**Introduction to Spatial Models**

Today, we will be working with our first spatial model. This will be a modification on a basic SIR model, and the implementation we are working with is programmed in R and is written to work in discrete-time. This model is based on a model used previously to study the spread of COVID-19 dynamics, and the original form can be found here: https://github.com/wpgp/BEARmod.

Today you will learn:

* How to use and edit an existing R model
* How space influences the spread of disease
* How to plot data from a spatial model

**PART 1: Implementing the model**

First, we will load “modelfx.R”. This file contains all the functions used to run the model, and each step (infection, recovery, and movement of infected people) occurs separately in this model. Here’s a brief description of the functions; see if you can walk through them and figure out how they work.

* initiatePop(): This function creates the initial population. Each patch can have different values of beta (transmission rate) and gamma (recovery rate)
* recovery\_timestep(): This function uses a recovery rate, and calculates numbers of people infected and recovered over time.
* exposure\_timestep(): This function calculates newly infectious people.
* movement\_timestep(): This function moves Infectious people from one place to another.
* runSim(): This function packages everything together and runs the simulation.

In equations, this model approximates within each patch:

Where exposure\_timestep calculates and recovery\_timestep calculates *.*

Then, we have theoreticalmodel.R that runs this file, loads in a dataset, and prepares a simulation run. In this case, we are starting with a mobility data file that is fairly similar to the ones you might find in the real world:

A screen shot of a computer

Description automatically generated

In other words, the first row indicates that 10 out of 100 people in patch 1 moved to patch 2, the second row indicates that 5 people moved from 1 to 3 out of 100, etc.

**TASK 1:** Given the movement patterns shown in the movement\_data file, if an outbreak begins in patch 5, where do you think it would go from there? Why?

Now, let’s try running the simulation. You can keep things as-is, where the simulation sets a beta (transmission rate) value of .5 for all patches, and a gamma (recovery rate) value of .25. We also start this simulation with 10 infected people in patch 5, and 0 elsewhere.

**TASK 2:** If you run through line 35, you will create a plot that shows the epidemic curve across all patches. Paste the figure below. What do you observe? Is it similar to what you expected in Task 1?

**PART 2: Exploring space**

Now, let’s start changing the transmission rates around. Around line 27, you will see

beta\_vec = rep(.5,5)

which indicates that all 5 patches will have a transmission rate of .5. Let’s make certain patches have higher transmission rates than others; specifically, let’s make patch 1 high transmission, and the rest low transmission. You can do that by replacing the original beta\_vec with this line:

beta\_vec = c(1, .25, .25, .25, .25)

**TASK 3:** Rerun the model and paste the figures that show the patch-specific and overall epidemic curve below.

Let’s see what happens if we remove the effect of space. We can do this under line 7, which reads in movement\_data, using the line “movement\_data$movers = 0”. This line will set all the “movers” variables to zero—in other words, nobody is moving between patches anymore.

**TASK 4:** Once you’ve changed the number of people moving in our dataset, rerun the model and recreate the plot. How is it different from Task 3, when people were moving? Are there more or fewer people infected overall?