

BOMV Transmission – Spring 2025

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Introduction

The infection dynamics of filoviruses, a clade including ebolaviruses and Marburg virus, are necessary to understand for their wide-ranging impacts on public health. To develop an understanding of these dynamics, we must consider the influence of the virus' reservoir population dynamics. Molossid, or free-tailed, bats are an implicated reservoir of ebolaviruses whose population dynamics have only recently been documented. We aim to evaluate the effect of the newfound Molossid bat population dynamics on the dispersal of ebolaviruses. More specifically, by creating a species-specific model that accurately describes Molossid bat birth pulses and other key features of Molossid ecology and physiology, we can infer its effects on ebolavirus transmission. To construct this model, we will be utilizing field data collected in rural south-eastern Kenya on *Mops condylurus*, the Angolan free-tailed bat.

As building structures in rural Kenya modernize, bats can roost in homes in higher numbers than previous, increasing exposure risk and potentially altering the spatial patterns of bats infected with Bombali ebolavirus (BOMV). I have created a model to simulate BOMV epidemics in either a computer-generated or real landscapes of roosts to determine how changing roost size will impact the persistence, peak size, force of infection, and spatial extent of BOMV epidemics. Here, I detail this model.

Next, we hope to apply this model to real landscapes in Taita-Taveta County, Kenya where we have roost occupancy data and real latitudes and longitudes of buildings. Paired with data from PIT-tagged bats, we can simulate accurate roost fidelity and bat dispersal.

We hope to answer the following question: how does the distribution of building types in the landscape affect the distribution of exposure risk? We expect that the distribution of risk matches the distribution of building sizes and that at equilibrium, the risk of exposure will be proportional to the number of bats in a roost. However, particular spatial structures may invalidate this.

Model Initialization

First, we define some important model parameters. The model uses SIR dynamics with constant population size, so we only need a transmission and recovery rate. The landscape of roosts is created with three important parameters. `num_roosts` is the total number of desired roosts. `num_clusters` describes the number of spatial clusters we want on the landscape. `sd` is the desired standard deviation of roosts within a single cluster.

```
#Define SIR Model Parameters
SIR_parms <- c(beta = 0.1, #transmission rate
               gamma = 0.03) # recovery rate

roost_parms <- c(num_roosts = 10, # number of roosts
                 num_clusters = 3, # number of clusters
                 sd = 0.1) # standard distance from cluster center
```

roostMap() creates a map of roosts on the unit square. It selects the first num_clusters roosts to be the centers of each cluster, and their location is determined by a uniform distribution across (0,1) for x and y. The remaining num_roosts-num_clusters roosts are randomly sorted into a cluster. Their location is then determined by a truncated normal distribution centered on the first roost in the respective cluster (Figure 1). Each roost is assigned a maximum occupancy at random. We also create a matrix storing pairwise distances between roosts in roost_dist.

```
source("Functions/roost_map.R")

roost_map <- roostMap(roost_parms)
roost_dist <- distMatrix(roost_parms[1], roost_map)

library(ggplot2)

ggplot(roost_map, aes(x,y, color=bin, label = lbl, size=N_max)) + geom_text()
+ xlim(0,1) + ylim(0,1)
```

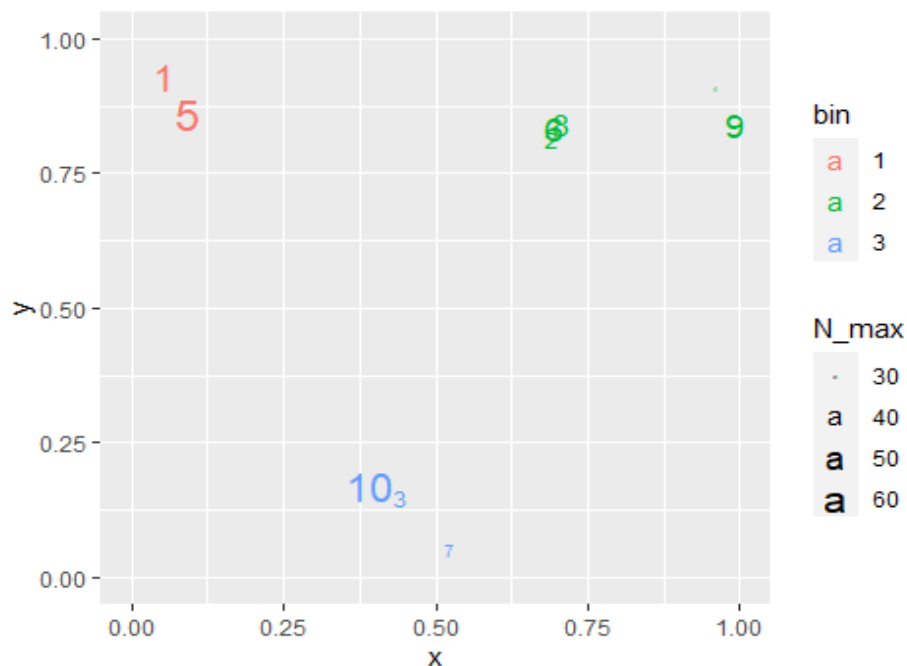


Figure 1 Map of randomly determined roost locations on the unit square. Color indicators the cluster each roost is placed in. The size of each label reflects the roost's maximum occupancy.

Next, we create a dataframe storing the number of susceptible (S), infected (I), recovered (R), and total bats (N) in each roost. These roosts are populated with two-thirds of their maximum occupancy, and a single infected individual.

A vector of scores is created to determine the connectivity of each roost. A roost's score is the sum of its distance from every other roost divided by the total distance in the system.

```
roosts <- data.frame(  
  S = vector("numeric", length=roost_parms[1]),  
  I = vector("numeric", length=roost_parms[1]),  
  R = vector("numeric", length=roost_parms[1]),  
  N = vector("numeric", length=roost_parms[1]),  
  N_max = roost_map$N_max  
)  
  
#Populate Roosts  
roosts$N <- round(roosts$N_max/1.5)  
roosts$S <- roosts$N-1  
roosts$I <- roosts$N-roosts$S  
  
#Total distances between any 2 roosts  
total_dist <- 0  
for(i in 1:roost_parms[1]) {  
  for(j in 1:i) {  
    total_dist <- total_dist + as.numeric(roost_dist[i,j])  
  }  
}  
  
#Score, a measure of isolation. greater score ==> greater isolation  
scores <- vector("numeric", length=roost_parms[1])  
for(i in 1:roost_parms[1]) {  
  tot <- sum(roost_dist[i,])  
  scores[i] <- tot/total_dist  
}  
  
source("Functions/single_day.R")  
  
roost_series <- list()  
roost_series[[1]] <- roosts  
for(i in 2:1000) {  
  roost_series[[i]] = movement2(as.data.frame(roost_series[[i-1]]),  
num_roosts=roost_parms[1], phi_max=0.25, roost_dist, scores)  
}
```

Inter-roost Movement and Transmission

Inter-roost movement has several steps. We assume that bats have knowledge of the locations of other roosts and their occupancy. First, a proportion of bats are chosen to emigrate from a roost. This proportion is determined by the isolation of a single roost via the roost's score. The greater the isolation of a roost, the lesser the number of bats that will leave it. Once these bats are selected, they are sorted into other roosts based upon the distance to other roosts and their percent occupancy. The distance-dependent component of immigrant likelihood exponential decays with distance. Roost occupancy linearly increases attractiveness, but when a roost reaches maximum occupancy, no more bats may immigrate to said roost.

In Figure 2, I show the occupancy of all roosts over 250 days. Roosts with low maximum occupancy and high isolation stay at low occupancy and are sometimes empty. Though the system does not equilibrate, it does establish a trend showing highly connected roosts to hold the most bats over time. We see that the trend in recovered individuals converges to the trend shown in the total number of bats, as expected.



Figure 2 Number of total, susceptible, infected, and recovered bats, as well as the percent occupancy, of each roost.

To determine the magnitude of stochasticity in the model, we can examine the occupancy of a single roost for ten realizations given equal initial conditions and model parameters. In Figure 3, we look at roost #2 and see a relatively consistent pattern, with peaks and troughs occurring nearby between realizations.

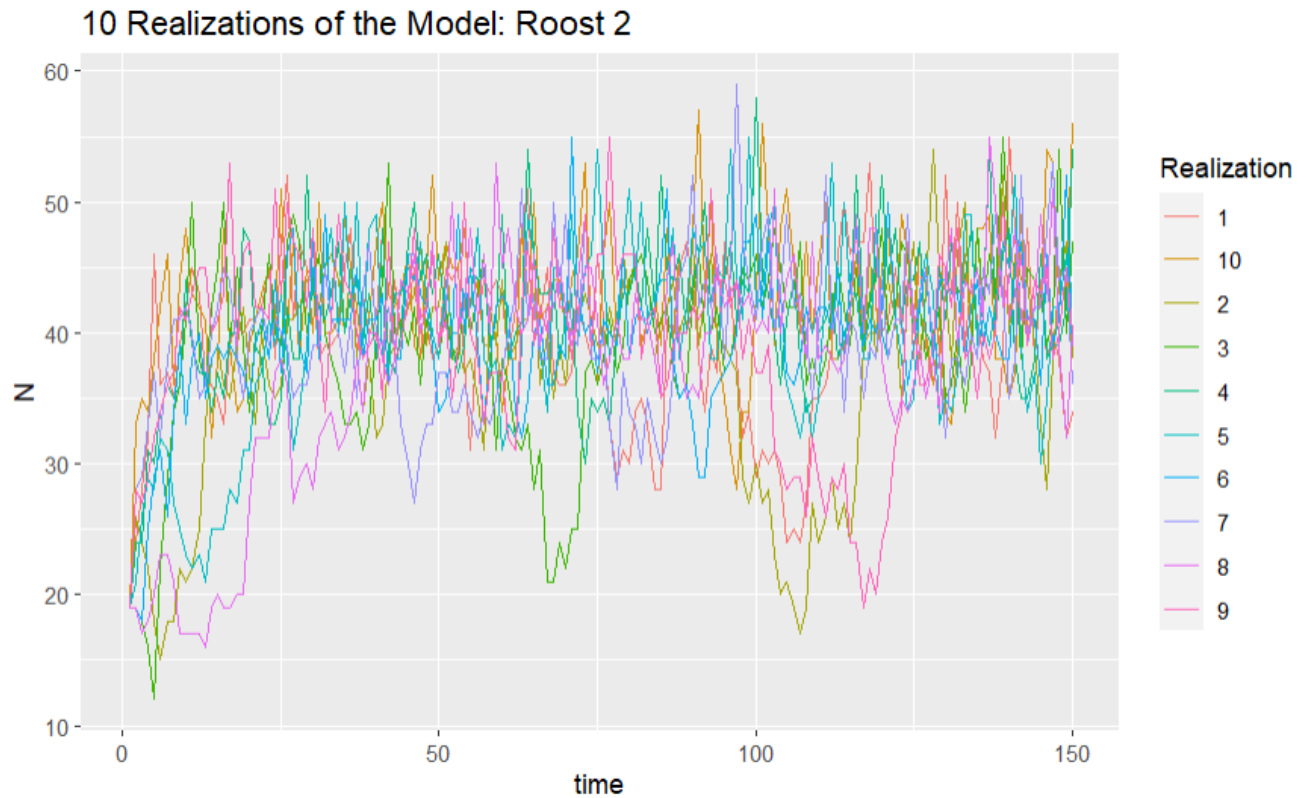


Figure 3 Total number of bats in a single roost across 10 realizations of the model.

Let us also consider a well-mixed realization of the model (Figure 4). Now, there is no spatial structure and no bat returns to the same roost as the night before. We see that roost occupancy is similar for all roosts and compartments of the SIR model follow tightly between roosts.

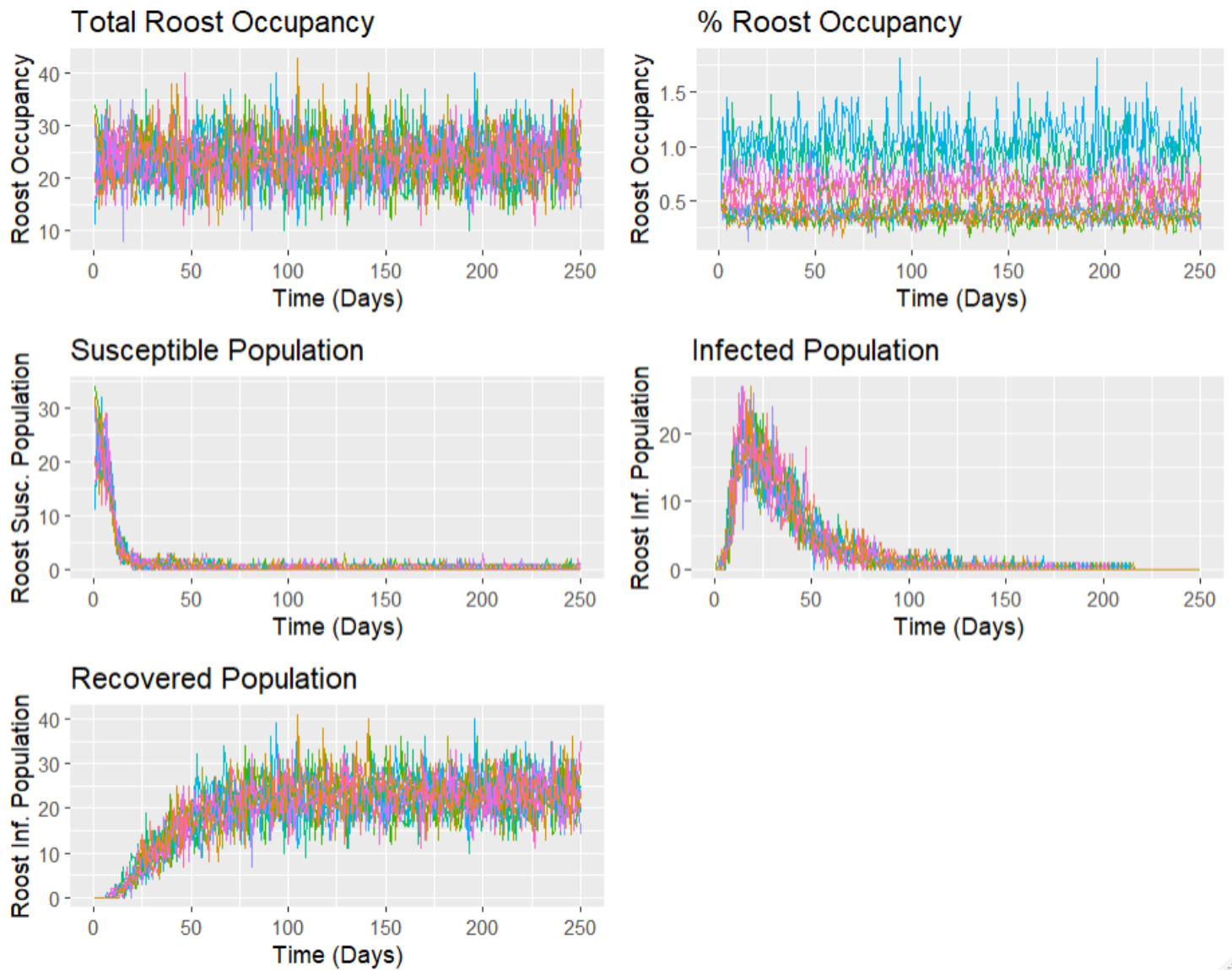


Figure 4 Number of total, susceptible, infected, and recovered bats, as well as the percent occupancy, of each roost for a single realization of the well-mixed model.