Overview

We build the model in the MASON toolkit, which is a Java-based agent-simulation library (Luke et al. 2004). We have described our model here following the Overview, Design concepts, and Details (ODD) protocol (Grimm et al., 2006, 2010).

Purpose

The purpose of the model is to understand how host mobility affects disease transmission. More specifically, we examine the impact of seasonal movements and daily grazing activities of mobile pastoralists on the transmission of foot-and-mouth disease (FMD) in the Far North Region of Cameroon.

State variables and scales

Mobile pastoralist

The agents represent mobile pastoralists that have herds consisting of 200 animals. The risk of disease transmission increases when agents are in close proximity, for example when sharing common grazing areas or transhumance routes. To represent the risk of transmission due to proximity we use a buffer with a fixed radius for all agents for the entire year. We change the buffer size to explore different scenarios of the geographic extent of contact among agents through unrecorded animal movements, shared grazing areas, human movements, and possible environmental transmission.

Each agent has an associated number of cattle in the S, I, and R states. As an attribute. If an agent has at least one infected animal, it can transmit the FMD virus not only to the cattle in the same agent but also to other agents. Table 1 summarizes the parameters used in the study.

Agents move based on their orbit (see Figure 4). Within a season, herds stay at a location for around 20±2 days. After 20±2 days, they move to a random location within the seasonal zone. At the end of the season, agents move toward the next seasonal zone. While in transit, they stay at one location for 26 days.
**Spatial and temporal scales**

The landscape for the model is 200 km by 200 km. There are 9 seasonal zones: three rainy, two cold dry, three hot dry and one transition season (see Figure 3). One time step in the model is a day. Each simulation runs for 365 days.

**Process overview and scheduling**

The model proceeds in daily time steps. Within each time step, agents decide whether they stay at the current location or move toward the next location. If they decide to move, then they determine the next place according to their orbits. The next step is to examine the spread of FMD virus. The model investigates all infected agents and the agents that are within the buffer of infected agents or have buffers that overlap the buffers of infected agents as neighboring agents. All neighboring agents to infected agents are set as an initial population in the SIR model. The SIR model is run for one time step. After completion of SIR model, the updated values of S, I, and R for the cattle are redistributed back to each agent. This process continues until the end of the simulation. The model process is presented in the following pseudo code.

**INITIALIZATION**
Set user defined parameters
Create agent world and seasonal zones
Create orbits for agents
Place the agents in the rainy seasonal zones

**EACH TIME STEP**
Each agent:
  If the time step is in the rainy or dry season
    If the agent stays at a location more than 20 Âś2 days then
      Moves to a random location within the seasonal zone
    End if
  Else
    If the agent stays at a location more than 4 Âś2 days then
      Moves toward the next seasonal zone
    End if
  End if

Set up population groups
For 1 to the total number of agents
  If an agent has at least one infected animal and has not been assigned to any population group then
    Assign this agent to a new population group
    Investigate the agents that neighbor this agent
    Assign the agents to the same population group with this agent
  End if
Next agent

For 1 to the total number of population group
  Run SIR model
  Redistribute the updated values of S, I and R to each agent
  (as specified in Equation 3)
Next population group
Store the values of S, I and R for each agent

**DESIGN CONCEPTS**
Emergence: Spatiotemporal dynamics of foot-and-mouth disease epidemics emerge from daily and seasonal movements of herds and the transmission of the disease. Stochasticity: At the beginning of the simulation, all agents are randomly distributed in the rainy season zones. Although they migrate along their annual orbits, their specific locations within each zone and in transit are decided randomly because the orbits have only seasonal zone order. In addition, FMD virus is started in a randomly selected animal. Interaction: Interactions among agents are through shared space and the FMD virus is transmitted from infected animals to susceptible animals. Observation: The total number of individuals in each compartment (S, I and R) is collected at every time step.
Details

Initialization

All agents are initially in the susceptible category. The starting day of the model is always August 16, to be consistent with the survey data. The location at which FMD outbreak starts is randomly selected. We design three experiment scenarios: FMD starts at day 1 and day 31 when pastoralists are still in their rainy season zones and at day 61 when they migrate to cold dry season zones along transhumance routes where agents are spatially close.

Input data

To assign the movement rule to each agent, we import 8 different orbits and 9 seasonal zones that we identified from transhumance survey data.

Submodels

Movement model: Between the arrival and leaving dates, an agent randomly finds a location within the corresponding zone (this random location can have any x and y coordinates within the zone) and stay there for a number of days that follows a uniform distribution between 18 and 22 days. This range is used because (1) 20 days of stay was used to identify the zones and (2) it gives certain randomness in the stays for each agent. Before the leaving date is reached, the agent continues to choose a random location and duration of stay in the zone. At the leaving date, the agent starts a directional movement toward the next zone in the orbit. The direction of the movement is determined by the angle between the current location of the agent and the center point of the next zone. A linear movement is used to guide the agent move toward the next zone. The agent stays at each location on the line for 2 to 6 days (randomly chosen using a uniform distribution). The distance of each move on the line between two stops is randomly decided following a uniform distribution between 9 to 11 km (the average moving distance in the data is 10 km with a standard deviation of 0.7 km). Once the arrival date of the next zone is reached, the agent resumes the mode of moving randomly in the zone and staying in each location between 18 and 22 days.

Disease model: To simulate the transmission of FMD among agents, we use an SIR model that analyzes the change of three population portions representing three critical stages of FMD: susceptible (S), infectious (I), and recovered (R). In our SIR model, we assume that the recovered individuals are immune for the whole year. We also do not consider births and deaths in a year, because it is a relatively short epidemic time scale and thus we ignore the demographic effects on the population. As a result, the frequency-dependent SIR model calculates transitions of individuals among compartments using the following equations:

\[
\begin{align*}
\frac{dS}{dt} &= -\beta \frac{SI}{N} \\
\frac{dI}{dt} &= \beta \frac{SI}{N} - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{align*}
\]

(1)

where S is the number of susceptible individual animals in the population, I the number of infected animals, R the number recovered animals, N the total population, \(\beta\) the disease transmission rate, and \(\gamma\) the recovery rate.

The model treats all infected agents and their neighbors as a population in the SIR model. After the completion of the SIR model, the updated values of S, I, and R for the cattle are redistributed back to each agent. This process continues until the end of the simulation.

After each time step (1 day), we recalculate the S, I, and R values for each agent using the proportion of the previous values for each agent. Specifically, we have

\[
\begin{align*}
\frac{dS_i(t)}{dt} &= \frac{S_i}{S} dS(t) \\
\frac{dI_i(t)}{dt} &= \frac{I_i}{I} dI(t) \\
\frac{dR_i(t)}{dt} &= \frac{R_i}{R} dR(t)
\end{align*}
\]

(2)

JASSS, 19(2) 6, 2016 http://jasss.soc.surrey.ac.uk/19/2/6.html Doi: 10.18564/jasss.3064
where subscript $i$ is used to indicate the $i$-th agent in the model, $dS_i$, $dI_i$, and $dR_i$, respectively are change rates of the number of susceptible, infected, and recovered, in the $i$-th agent, $S_i$, $I_i$, and $R_i$ respectively are the number of susceptible, infected, and recovered animals before the current day for the $i$-th agent, $S_i$, $I_i$, and $R_i$ respectively are the total number of susceptible, infected, and recovered animals before the current day for the entire cluster, and $dS$ and $dR$ are calculated using the SIR model described above for the entire cluster.

References

URL http://dx.doi.org/10.1016/j.ecolmodel.2006.04.023

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