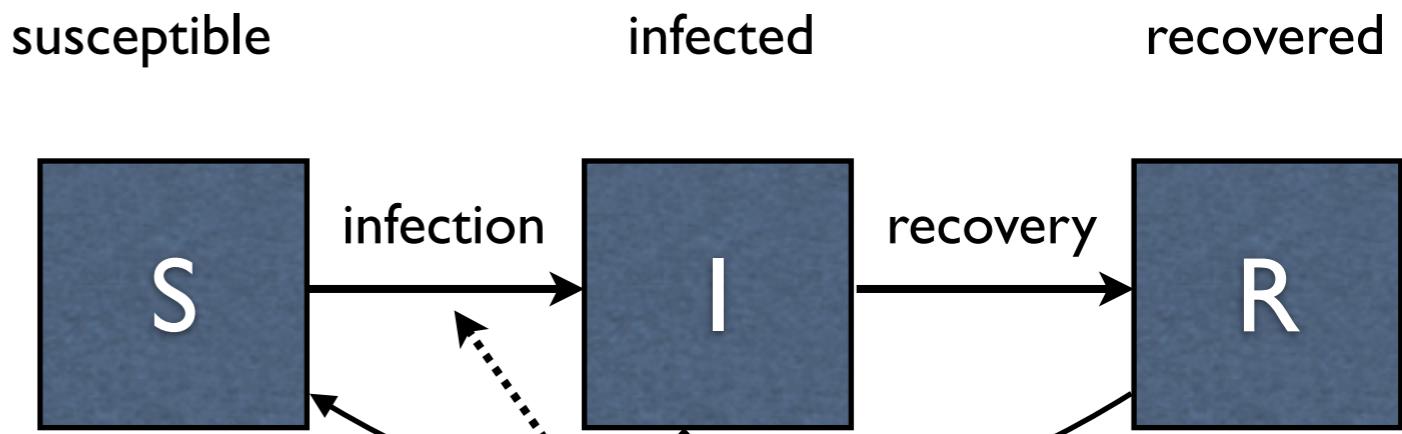
Parameters

β_V : transmission rate

μ : birth rate

σ : death rate

Humans



Vectors



The basic vector model

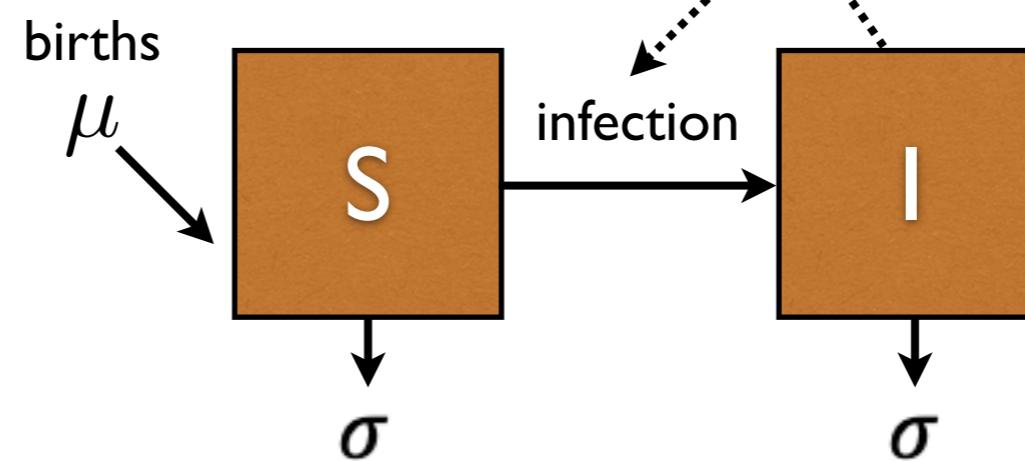
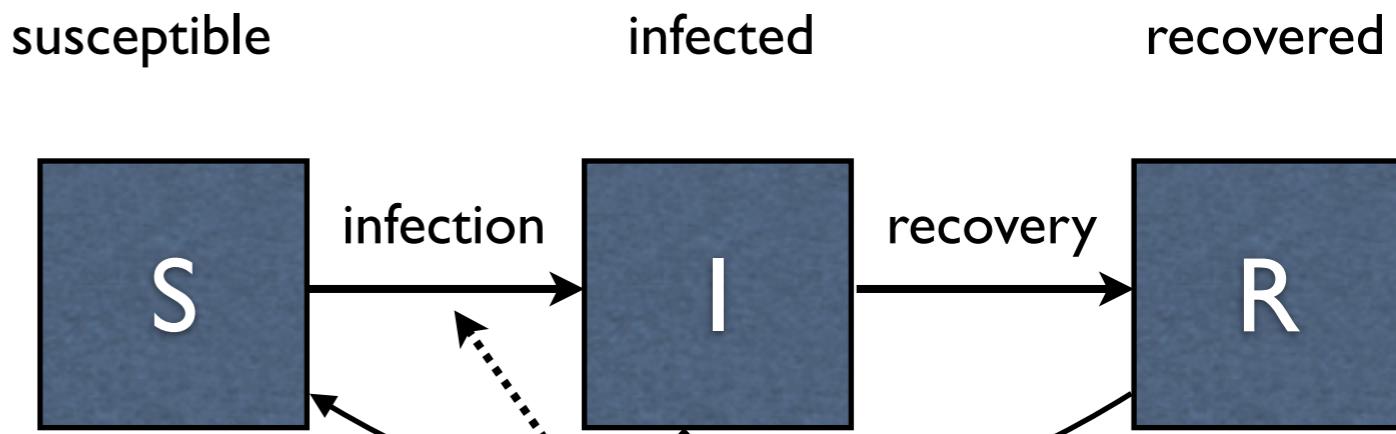
Parameters

β_V : transmission rate

μ : birth rate

σ : death rate

Humans



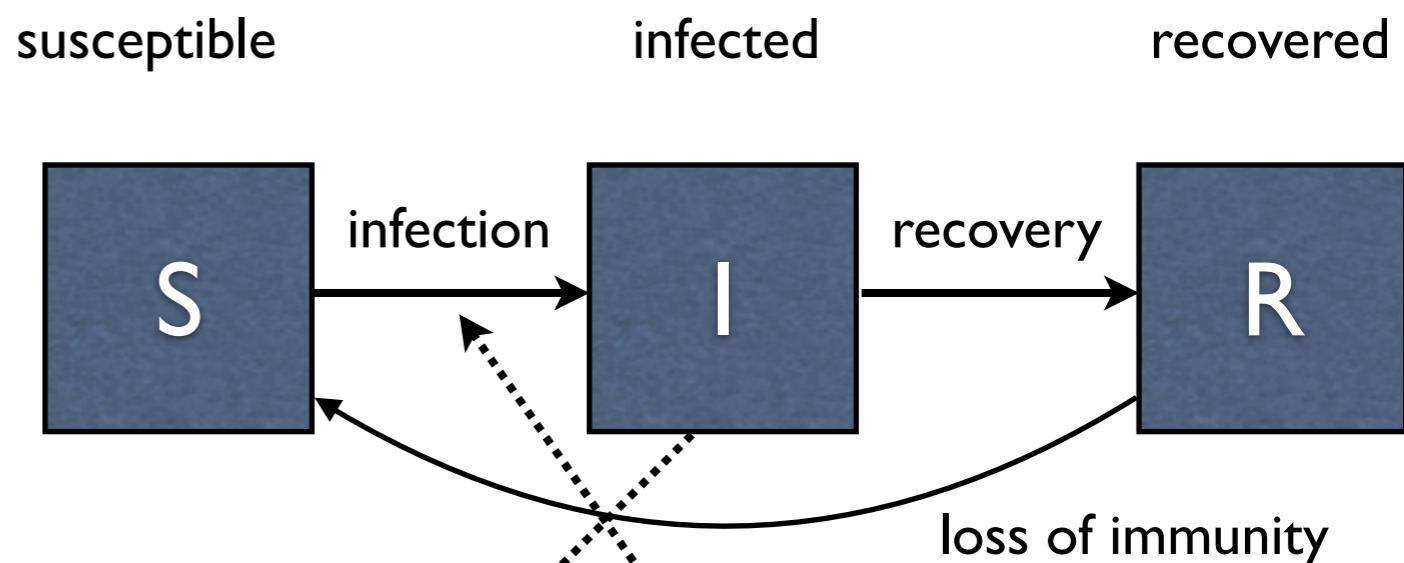
Vectors

$$\frac{dS_V(t)}{dt} = \mu - \beta_V S_V I_H - \sigma S_V$$

$$\frac{dI_V(t)}{dt} = \beta_V S_V I_H - \sigma I_V$$



The basic vector model



Humans

$$\frac{dS_H(t)}{dt} = -\beta_H S_H I_V + w R_H$$

$$\frac{dI_H(t)}{dt} = \beta_H S_H I_V - \gamma I_H$$

$$\frac{dR_H(t)}{dt} = \gamma I_H - w R_H$$

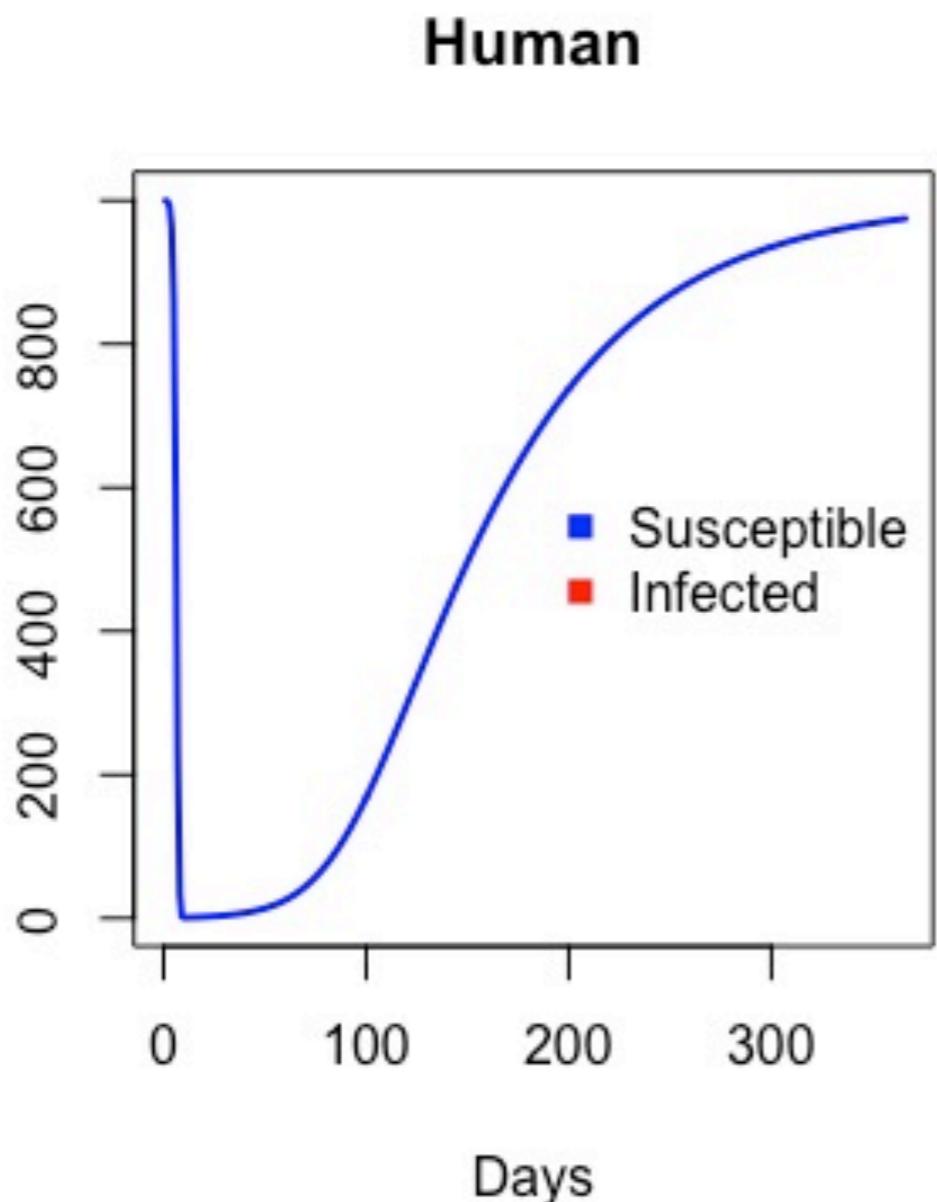
Vectors

$$\frac{dS_V(t)}{dt} = \mu - \beta_V S_V I_H - \sigma S_V$$

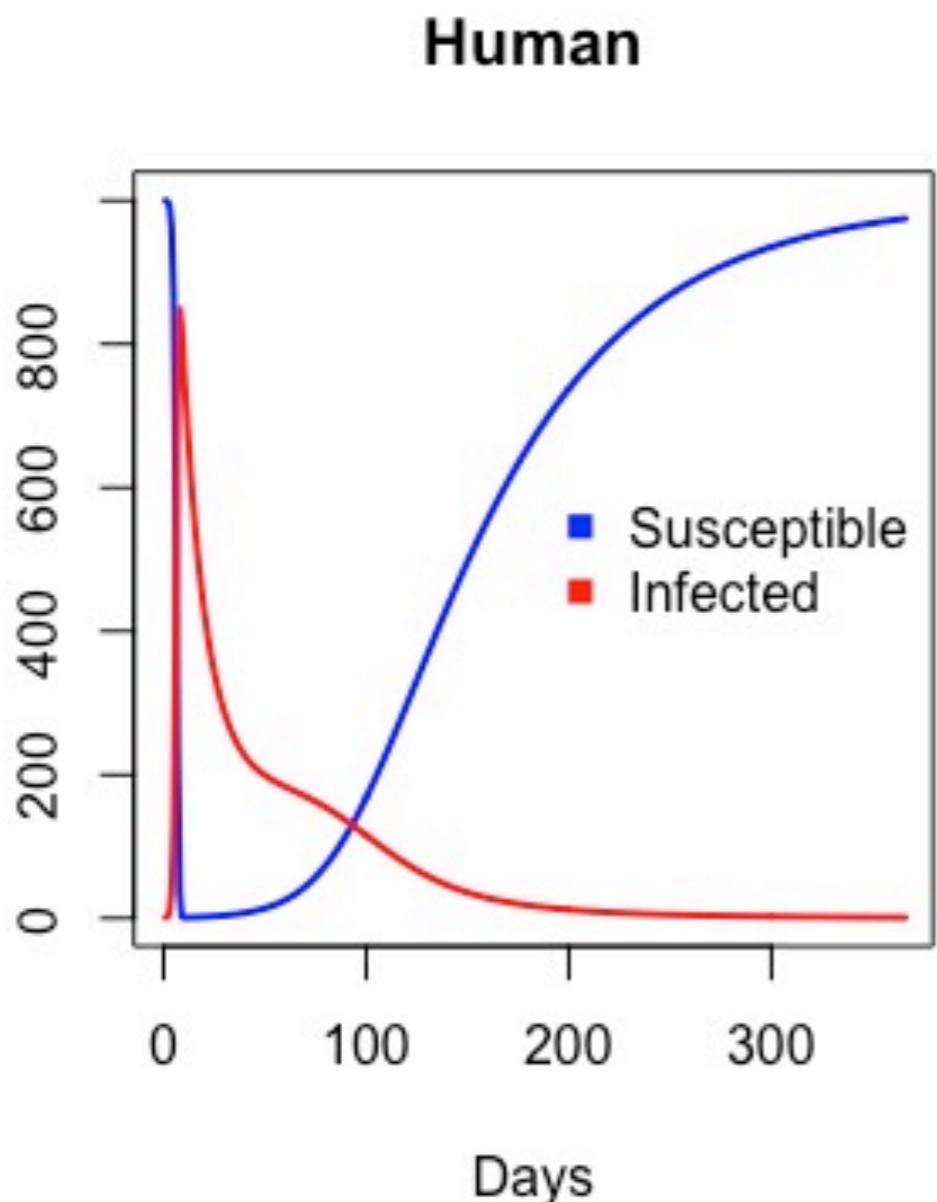
$$\frac{dI_V(t)}{dt} = \beta_V S_V I_H - \sigma I_V$$



The basic vector model: dynamics

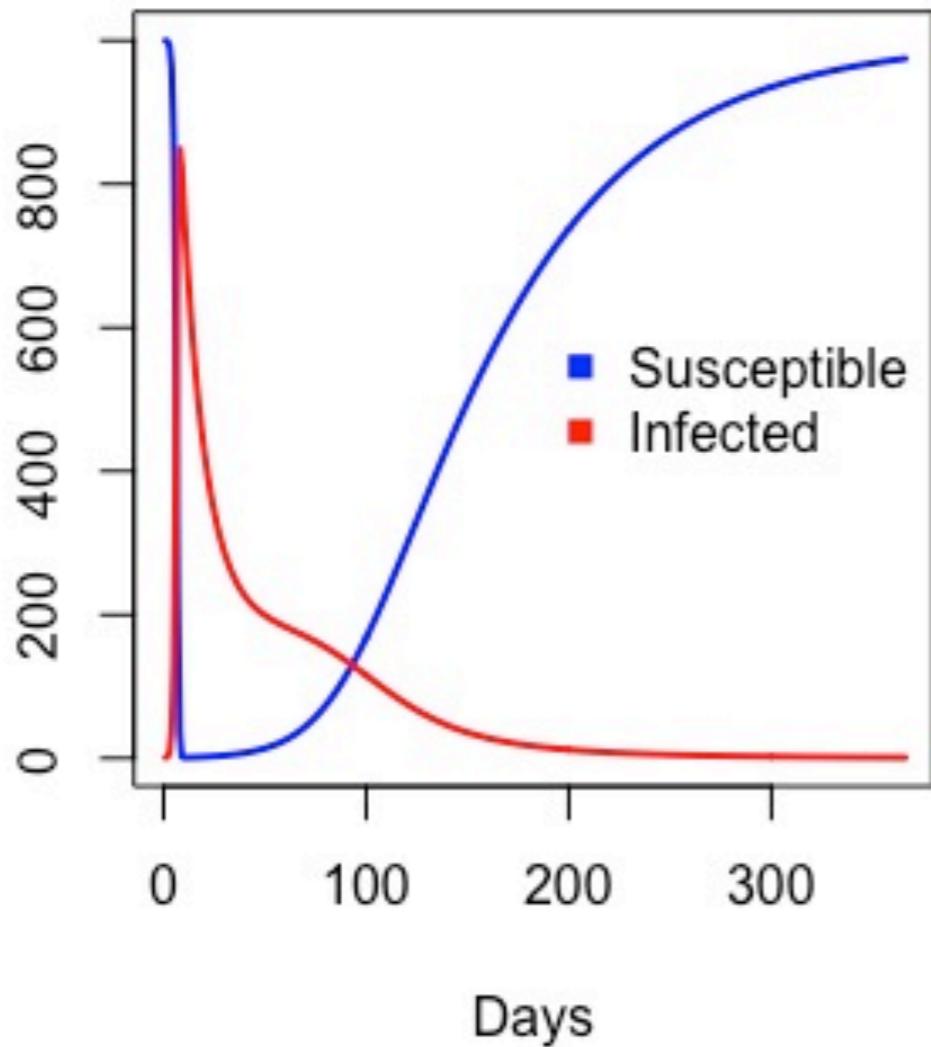


The basic vector model: dynamics

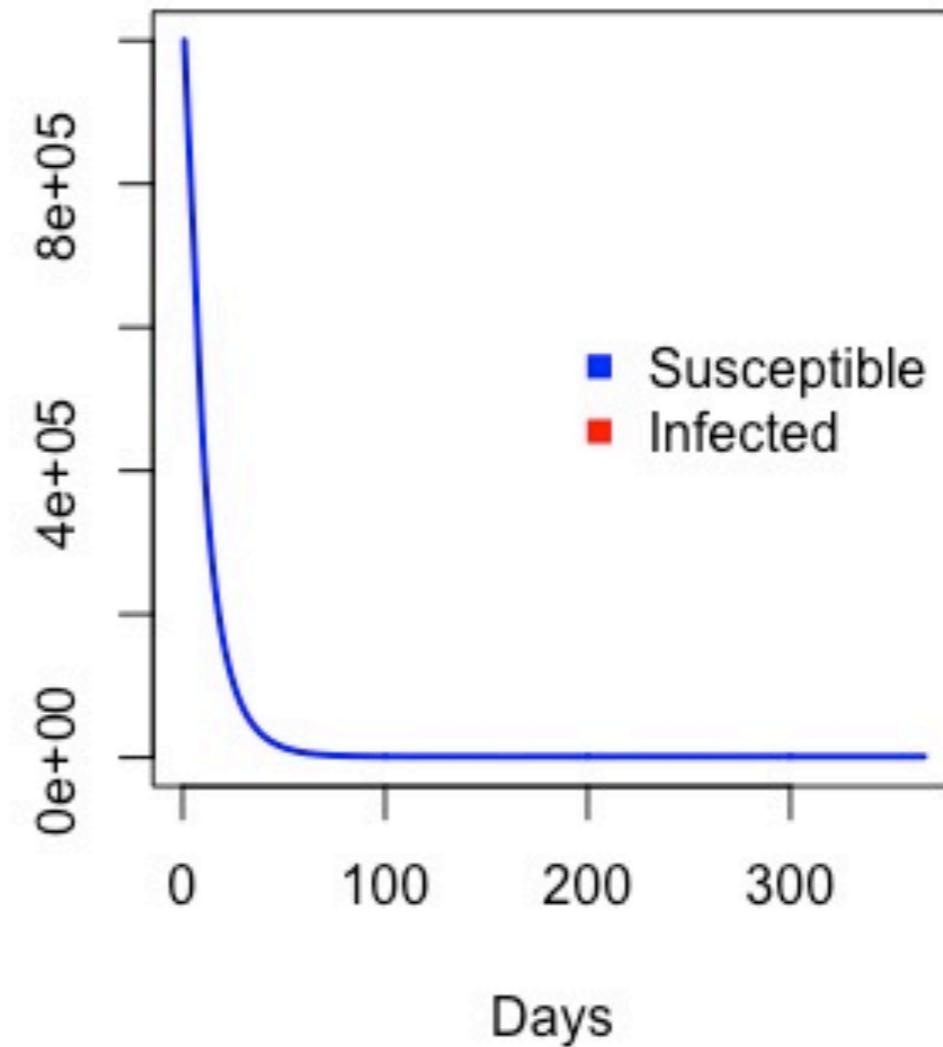


The basic vector model: dynamics

Human

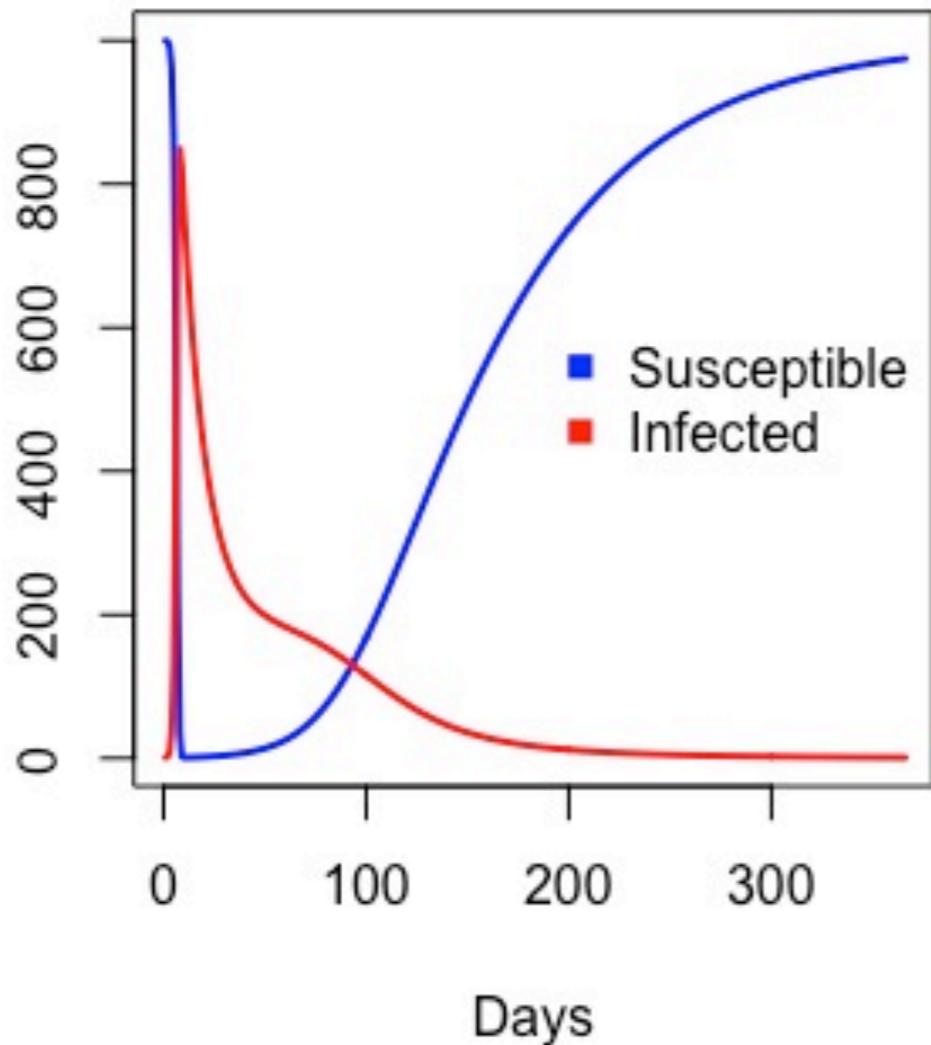


Vector

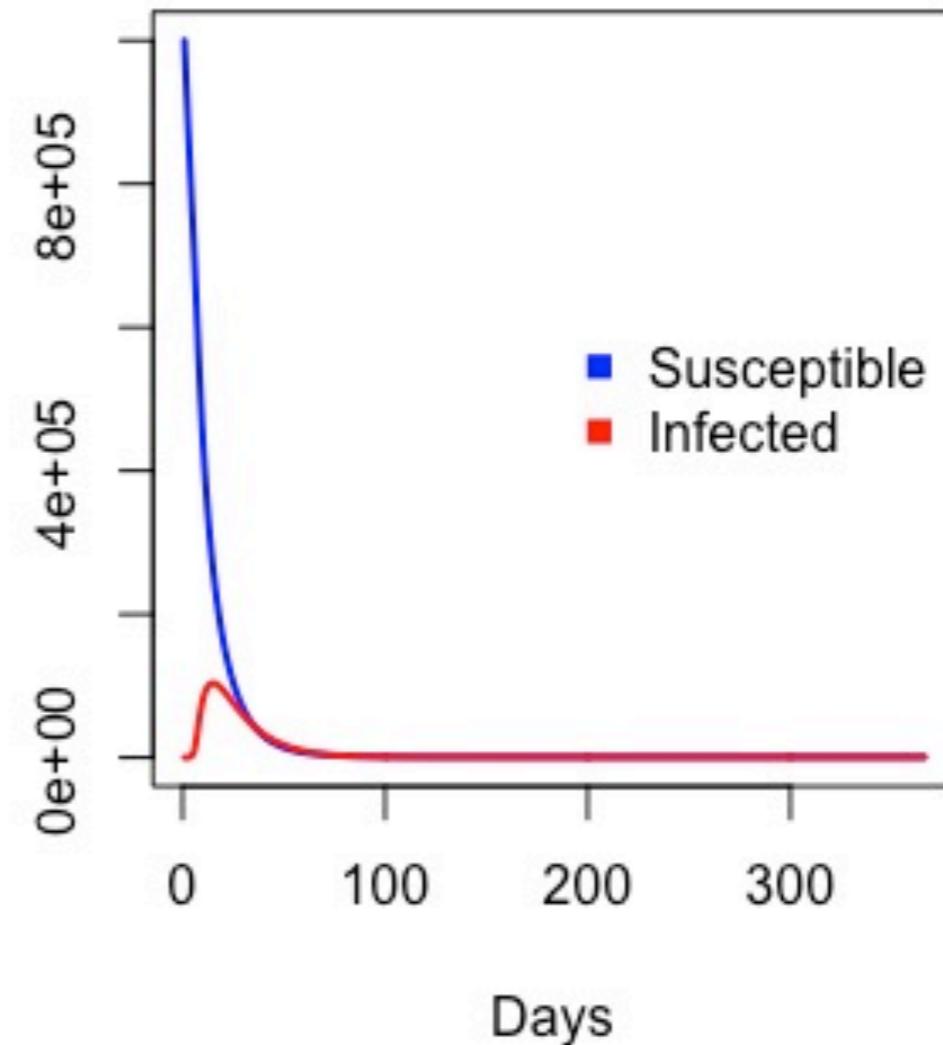


The basic vector model: dynamics

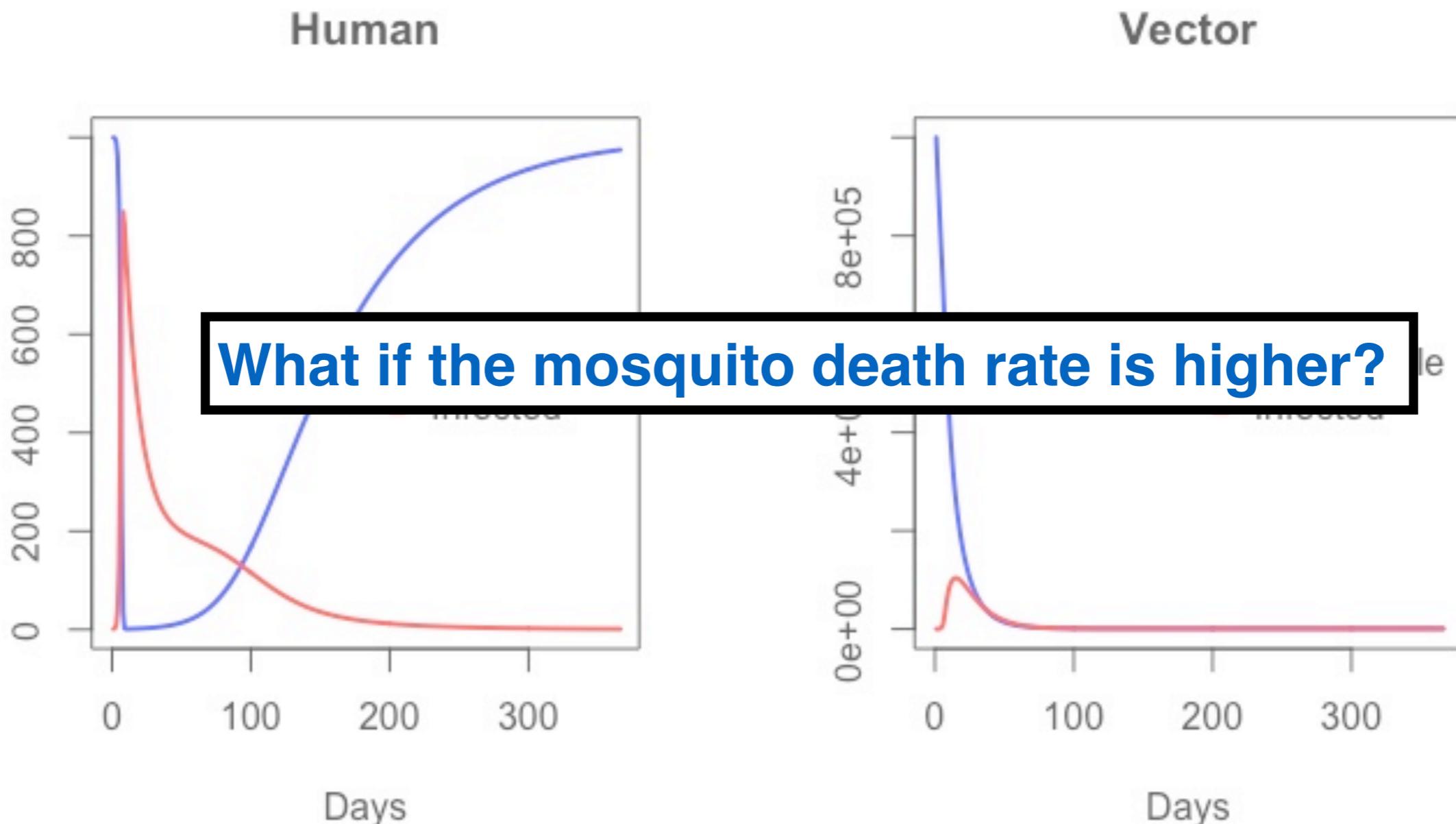
Human



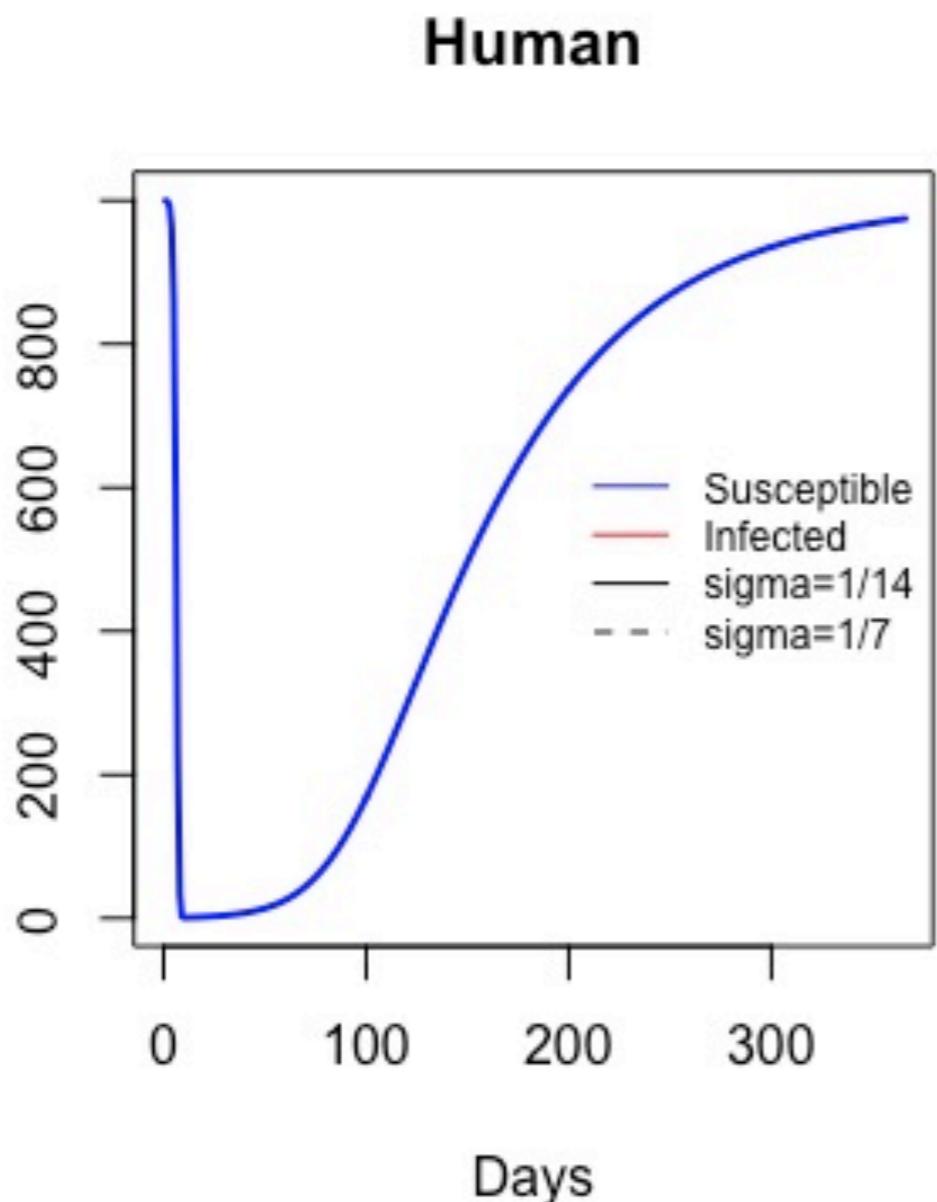
Vector



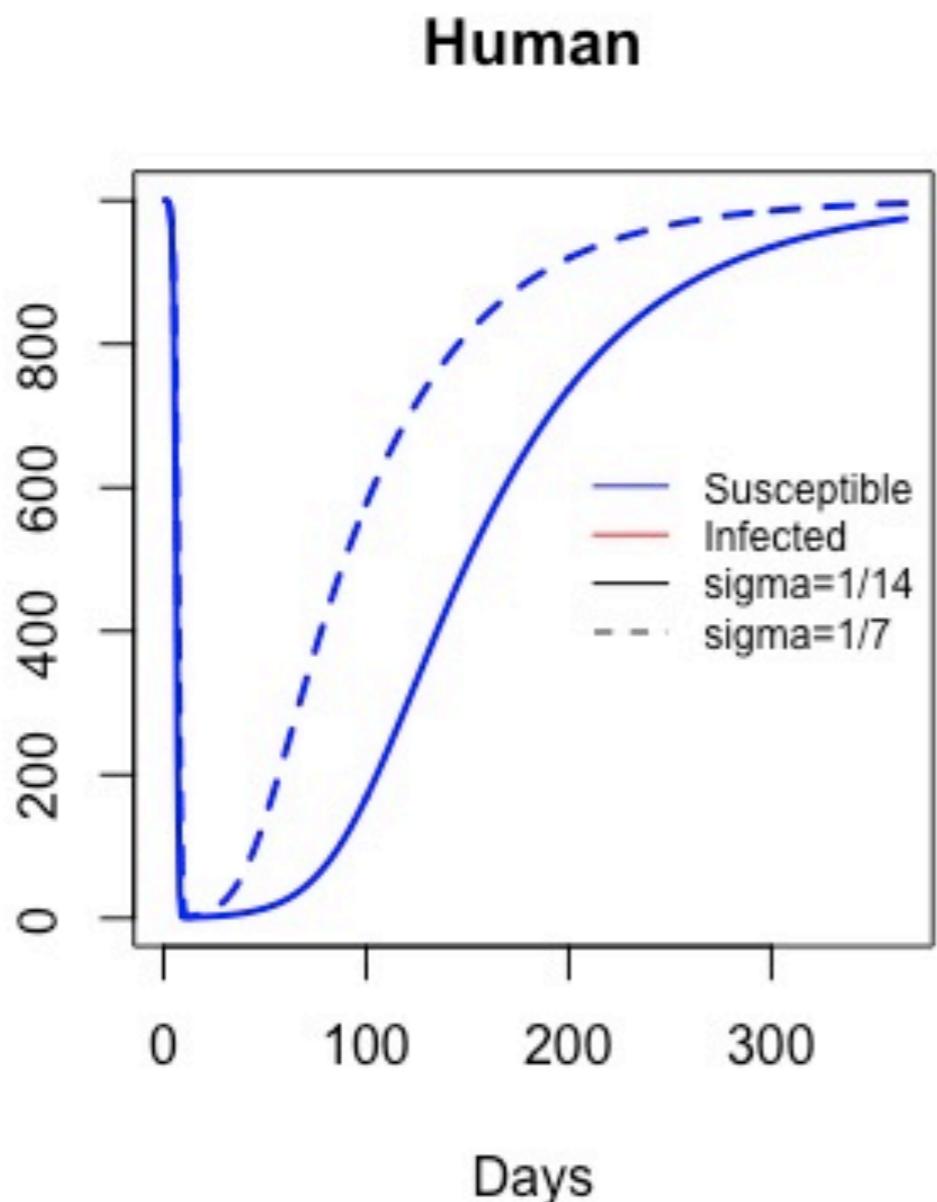
The basic vector model: dynamics



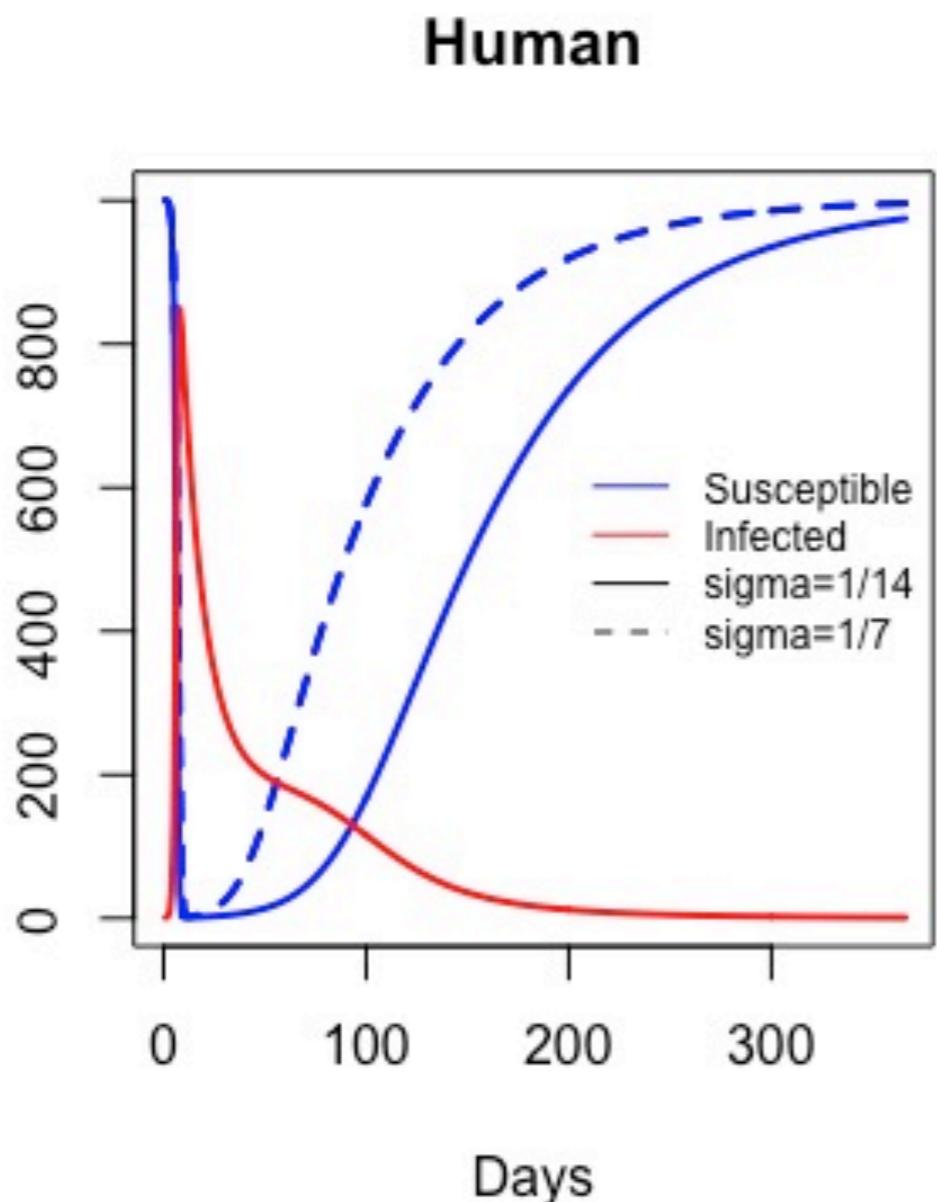
The basic vector model: dynamics



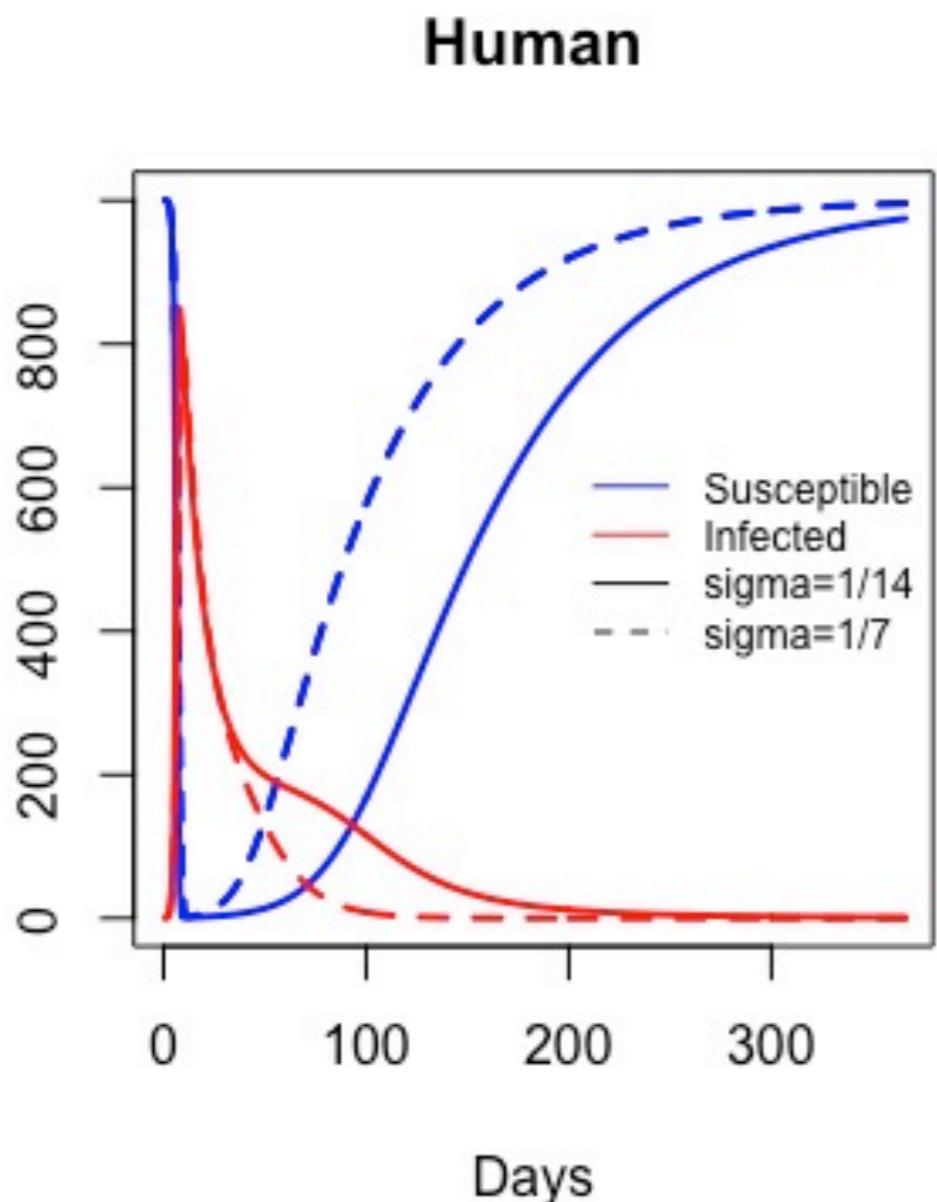
The basic vector model: dynamics



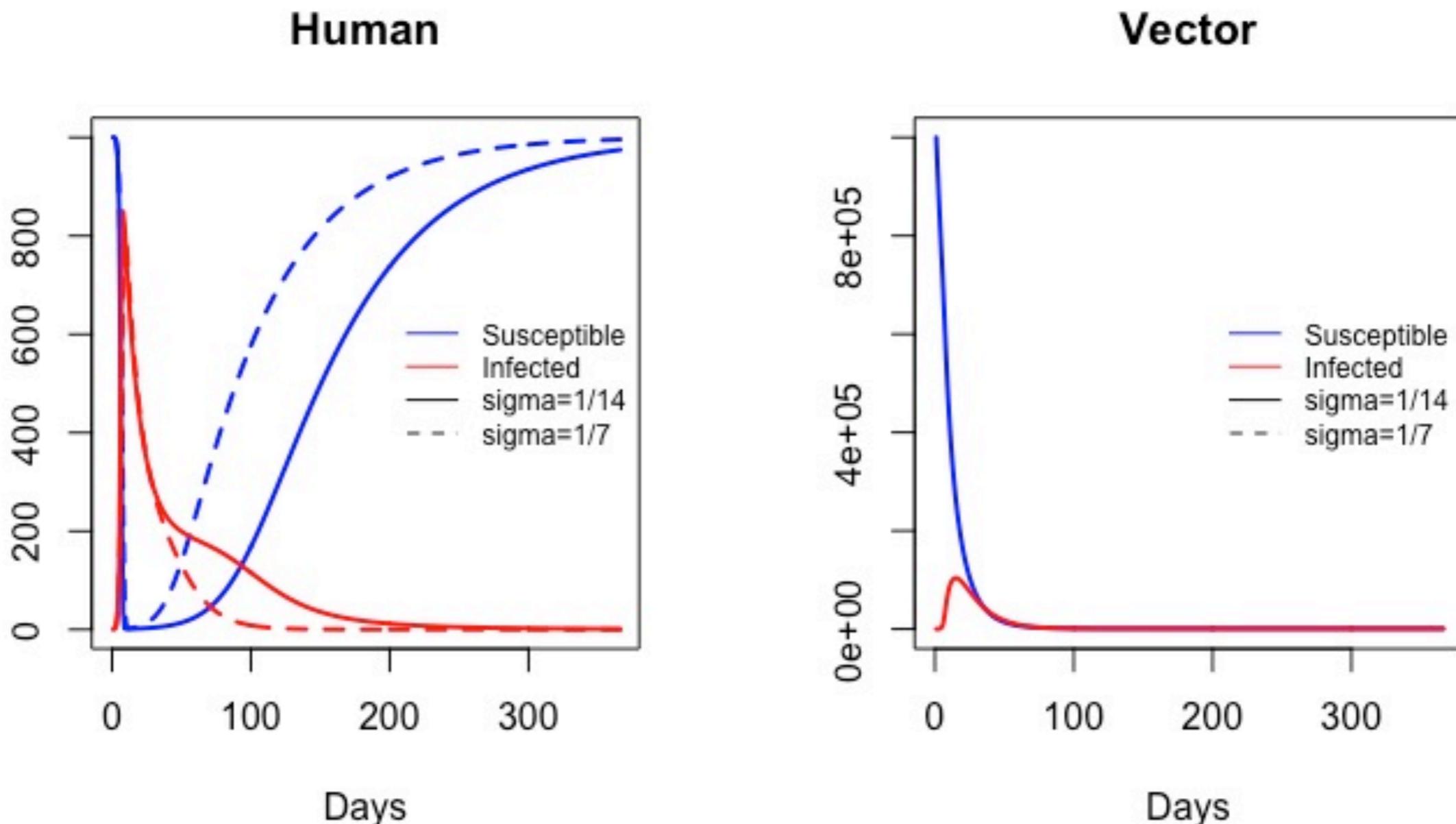
The basic vector model: dynamics



The basic vector model: dynamics

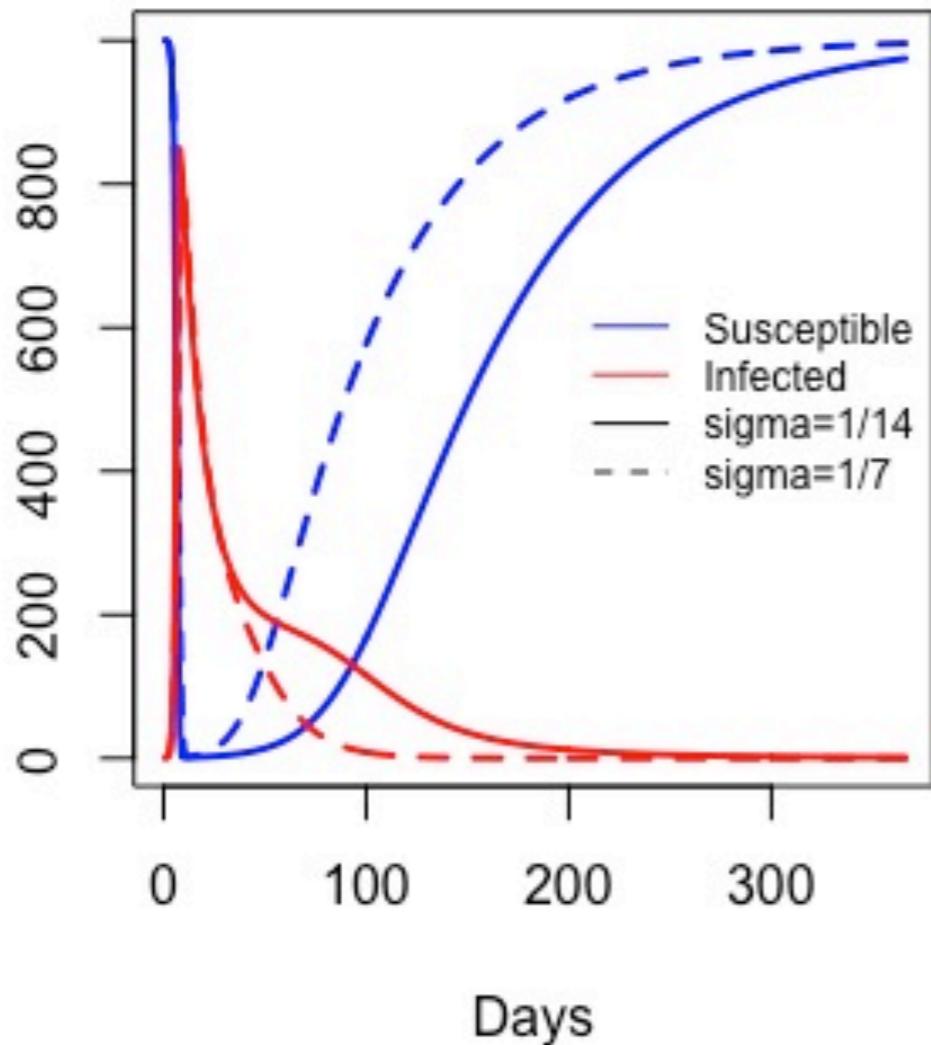


The basic vector model: dynamics

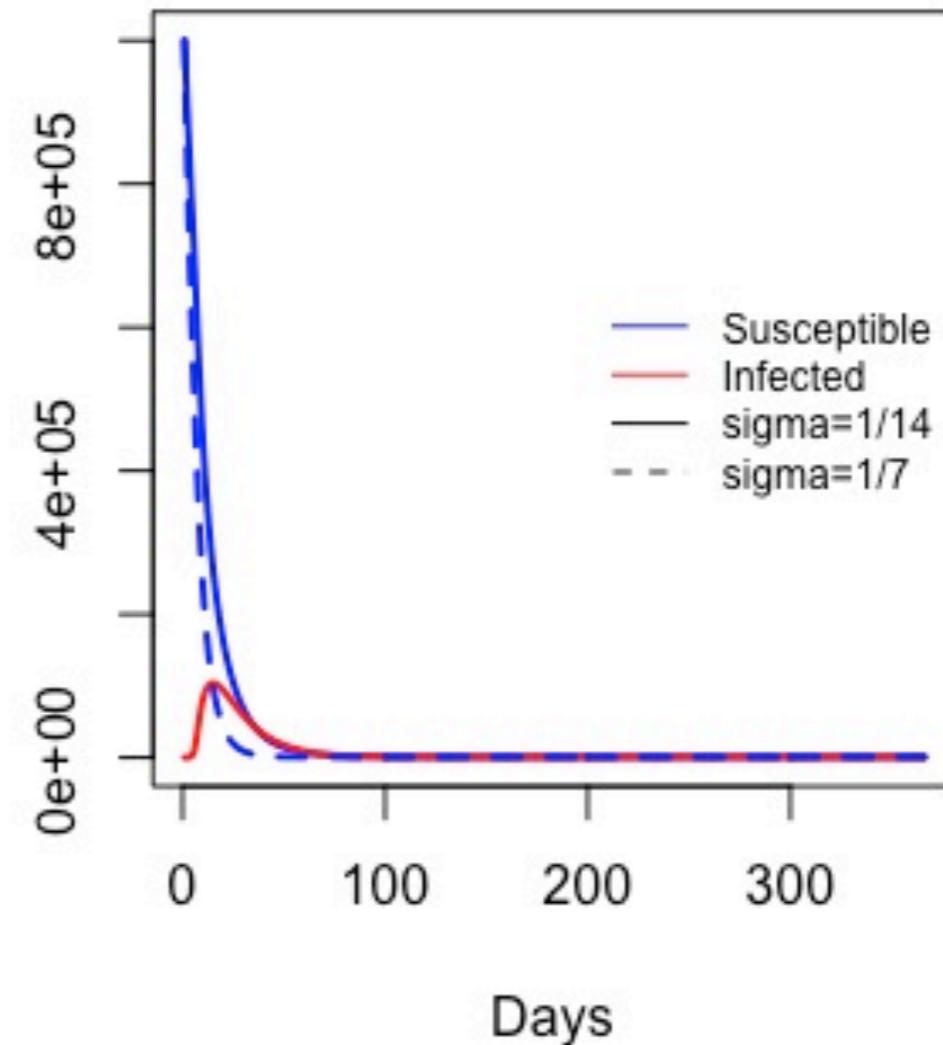


The basic vector model: dynamics

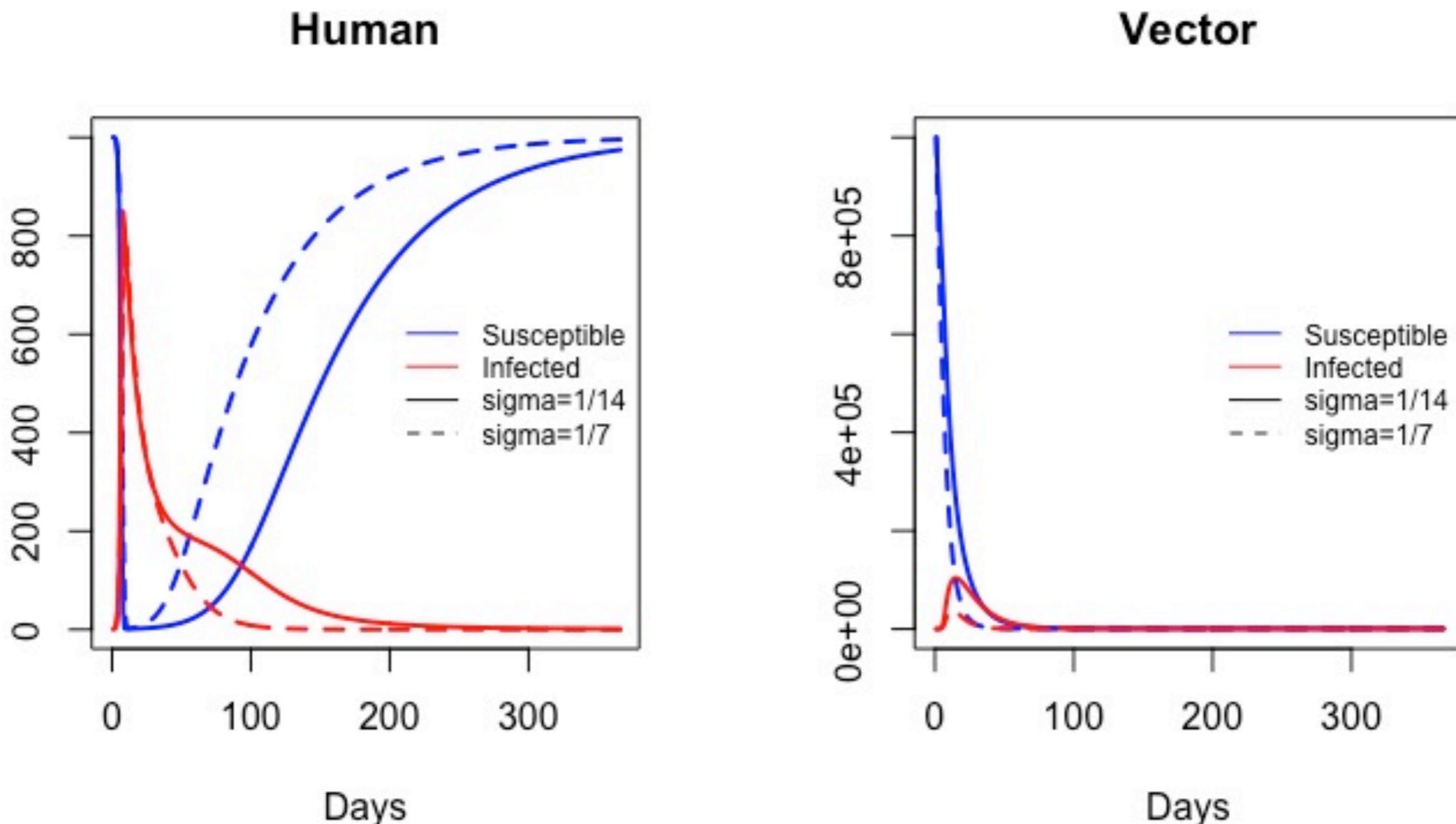
Human

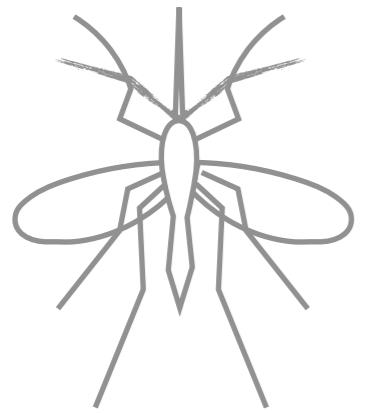


Vector



The basic vector model: dynamics

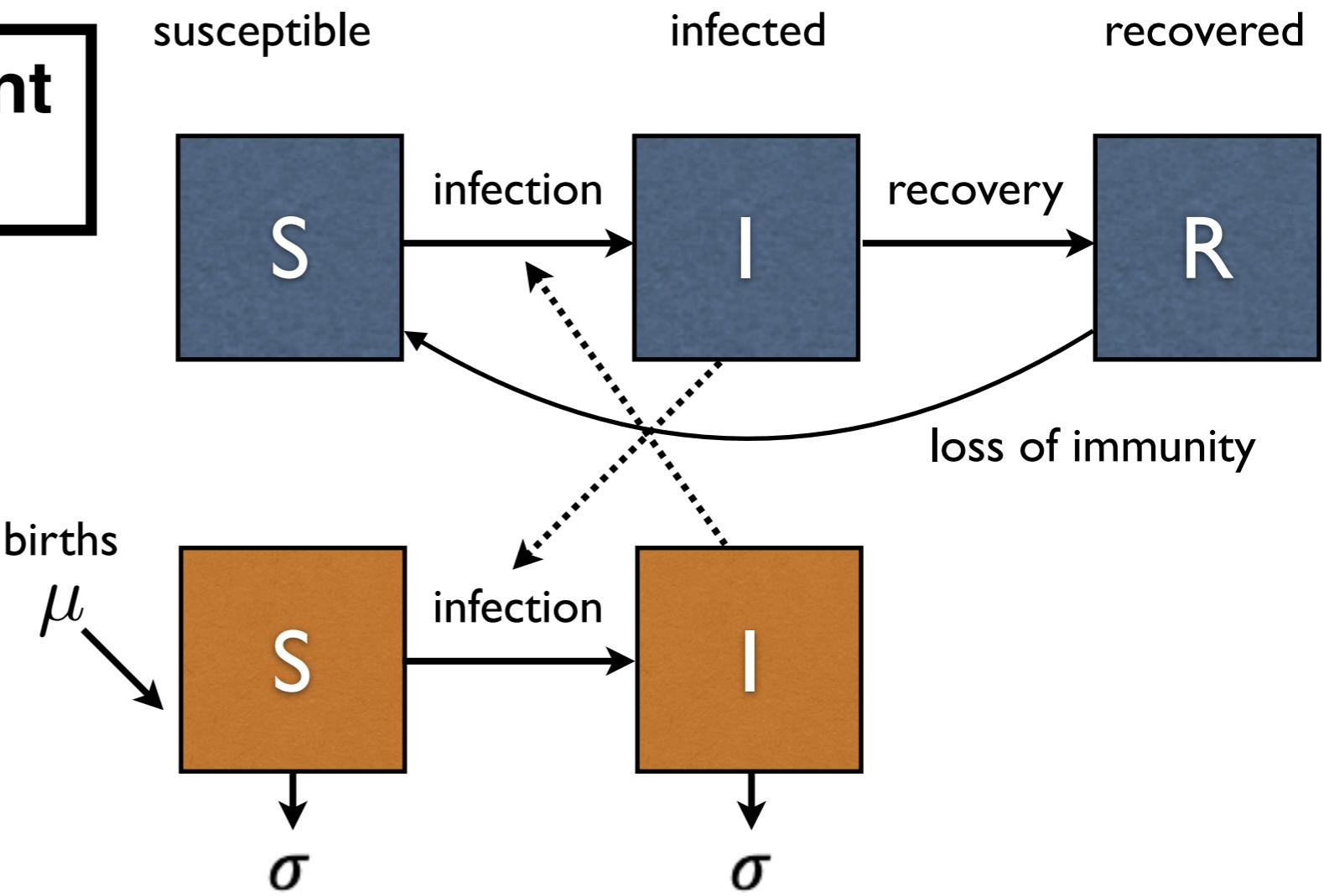




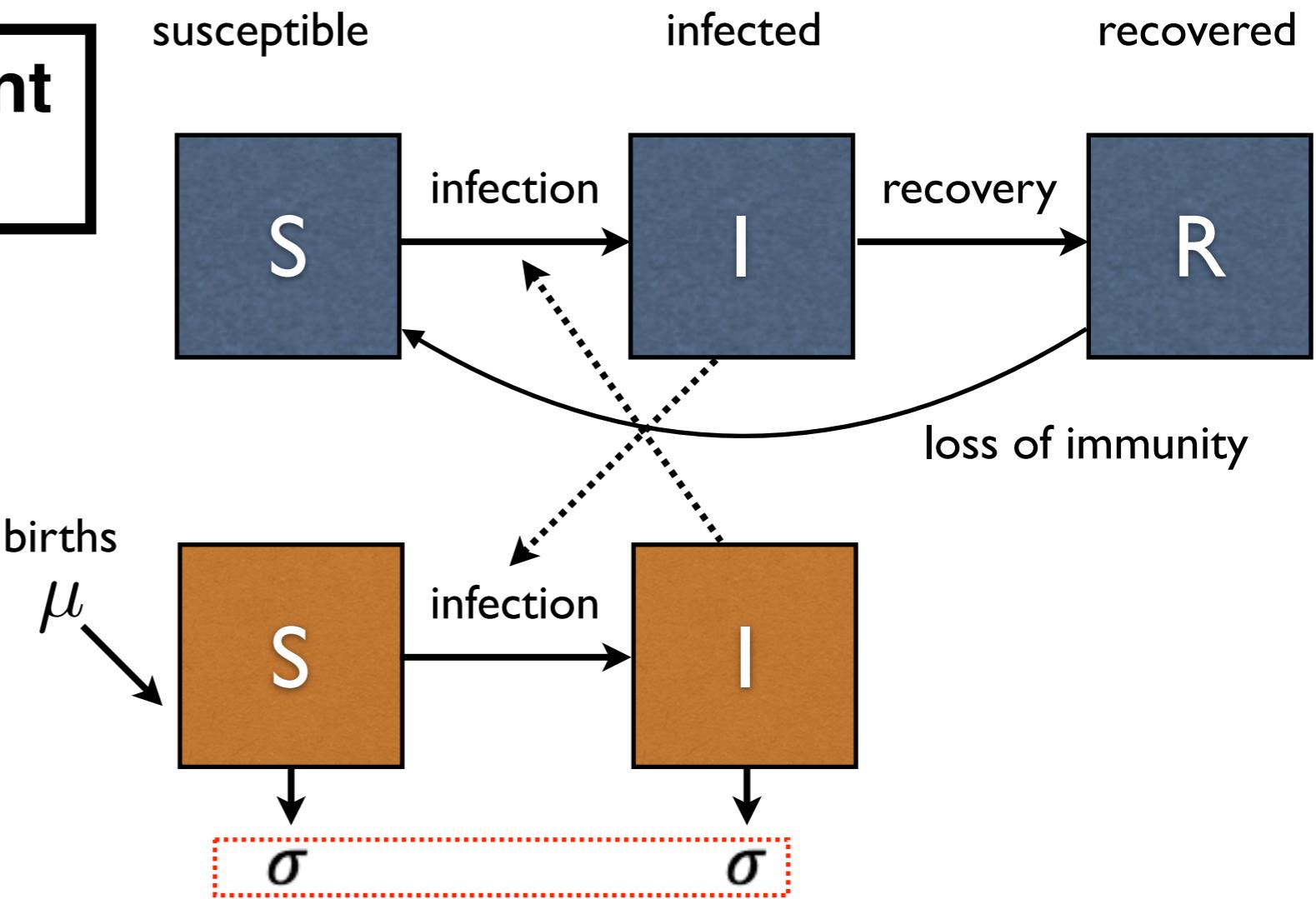
2. Incorporating temperature



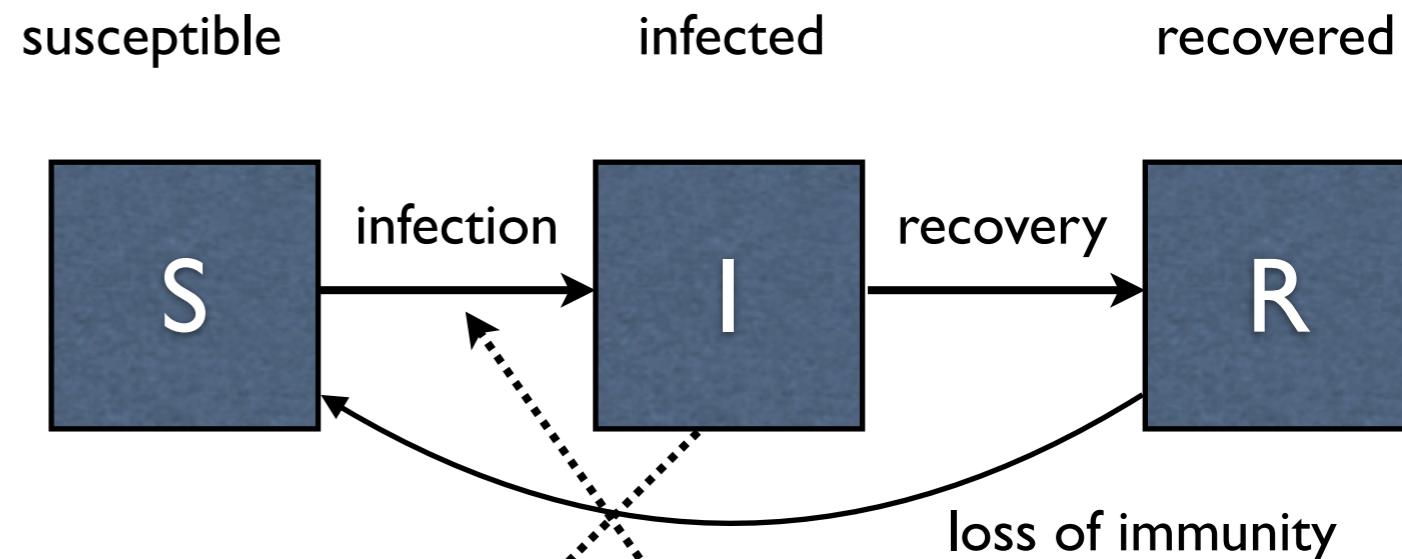
Temperature dependent vector mortality



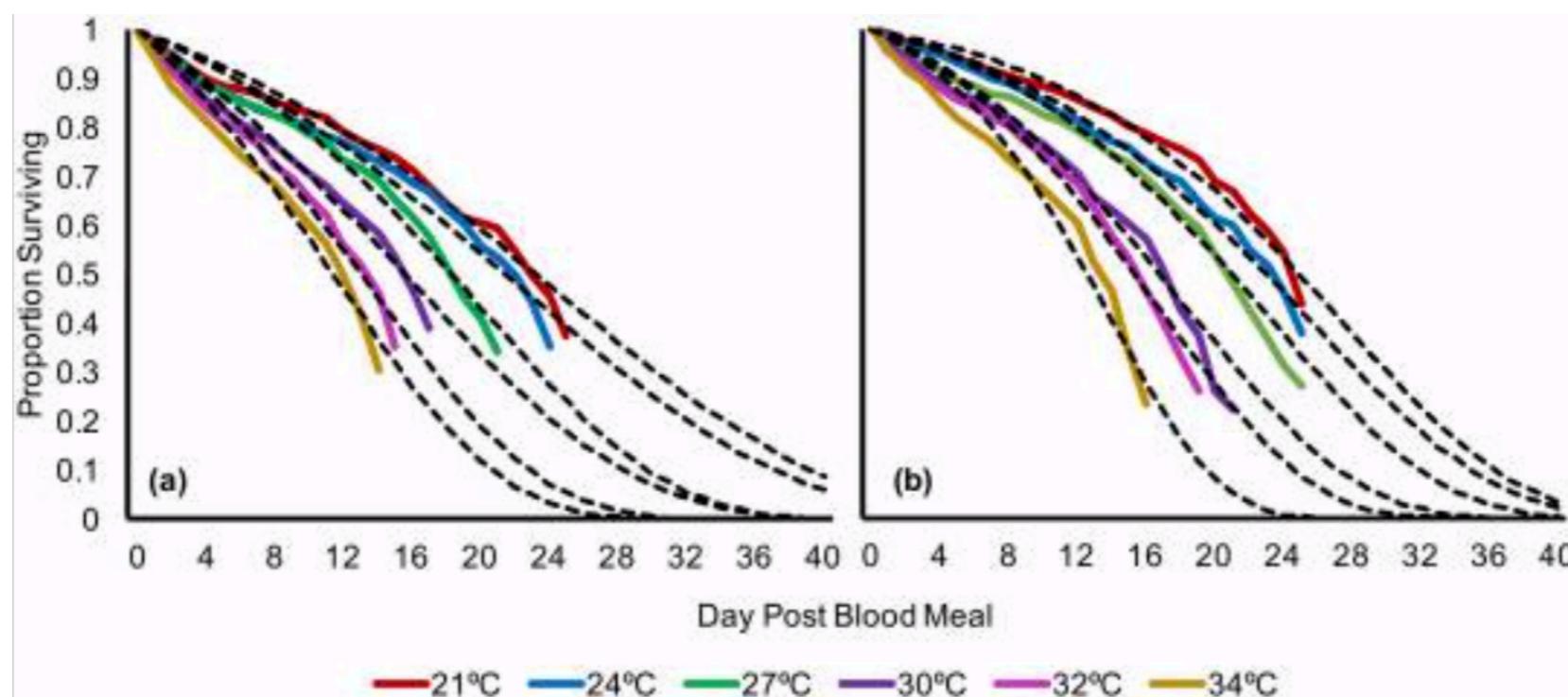
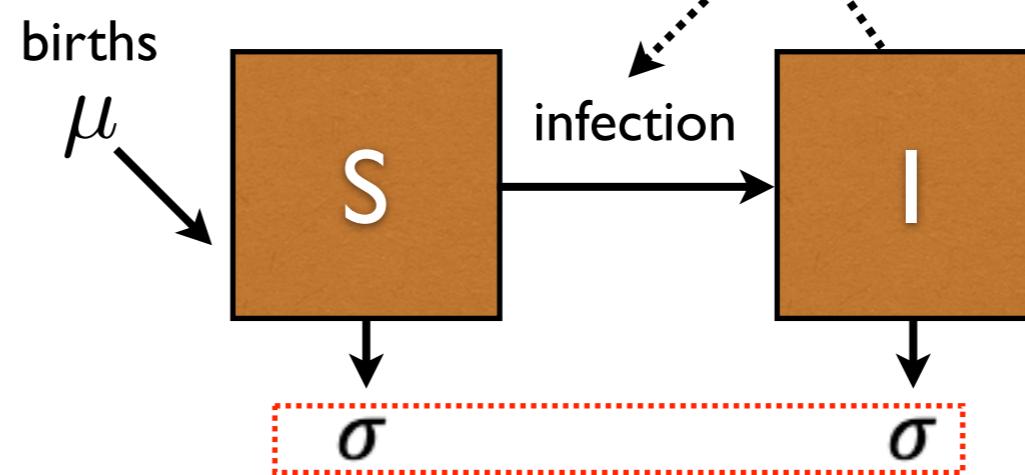
Temperature dependent vector mortality



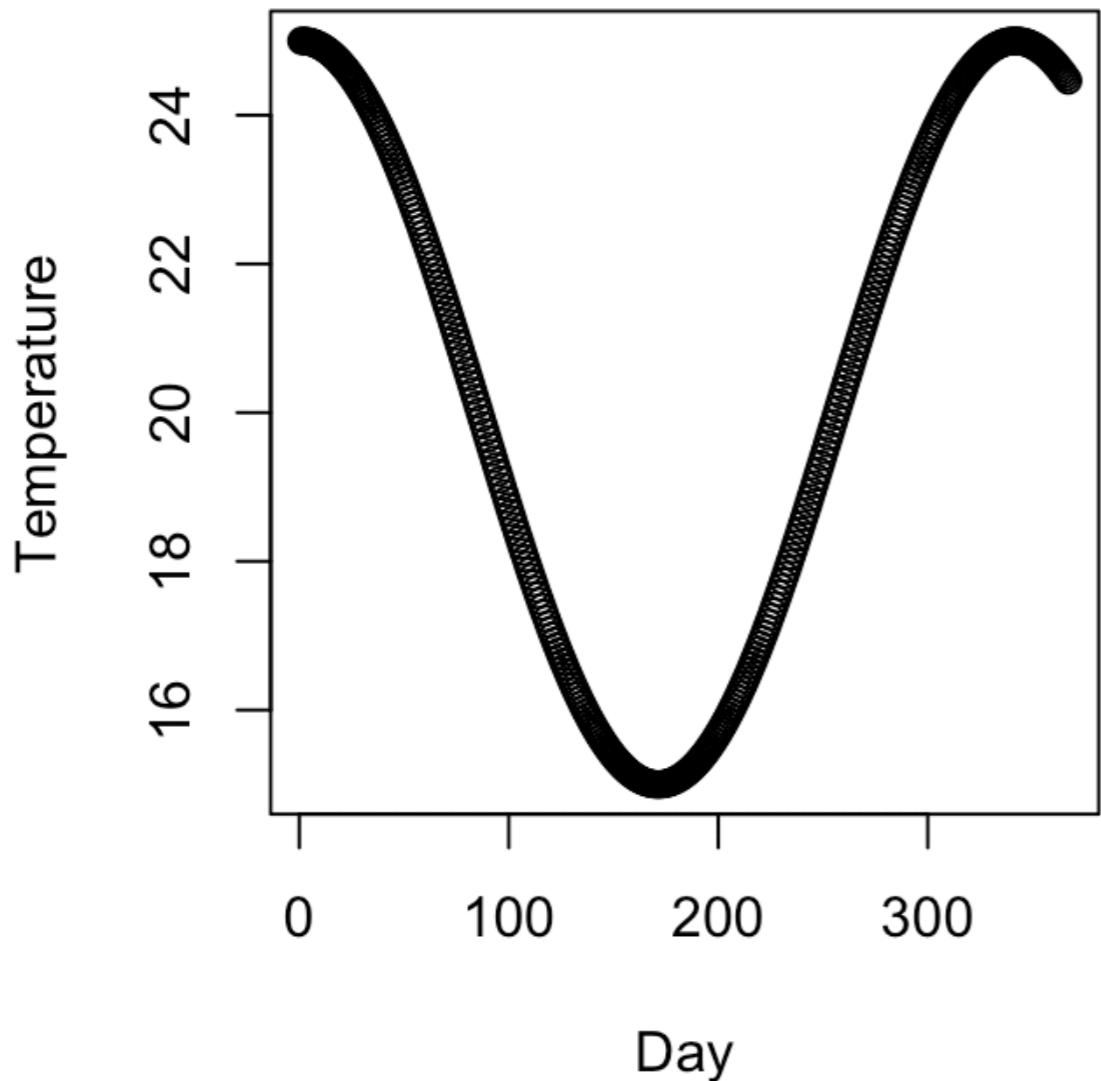
Temperature dependent vector mortality



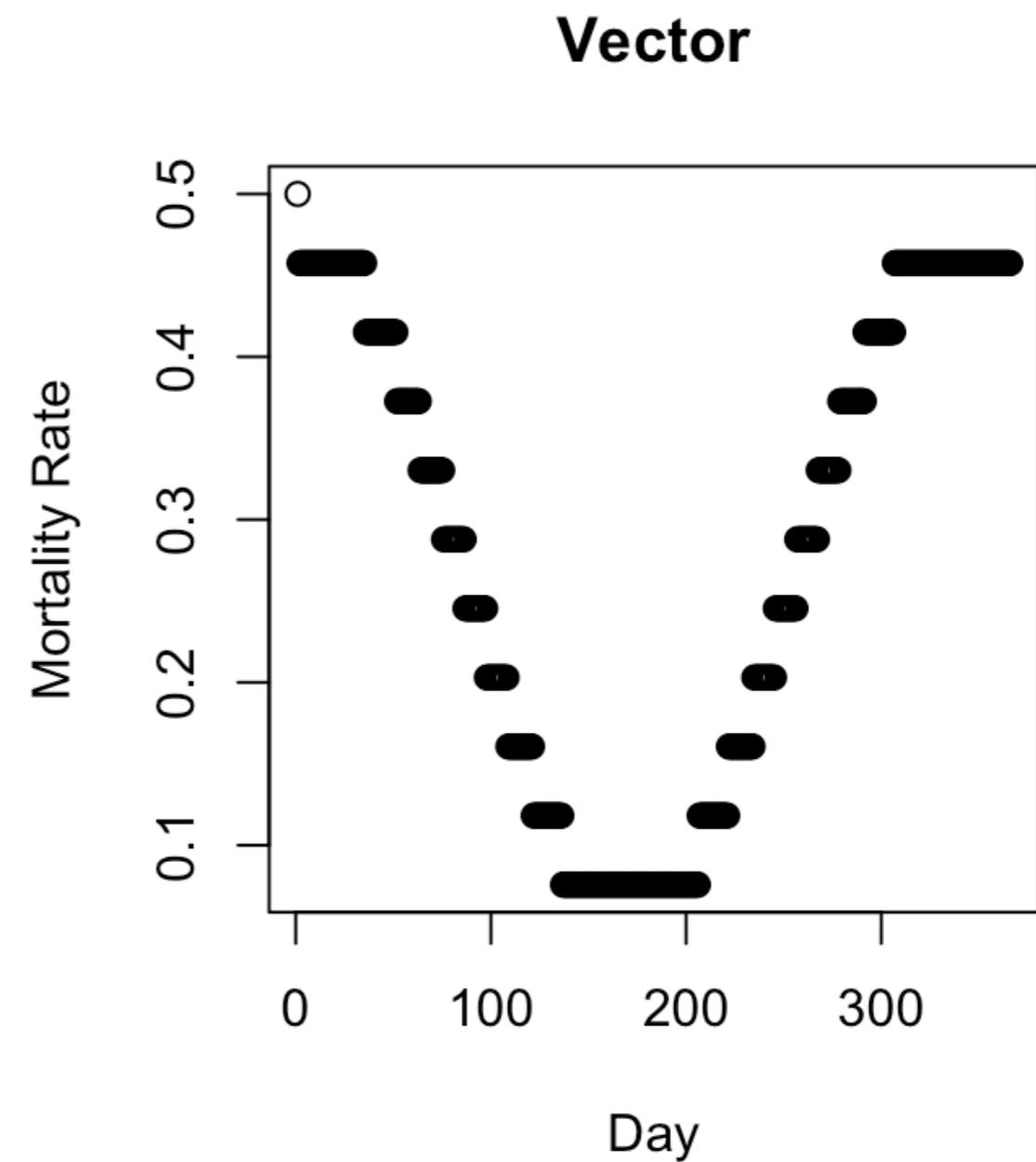
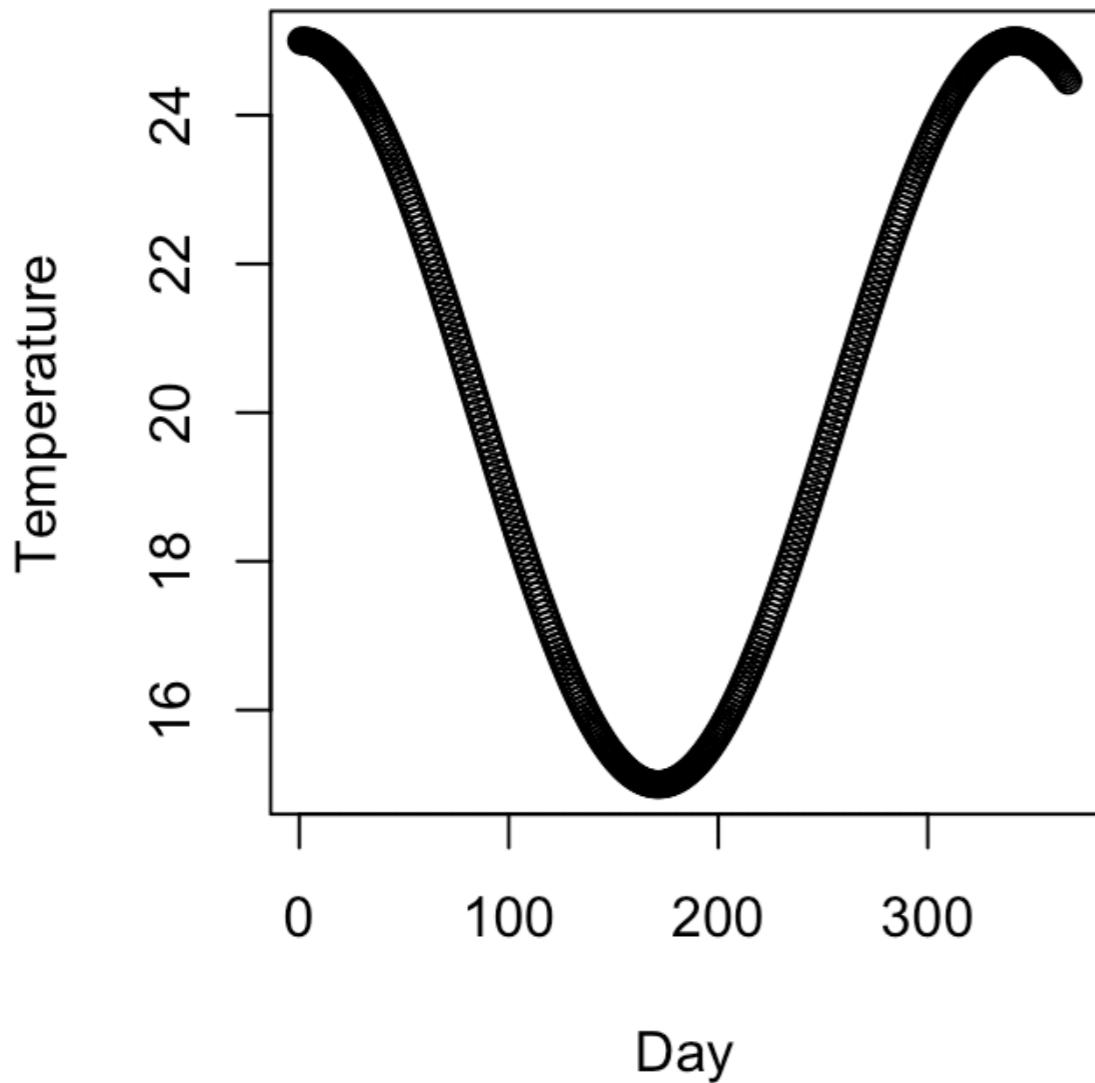
Shapiro LLM. et al. (2017). Quantifying the effects of temperature on mosquito and parasite traits that determine the transmission potential of human malaria. *PLoS Bio*, 15(10): e2003489.



Temperature dependent vector mortality: dynamics

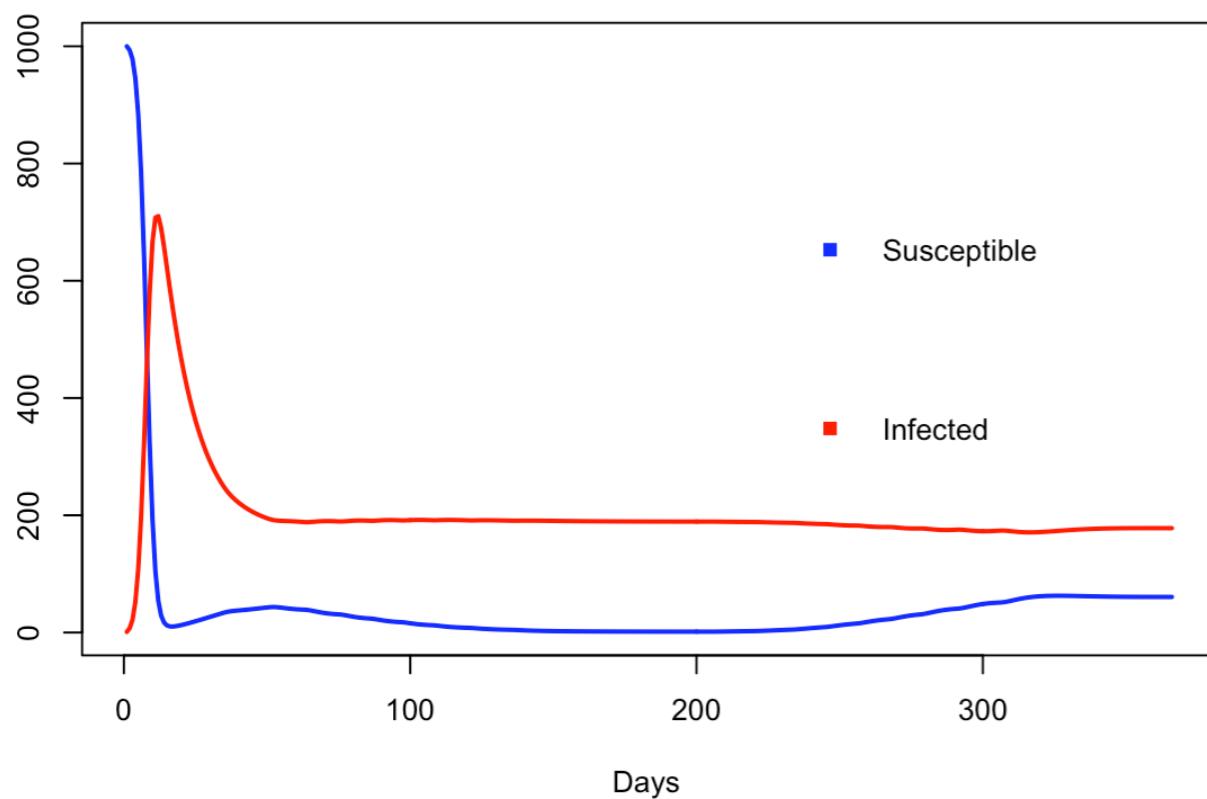


Temperature dependent vector mortality: dynamics

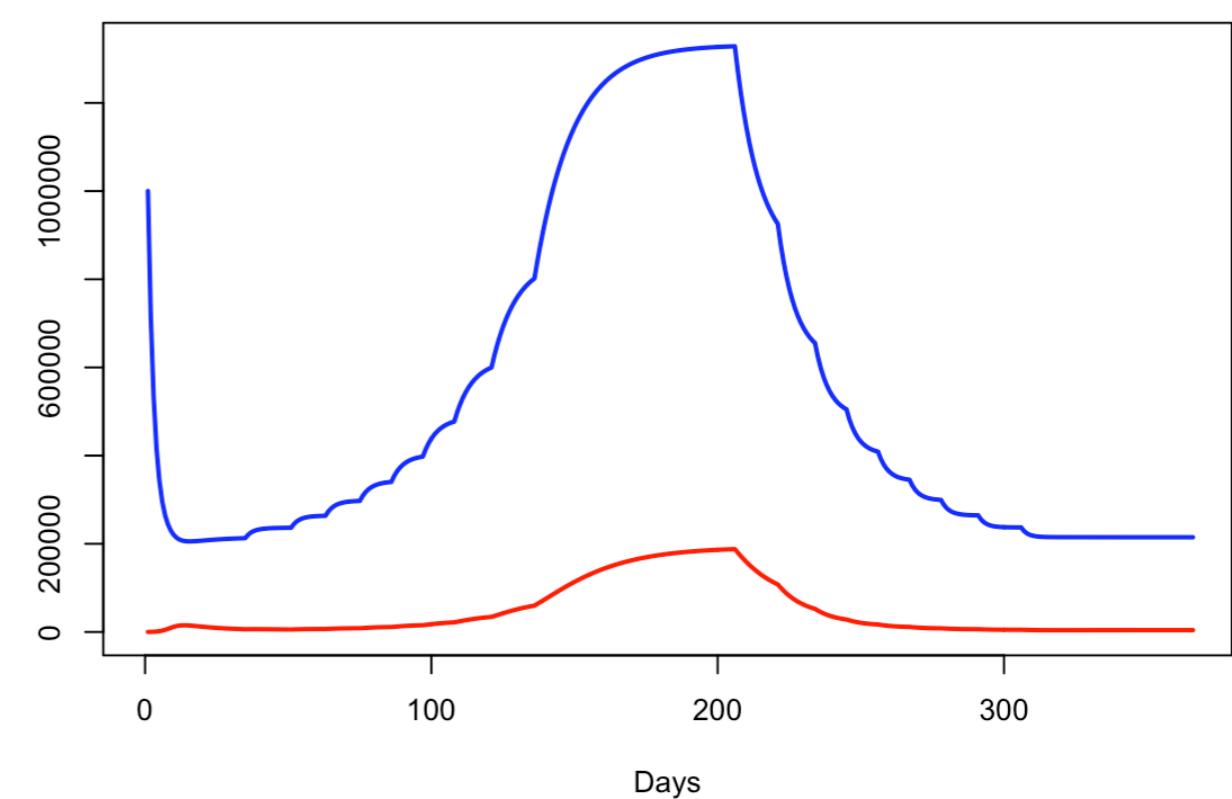


Temperature dependent vector mortality: dynamics

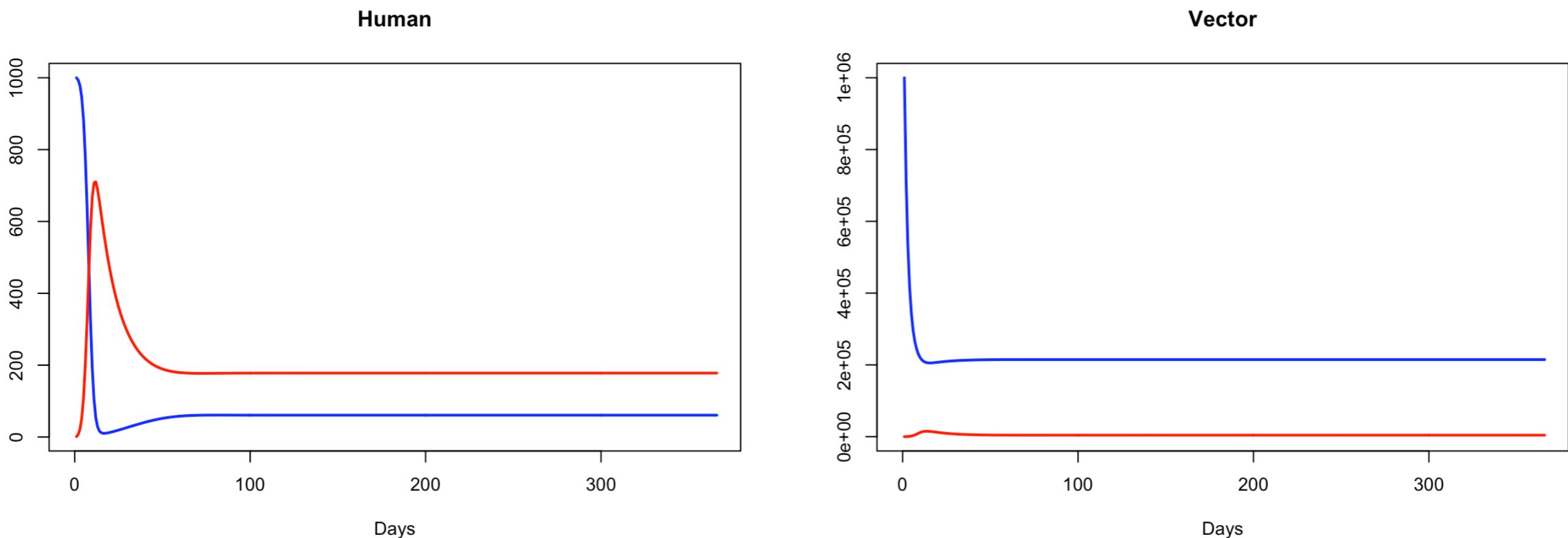
Human

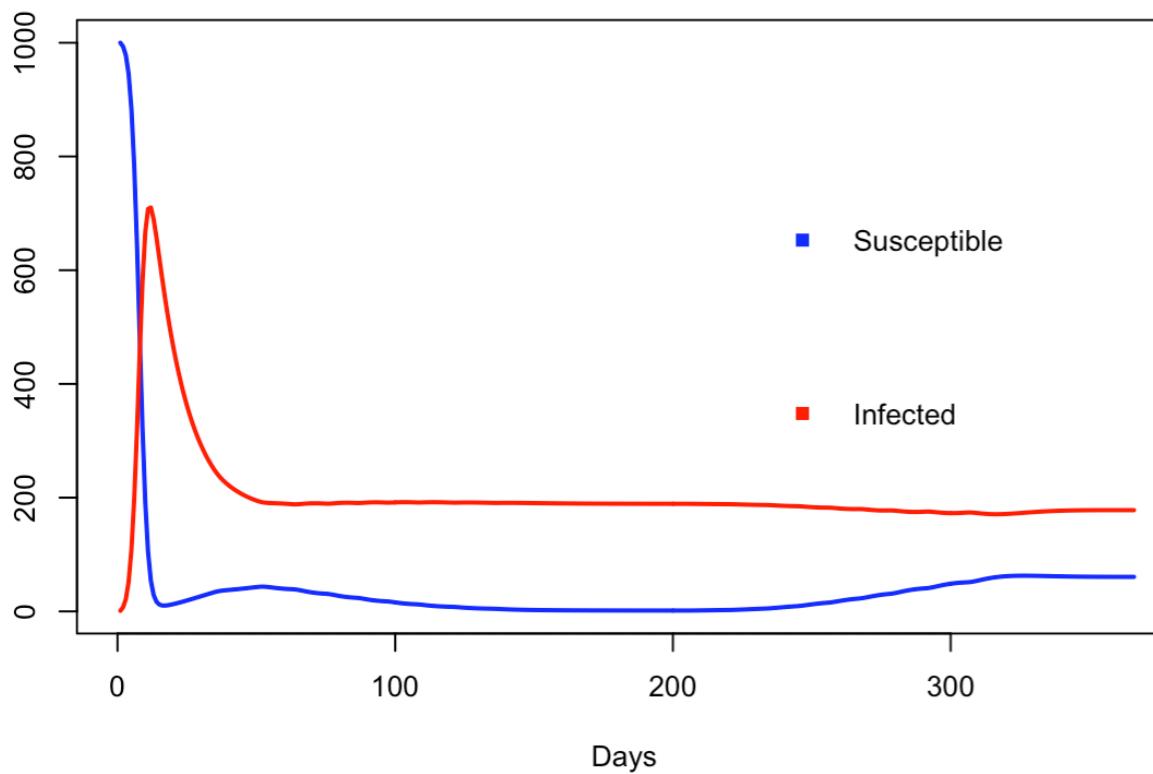
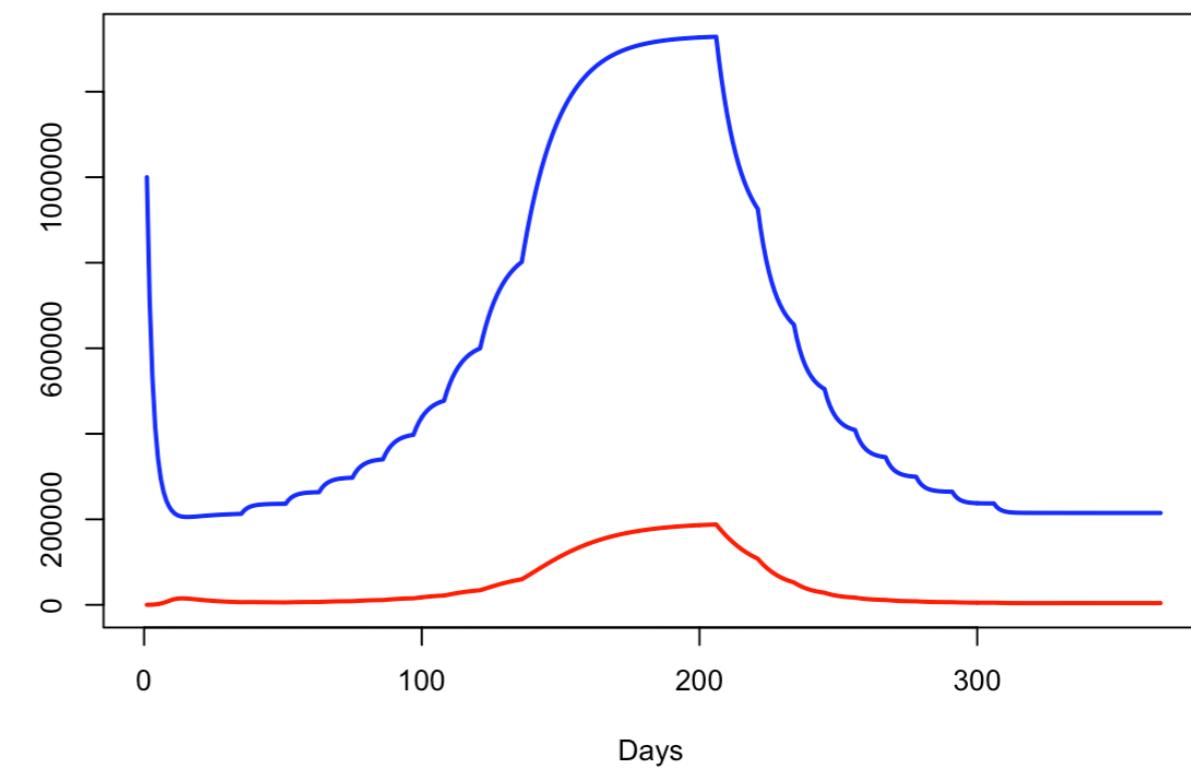
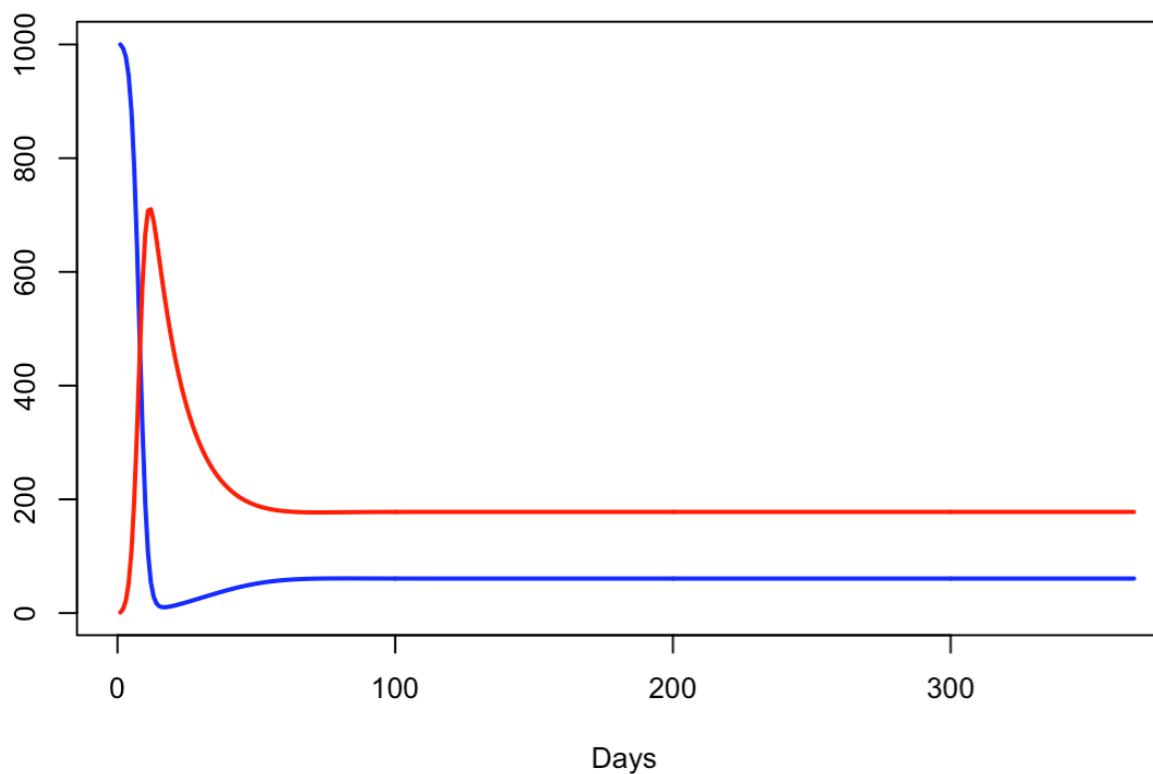
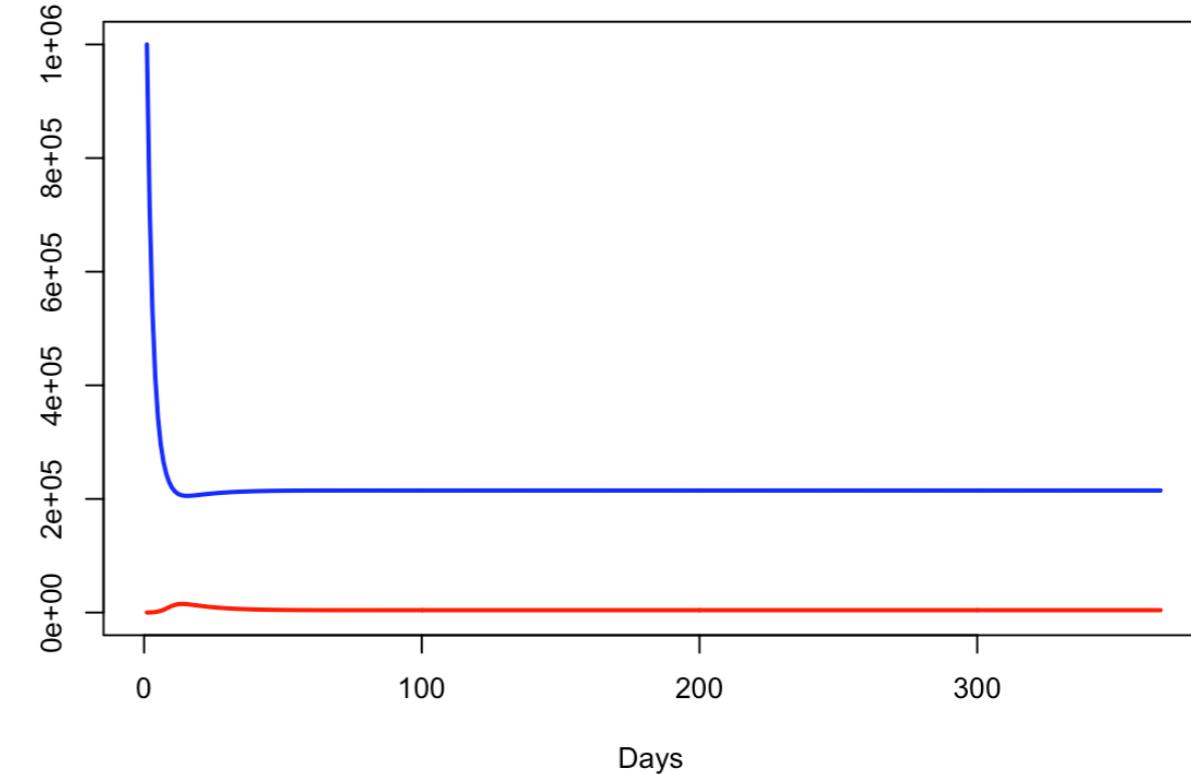


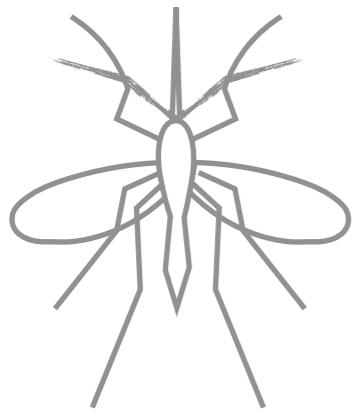
Vector



Temperature dependent vector mortality: dynamics



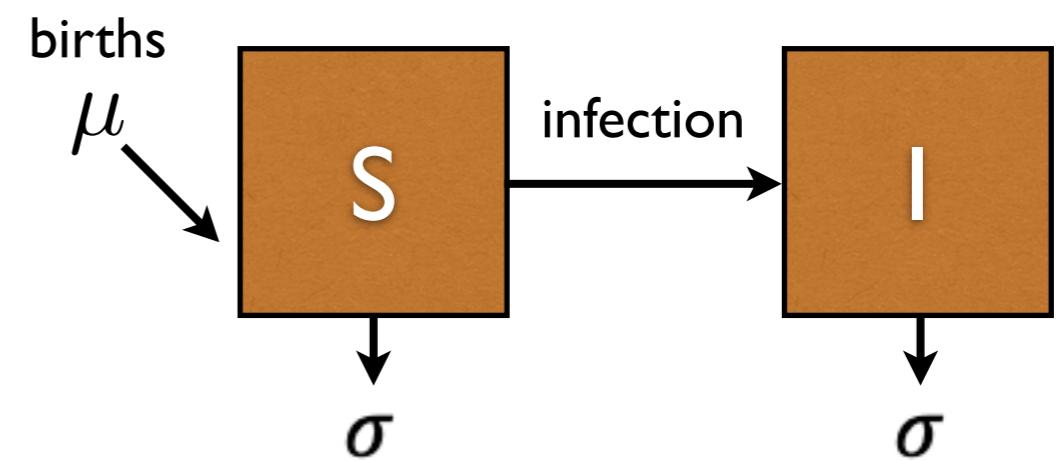
Human**Vector****Human****Vector**



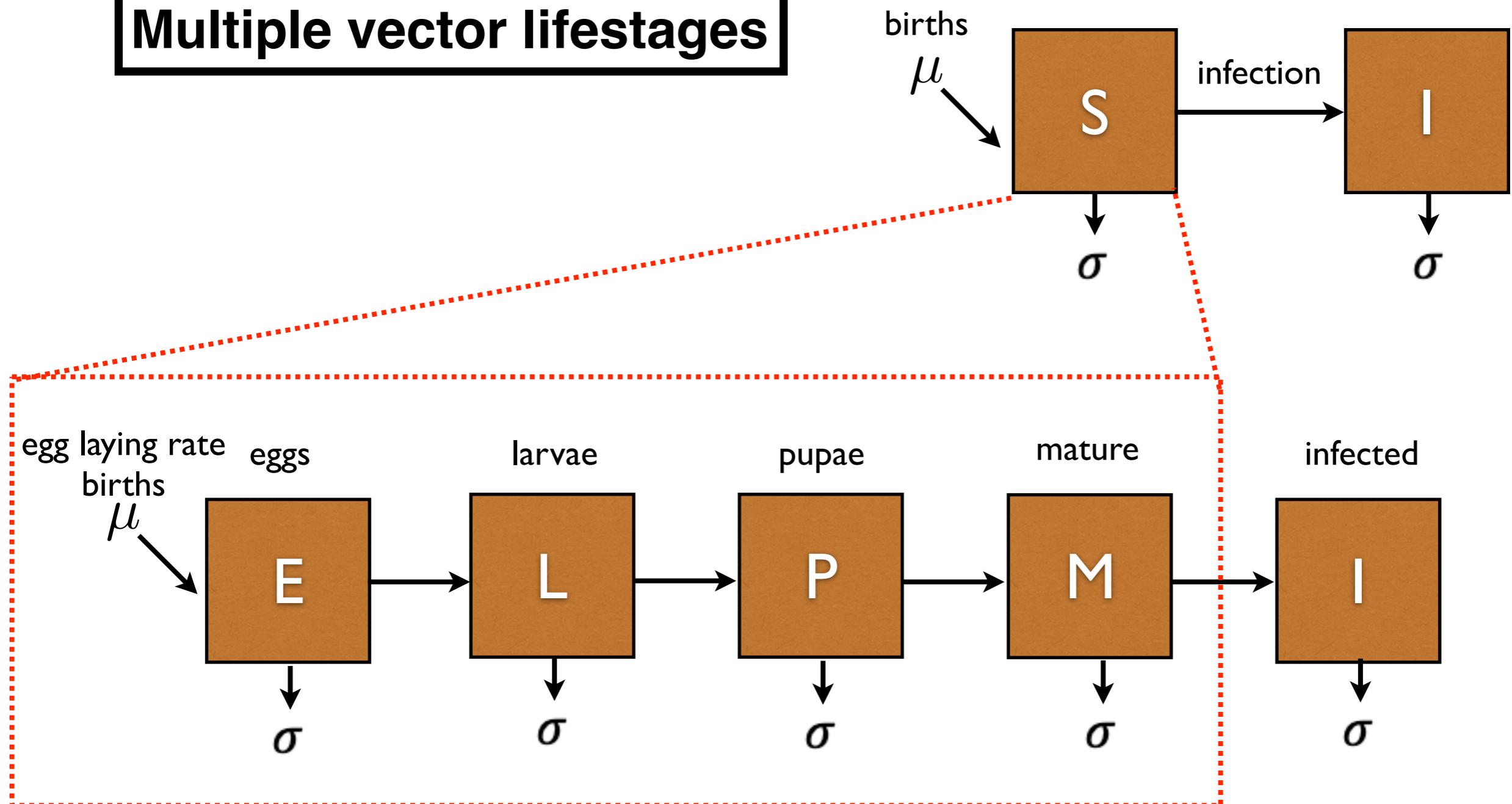
3. Increasing complexity about the vector lifecycle

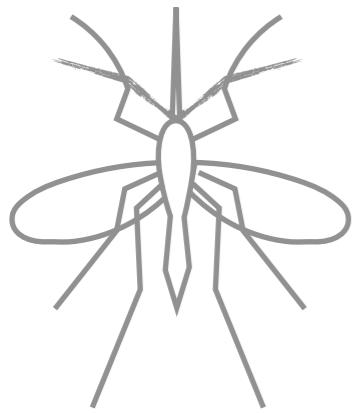


Multiple vector lifestages



Multiple vector lifestages





4. How can the dynamics be used for disease control?



What is malaria?

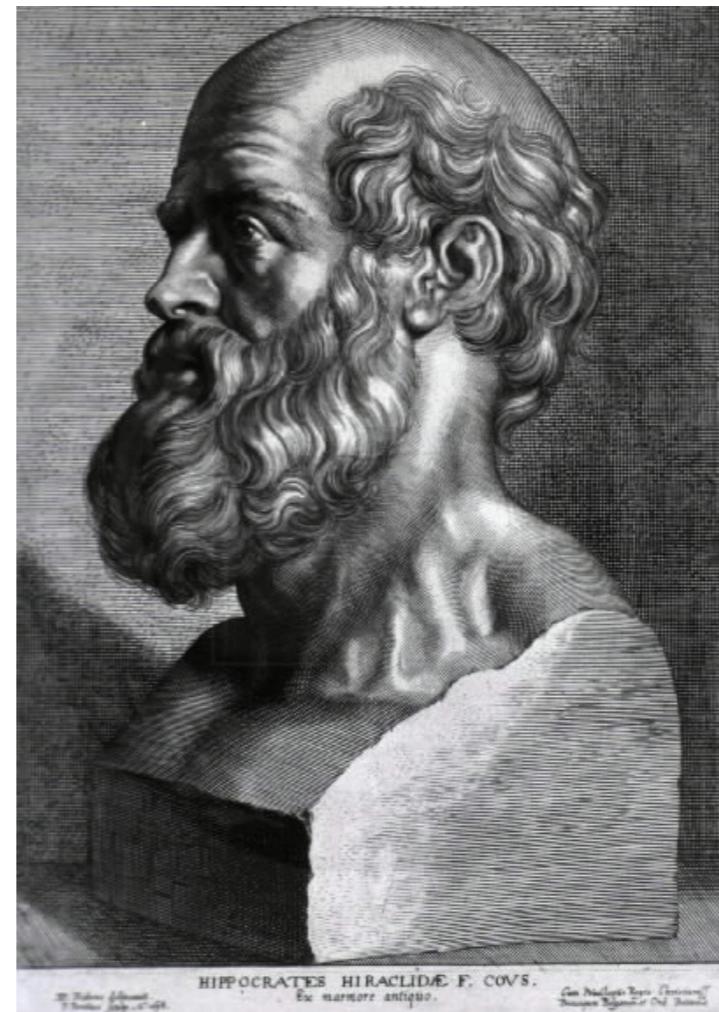
Ebers papyrus

mentions fevers,
rigors, splenomegaly.



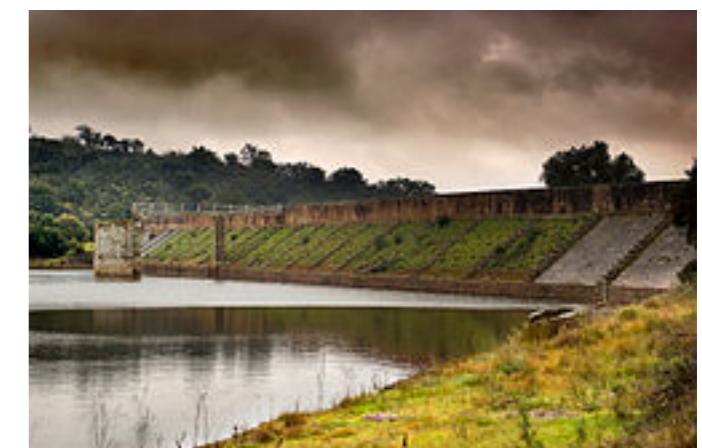
1550 BC

Hippocrates connected stagnant bodies of water and occurrence of fevers in local populations.



460 BC

Romans also associated marshes with fever and pioneered efforts to drain swamps.



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Mosquitoes and malaria



Ronald Ross comments on cells outside the stomach of the Anopheles mosquito:

"but what now arrested attention was the fact that each of these bodies contained a few granules of black pigment absolutely identical in appearance with the well-known and characteristic pigment of the parasite of malaria (large quartans and crescent-derived spheres)."

Ross, Ronald British Medical Journal
1:1786-1788 (1897)



The burden of malaria

Estimated one death every 30 seconds.

Infection in pregnancy (low birth weight, pre-term delivery)

Acute febrile illness (cerebral malaria, respiratory distress, hypoglycaemia)

Chronic, repeated infection (severe anaemia)

Considerable economic impacts

Up to **40% all health expenditure**; 1.3% reduction in GDP
sustained national differences; \$12 billion p.a. in Africa

Poverty traps and cycles.

Sachs, J. and Malaney, P. (2002). The economic and social burden of malaria. *Nature*, **415**: 680-685.



Control options

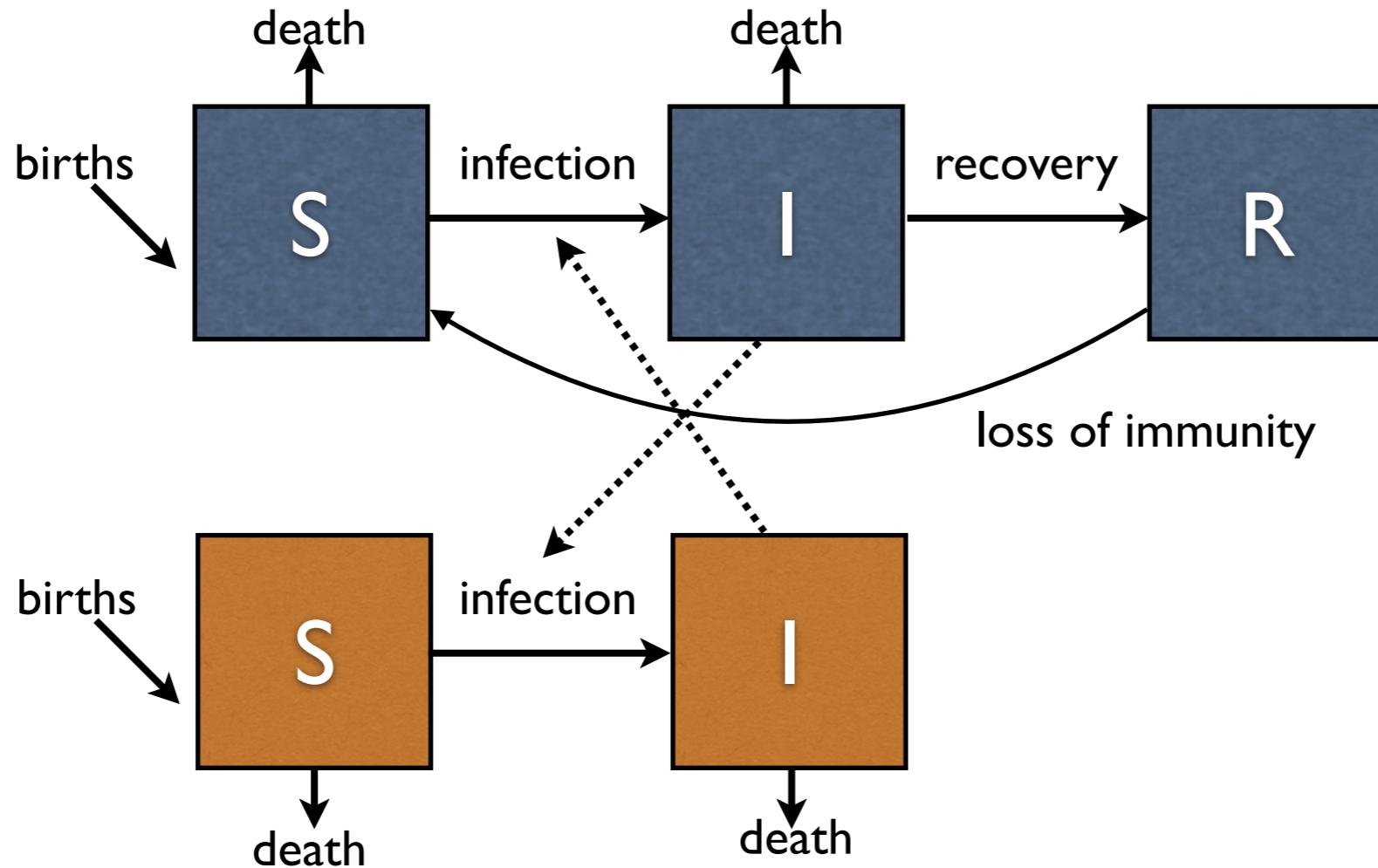
Environmental modification and species sanitation - reasonable history of success in temperate regions.

Adult vector control - current primary public health intervention - key players: indoor residual spraying (IRS), insecticide-treated mosquito nets (ITNs) and long lasting insecticide impregnated nets (LLINs)

Drugs and treatment - increasing access to drug treatment and availability



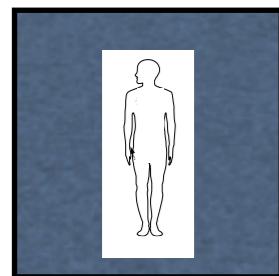
Implications for control



Implications for control

Assuming pops broadly at equilibrium – so don't worry about details of births and deaths and focus on proportions.

Version of the Ross Macdonald model



x = proportion of infectious humans

no female mosquitoes per human host prob human infection per bite human recovery rate

$$\frac{dx}{dt} = mabz(1 - x) - rx$$

number bites per mosquito per unit time



z = proportion of infectious mosquitos

prob mosquito infection per bite

$$\frac{dz}{dt} = acx(1 - z) - gz$$

mosquito death rate



How to interpret? Can we estimate R_0 ?

R_0 is the number of new infections for one infected human in a completely susceptible population.

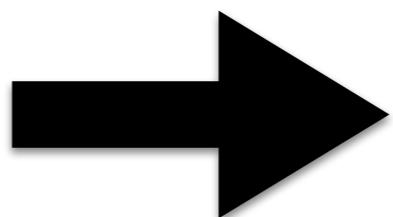
$R_0 > 1$ implies that the infection will spread - one infection will result in more than one new infection.

$R_0 < 1$ implies that the infection will go extinct - and thus also represents the condition for successful control.



Assume no infected humans ($x=0$)

$$\frac{dx}{dt} > 0$$



$$\frac{ma^2bc}{g} - r > 0$$

$$R_0 = \frac{ma^2bc}{gr}$$



Elimination

$$R_0 = 1$$

means that:

*no female mosquitoes
per human host*



$$m = \frac{rg}{mba^2c}$$

Using similar results, Ross identified that there is a **critical density of mosquitoes**, below which malaria cannot be sustained.

!You don't need to kill every mosquito to eliminate malaria!

Led to a huge focus on vector control..

