10.4 Movement of Ants

R Quick Review Questions

Introduction to Computational Science:

Modeling and Simulation for the Sciences, 2nd Edition

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This file contains system-dependent Quick Review Questions and answers in *R* for Module 10.4 on "Movement of Ants." Complete all code development in *R*.

Grid Initializations

Quick Review Question 1 This question refers to the initialization of the grid for ant movement. In an M-file, we define a function *gridInit* to return an initial grid, *grid*. The function begins as follows:

```
initAntGrid<- function(n, probAnt)
% INITANTGRID - initialization of n+2-by-n+2 array for ant simulation
% probAnt is the probability that a site has an ant.
global EMPTY NORTH EAST SOUTH WEST STAY BORDER
EMPTY = 0
NORTH = 1
EAST = 2
SOUTH = 3
WEST = 4
STAY = 5
BORDER = 6</pre>
```

- **a.** Initialize *grid* to be an n+2-by-n+2 array of value *BORDER*.
- **b.** Write a statement to return a random integer between 1 and 4 representing the four directions.
- **c.** Complete the code to assign values to the interior of the two-dimensional array *grid*. With a probability of *probAnt*, a site contains an ant that faces in a random direction. Otherwise, the site does not contain an ant.

Quick Review Question 2

- **a.** Assign to *pherGrid* a n+2-by-n+2 array of value grid of zeros.
- **b.** Complete the loop to generate a chemical trail with no ants on the middle row of the grid, *grid*. The maximum amount of chemical, MAXPHER, which is a global constant, occurs in column n, and for column i+1 the amount of chemical is a fraction, i / n, expressed as an integer, of the maximum, MAXPHER. For example, if MAXPHER is 50, i is 10, and n is 17, then the amount of chemical in column 10 is the integer 29 because (50)(10)/17 = 29.41.

```
i = round(n/2);
for i = 1:n
    grid[mid, i+1] = ____;
end
```

Applying Diffusion

Quick Review Question 3 Complete the code for *applyDiffusionExtended* to apply the *diffusion* function to each internal cell and returns an (n + 2)-by-(n + 2) pheromone grid, keeping the border intact.

```
applyDiffusionExtended = function(matExt, diffusionRate)
n = ncol(matExt) - 2
pherGrid = matExt
for(i in
    for (j in ___
        site = matExt[i, j];
        N = matExt[i-1, j];
        NE = matExt[i-1, j+1];
        E = matExt[i, j+1];
        SE = matExt[i+1, j+1];
        S = matExt[i+1, j];
        SW = matExt[i+1, j-1];
        W = matExt[i, j-1];
        NW = matExt[i-1, j-1];
        pherGrid[i, j] = diffusionPher(diffusionRate,
               site, N, NE, E, SE, S, SW, W, NW);
return (phergrid)
}
```

Sensing

Quick Review Question 4

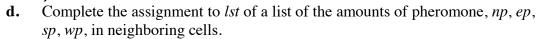
a. Complete the first line of the function M-file *sense.m*.

```
_____ <- ____ sense(site, na, ea, sa, wa, np, ep, sp, wp)
```

b. Complete the command in the function definition to indicate that *STAY* and *EMPTY* are not local.

c.

utils::globalVariables()
Complete the command to indicate that an empty site does not sense anything. Thus, its value remains the same.
<pre>if (site ==) direction =)</pre>



```
lst = ____
```

- e. This part refers to the second *sense* rule that an ant does not turn to a cell from which the creature just came. Suppose *site* is the direction from which the ant came. Write the statement to do the following: If *site* is less than or equal to 4 (i.e., not *STAY*), make the corresponding value of *lst* be a small number, -2.
- f. This question refers to the fourth *sense* rule: An ant does not turn to a location that currently contains an ant. Suppose *na* is the ant grid value for the neighbor to the north. Assuming *neighbors* is defined as [*na*, *ea*, *sa*, *wa*], write the loop to do the following: If the neighbor in a direction contains an ant, make the corresponding element of *lst* be -2.
- **e.** Complete the statement to assign the maximum level from *lst* to *mx*.

```
mx =
```

f. According to rule 6, if no neighboring cell is available, the ant will not plan to move. Start the *if* statement to test that the ant cannot (i.e., *mx* is negative), and if so the returned value is *STAY*

g. Parts g-j refer to Rule 5, which says that an ant turns in the direction of the neighboring available (not the previous, an occupied, or a border cell) with the greatest amount of chemical. Complete the statement to assign to *posList* a list of indices in *lst* where the maximum level, *mx*, occurs.

```
posList = ____(____)
```

h. Complete the statement to assign to *lng* the number of elements in *posList*.

```
lng = (posList)
```

i. Complete the statement to assign to *rndPos* a random integer between 1 and *lng*, inclusively, that is a possible index of *posList*.

```
rndPos =
```

j. Give the code to return the *posList* element with index *rndPos*.

k. Give this entire *sense* rule.

Quick Review Question 5 applySenseExtended is similar to applyPherExtended, except we change the value of the antGrid cell only if the cell contains an ant (i.e. is not EMPTY). Start the if statement to test that the ij element of antGrid is not EMPTY.

4

Walking

Quick Review Question 6

a. Complete the assignment so that the new amount in newPherGrid[i, j] is the maximum of 0 and the current amount minus EVAPORATE (rule 7).

```
newPherGrid[i, j] = ______
```

b. Give the ant-grid element to the north of antGrid[i, j].

Simulation

Quick Review Question 7

- **a.** Write a statement to assign to antGrids a page containing antGrid.
- **b.** Write a statement to append *antGrids* as the i + 1 element.

Visualizing the Simulation

- **Quick Review Question 8** Suppose *antGrids* is a list of ant grids, *pherGrids* is a list of pheromone grids, and *maxp* is the maximum amount of chemical in any cell of any grid in *pherGrids*.
 - **a.** Write a statement to assign to *m* the number of grids in *antGrids*.
 - **b.** Write a statement to assign to *n* the number of rows (or columns) on the interior of an individual grid.
 - **c.** Write a statement to initialize gr to be an $n \square \times n$ matrix of zeros.
 - **d.** Assign to a the kth element of antGrids.
 - **e.** Assign to *map* the appending of the *rgb* value for red and the gray scale sequence from 0 to 1 with *maxp* number of values.
 - Suppose p is the kth element of pherGrids. Complete the nested loops to assign to gr[i-1,j-1] an appropriately scaled pheromone value from p[i,j] if a[i,j] is EMPTY and 0 otherwise, when an ant is present. We subtract one from the indices of gr because we are not including the border. To scale, we first add 1 to p[i,j] to eliminate the possibility of zero, and then we divide by (maxp+1) to obtain a value greater than zero but less than or equal to one. Finally, to have the larger amounts of chemical be darker, we subtract the result from one.

```
for (i in 2:(n+1)){
   for (j in 2:(n+1)) {
```

}

```
if (a[i, j] == EMPTY) {
    gr[i-1, j-1] = ____ # most chem->black
    }
else {
    gr[i-1, j-1] = ____ # make ant lowest value, -> red
  }
}
```

g. Write statements to produce an image of gr using the color map map, no axes, and a box around the image.

Answers to Quick Review Questions

```
1.
    a.
         grid = BORDER*matrix(rep(1,(n+2)*(n+2)),ncol=n+2)
    b.
         floor(runif(1,1,5))
    c.
         for (i in 2:n+1){
             for( j in 2:n+1){
                  if (runif(1) < probAnt){</pre>
                      grid[i, j] = floor(runif(1,1,5))
                  else
                      grid[i, j] = EMPTY
             }
         }
2.
         grid = matrix(rep(0,(n+2)*(n+2)),ncol=n+2)
    a.
    b.
         i = floor(n/2) + 1
         for (j in 1:n){
             grid[mid, i+1] = i/n*MAXPHER;
         }
3.
    applyDiffusionExtended<-function (matExt, diffusionRate) {
         n = ncol(matExt) - 2
         pherGrid = matExt
         for (i in 1:n+1){
            for (j in 2:n+1){
               site = matExt[i, j]
                N = matExt[i-1,j]
               NE = matExt[i-1, j+1]
                E = matExt[i, j+1]
                SE = matExt[i+1, j+1]
                S = matExt[i+1, j]
                SW = matExt[i+1, j-1]
               W = matExt[i, j-1]
               NW = matExt[i-1, j-1]
                pherGrid[i, j] = diffusionPher(diffusionRate,
                     site, N, NE, E, SE, S, SW, W, NW)
             }
          }
          return(pherGrid)
    }
```

2. a. sense <- function(site, na, ea, sa, wa, np, ep, sp, wp)

```
b.
    utils::globalVariables(c("STAY", "EMPTY"))
c.
    if (site == EMPTY){
        direction = EMPTY
d.
    lst = c(np, ep, sp, wp)
e.
    if (site < STAY){
        lst(site) = -2
f.
    for (i in 1:4){
        if (neighbors[i] > 0){
             lst[i] = -2
        }
    }
e.
    mx = max(lst)
f.
    if (mx < 0){
        direction = STAY
g.
    posList = which(lst == mx)
h.
    lng = length(posList)
i.
    rndPos = ceiling (runif(1,0,lng))
j.
    posList[rndPos]
k.
    sense = function(site, na, ea, sa, wa, np, ep, sp, wp)
    global STAY EMPTY
    if (site == EMPTY){
        direction = EMPTY
        return
    }
    lst = c(np, ep, sp, wp)
    # don't allow ant to turn to previous cell, so make value artificially
    # small
    if (site < STAY){
        lst(site) = -2
    }
    # don't allow ant to turn to cell with another ant, so make value
    # artificially small
    neighbors = c(na, ea, sa, wa)
    for (i in 1:4){
        if (neighbors[i] > 0){
             lst(i) = -2
        }
    }
    mx = max(lst)
    if (mx < 0){
        direction = STAY
    }else{
        posList = which(lst == mx)
        lng = length(posList)
        rndPos = ceiling(runif(1,0,lng))
        direction = posList[rndPos]
```

```
}
5.
    if (antGrid[i, j] != EMPTY)...
6.
         newPherGrid[i, j] = max((newPherGrid[i, j] - EVAPORATE, 0));
    a.
    b.
         newPherGrid[i - 1, j]
7.
         antGrids[, , 1] = antGrid
    a.
    b.
         antGrids[, , i+1] = antGrid
8.
    a.
         m = length(antGrids[1,1,])
    b.
         n = length(antGrids[,1,1]) - 2
    c.
         gr = matrix(rep(0,n*n), nrow=n)
    d.
         a = antGrids[, , k]
    e.
         map = append(rgb(1,0,0), gray(seq(0,1,length=maxp)))
    f.
         for (i in 2:(n+1)){
             for (j in 2:(n+1)) {
                 if (a[i, j] == EMPTY) {
                     gr[i-1, j-1] = 1 - (p[i, j]+1)/(maxp+1) # most chem->black
                      }
                  else {
                      gr[i-1, j-1] = 0 # make ant lowest value, -> red
                 }
              }
    g.
         image(gr, col=map, axes=FALSE)
         box()
```