

Numerical Analysis of a Multi-Vector Disease Model

Colleen Thiersch

Mentors: Karen Wylie and Dr. Nina Fefferman

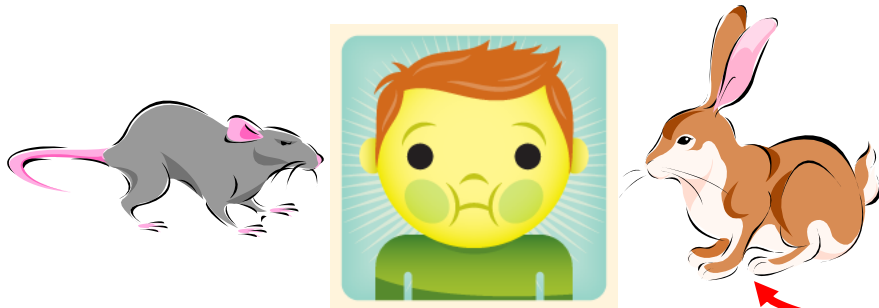
DIMACS 2012

Why Do We Model Disease?

- To obtain quantitative data without waiting for the spread of the disease
- To better understand the factors that are most (and least) important in epidemiology
- To predict the progression of an outbreak and the number of species that are alive at any time during an outbreak
- To prevent future disease outbreaks by changing factors that we can control to stop or suppress disease transmission

Hosts

(disease carriers)



Within each host population:

Susceptible

Infectious

Removed

Vectors

(disease transmitters)



Fleas & Ticks → live on a few individuals
and bite multiple times

Mosquitoes → bite multiple individuals a
few times and fly away

SIR Disease Model

Variables

- **Vector: Susceptible and Infectious Individuals**
- **Host: Susceptible, Infectious and Recovered Individuals**

Rates

- **Host death rate/recovery rate**
- **Vector birth and death rate**
- **Vector $\rightarrow$ Host and Host $\rightarrow$ Vector transmission rates**

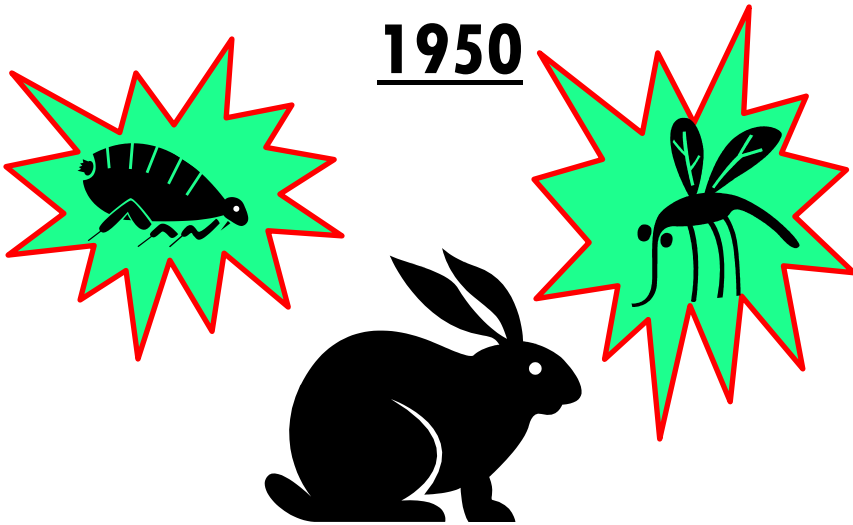
1850's



1880's

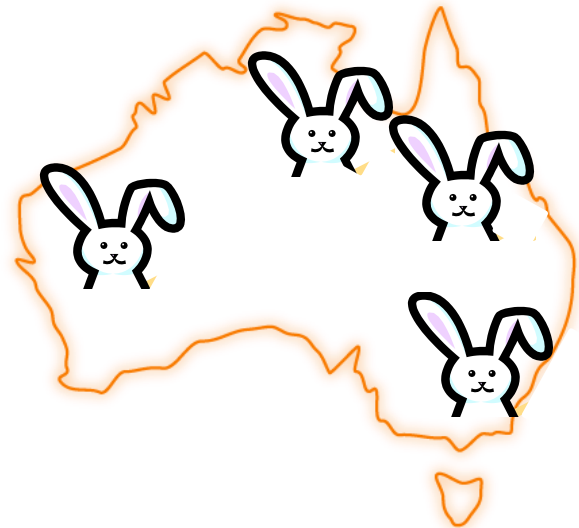


1950



Myxomatosis

1952



Summer Goals

- 1. Analyze and simplify the existing system of differential equations.**
- 2. Find a numerical solution for the model.**
- 3. Using the model, draw conclusions about the lifestyle and biting strategies of the different types of vectors**