Epimodel

Reed Scott

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Introduction

I am assuming that you have already read the document on simulating abundance of species in a meta-community. As a reminder, our goal is to understand whether or not landscape level R_0 is impacted by β diversity. We have simulated a dataset with abundances for each species. Now we need to see how the abundance of each species and the connectivty of patches interact to impact prevalence of the disease.

Initializing

The first step is to determine initial conditions. We need to determine the amount of susceptible individuals and infected individuals at the start of this simulation. For now, I have assumed that the most abundant species (spp1) is the most susceptible (highest probability of getting disease) while the least abundant spp (spp6) is the most resistant. Because this uses an SIS model, the number of infectious individuals I can be determined by the total population - S. Total population is also just S+I. Finally we have to determine a starting disease level. In this case, we are using the amphibian chytrid fungus as an example, so I have chose what I *think* is a reasonable starting number of 1000 zoospores.

```
S <- ceiling(meta_comm1[,1:6]*c(0.8,0.85,0.9,0.93,0.95,.99)) #starting value of susceptibles
I <- meta_comm1[,1:6] - S #starting value of infecteds
N <- S+I
Z <- 1000 #starting amount of zoospores
```

Species characteristics

Ater choosing the initial values, we must assign species specific traits to determine how their abundance will impact disease risk. These include a birth rate (b), death rate (d), tranmission coefficient(beta), recovery rate (v), dispersal rate (phi), and BD load / shedding rate (lambda). These are shown in the table below.

```
##   Species birth death   trans recovery dispersal shedding
## 1    Spp1   0.6  0.06 0.00013      0.4      0.09      3.0
## 2    Spp2   0.5  0.05 0.00012      0.5      0.08      2.5
## 3    Spp3   0.4  0.04 0.00011      0.6      0.07      2.0
## 4    Spp4   0.3  0.03 0.00010      0.7      0.06      1.5
## 5    spp5   0.2  0.02 0.00009      0.8      0.05      1.0
## 6    spp6   0.1  0.01 0.00008      0.9      0.04      0.5
```

Note: right now, these characteristics are relatively arbitrary. I came up with values that I think would be in the range of plausible values. However, these are essentially made up. A key next step is to find more realistics values. This may include asking Mark what values they observed in their study.

Lastly, we must set some more characteristics about the meta-community within which we are operating. We must establish gamma, or the decay rate of zoospores of Bd. We have to establish a matrix, c, of the connectivty values between patches. And we must establish the area of each patch. We also have to establish the length of time over which this will occur. In this case, I have set time = 90, to represent a potential 90 day field season.

```
# meta-community characteristics
gamma <- 0.001 #zoospore decay rate
c <- matrix(data = rnorm(n = num_patches^2, mean = 0.5, sd = 0.1),
            nrow = num_patches,
            ncol = num_patches)
#Connectivity of patches
A <- rnorm(n = num_patches, mean = 0.5, sd = 0.1) #area ratios
time <- 90 #how many "days" do I want in the season
```

Note: right now, c is a matrix of random values with mean 0.5 and sd = 0.1. This will likely need to be adjusted considerably in my opinion. We may need to set distance values between each pair of patches, and then consider how distance affects connectivty. Additionally, we have to consider that within this matrix, along the diagonal is the probability that an individual stays in the same patch. There will likely be a different formulation for this probability.

Running the simulation over time

Alright, we're finally at the main event! This is a relatively short bit of code, but it does a lot.

First, we'll want to establish an empty list, of length time. We will use this list to record the number susceptible individuals of each species, infectious individuals of each species, total number of individuals of each species, and the time (i.e. "day").

With that set we can start the for loop. The for loop runs for time t. There are 3 key steps to this loop.

1. Calculate delta_s, delta_I, and delta_Z. This is the number of new susceptible and ifnectious individuals for each species, as well as the number of zoospores being added to the pool.
2. Calculate the new S, I, Z, and N values. This just simply adds the delta values to their respective initial values to calculate the "new" values for S,I,Z, and N.
3. Package it all in a list. We will do this so that we get a nice output we can later use for analysis.

```
pop_list <- vector("list", length = time)
for (t in 1:time) {
  delta_s <- b*N - d*S - beta*S*Z + v*I + phi*sum(-c*S + c*S) #for now have excluded area of patches
  #may want to add that back in though
  delta_I <- beta*S*Z-(v+d)*I+phi*sum(-c*I + c*I)#for now have excluded area of patches
  #may want to add that back in though
  delta_Z <- sum(lambda*I - gamma*Z)
  S <- S+delta_s
  I <- I+delta_I
  z <- Z+delta_Z
  N <- S + I
  t = t
```

```
  pop <- list(Susceptible = S, Infectious = I, Zoospores = Z, Total = N, Time = t)
  pop_list[[t]] <- pop
}
```

I am not going to display pop_list because it's huge: it's 90 lists, each of which contain 5 dataframes. Additionally, right now the output is unrealistic. However, I think that as we fine tune the parameters, we will find this to be a good functional model.

Conclusion

I believe what I have now is solid progress and a really good start to the simulation! However, I have no delusions. There is still a lot of work to be done one this. Most important, I believe, is that I need to tune the parameters to be more biologicall relevant / realistic. I also still need to consider how I will be analyzing the output of this SIS model. Additionally, the goal is to simulate multiple different metacommunities and compare landscape R_0 values, which I have not yet done. So, yes, there is still a lot of work to do. I am nonetheless excited at the progress I've made.