

CSE 6010 / CX 4010 Assignment 6

Epidemic Network Model

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In this assignment, we develop `create_AdjMatrix_random` function to determine the connection between each agent at first. Then we use adjacency matrix in iteration function to update the state of each agent under some specified probabilities in each iteration. In these main functions, probabilities like `pInfection`, `pRecovery`, `pReplaceRandom` and `pDisconnect` affect the state of each agent. For performing these probabilities, we use `if` function to check whether the specified probability has effect on agents. Also, `srand` and `rand` functions are used to design how the probabilities will happen in each situation.

Sanity check

- To make sure the adjacency matrix is symmetric, we print the adjacency matrix to check whether the $\text{Adj}[i, j]$ and $\text{Adj}[j, i]$ are 1 if the edge between two agents, i and j , exists and 0 otherwise.
- To implement the experiment, we assume first agent is infected. Then we will check the effects in each iteration. To check the infected agents are infected reasonably through edges, we print adjacency matrix in first several iterations and ensure that the one who just gets infected has entry 1 in matrix with other infected agents.
- To ensure the sum of infected, recovered and susceptible agents are numAgents , we record the state of all agents in each iteration and print. In addition to check the all agents are in experiment, the non-decreasing numbers of recovered agents convince us that the state is reasonably changed from susceptible to infected and to recovered at the end.

Results of experiments

First column: The maximum number of infected individuals in a single iteration
Second column: The iteration number at which the maximum number of infected individuals occurs
Third column: The sum of the number of currently infected and recovered individuals after the last iteration.

| | pReplaceRandom = 0 | | |
|--------|--------------------|----|-------|
| | pDisconnect = 0 | | |
| | 27 | 29 | 150 |
| | 26 | 57 | 136 |
| | 21 | 25 | 64 |
| | 20 | 20 | 118 |
| | 12 | 16 | 24 |
| | 18 | 16 | 53 |
| | 14 | 19 | 21 |
| | 26 | 37 | 111 |
| | 23 | 97 | 127 |
| | 27 | 58 | 144 |
| | | | |
| MEDIAN | 22 | 27 | 114.5 |
| MAX | 27 | 97 | 150 |
| MIN | 12 | 16 | 21 |

| | pReplaceRandom = 0.25 | | |
|--------|-----------------------|------|-------|
| | pDisconnect = 0 | | |
| | 197 | 31 | 489 |
| | 183 | 24 | 488 |
| | 177 | 30 | 476 |
| | 195 | 32 | 492 |
| | 189 | 27 | 488 |
| | 185 | 32 | 483 |
| | 177 | 39 | 482 |
| | 187 | 32 | 487 |
| | 202 | 31 | 491 |
| | 188 | 32 | 478 |
| | | | |
| MEDIAN | 187.5 | 31.5 | 487.5 |
| MAX | 202 | 39 | 492 |
| MIN | 177 | 24 | 476 |

| | pReplaceRandom = 0 | | |
|--------|--------------------|------|------|
| | pDisconnect = 0.5 | | |
| | 9 | 67 | 41 |
| | 6 | 5 | 15 |
| | 2 | 2 | 6 |
| | 7 | 7 | 13 |
| | 2 | 2 | 3 |
| | 8 | 17 | 42 |
| | 8 | 12 | 14 |
| | 8 | 24 | 19 |
| | 11 | 9 | 35 |
| | 8 | 14 | 14 |
| | | | |
| MEDIAN | 8 | 10.5 | 14.5 |
| MAX | 11 | 67 | 42 |
| MIN | 2 | 2 | 3 |

| | pReplaceRandom = 0.25 | | |
|--------|-----------------------|----|-----|
| | pDisconnect = 0.5 | | |
| | 65 | 61 | 293 |
| | 59 | 55 | 336 |
| | 12 | 27 | 46 |
| | 53 | 91 | 225 |
| | 57 | 59 | 307 |
| | 53 | 57 | 283 |
| | 62 | 52 | 305 |
| | 39 | 72 | 252 |
| | 56 | 53 | 333 |
| | 42 | 84 | 232 |
| | | | |
| MEDIAN | 54.5 | 58 | 288 |
| MAX | 65 | 91 | 336 |
| MIN | 12 | 27 | 46 |

In experiment, we have to control two parameters, pReplaceRandom and pDisconnect. The pReplaceRandom represents the probability that agents can infect any other agent in addition to their closest neighbor. In other words, as pReplaceRandom is greater, the risk of infection is higher. From the results, we can tell that when pReplaceRandom is changed from 0 to 0.25, the data show that the number of infected individuals is greater. As for pDisconnect, it represents the probability that connection between each agent might be removed. That is, as pDisconnect is greater, the risk of infection is smaller. From the results, we can tell that when pDisconnect is changed from 0 to 0.5, the data show that the number of infected individuals is smaller. Therefore, we can conclude that this experiment works well and satisfies what we expect.

Division of Labor

- At first, Ting developed the network functions (`create_array`, `create_AdjMatrix_random`) to build up the network structure. Also, Chin started to build the basic model functions (`update_state`, `calculate` and `calculate1`). Then, we both presented our own ideas to make the iteration function. After that, we found out that Chin's code could perform the result correctly but Ting's not. Therefore, we used the iteration function which was based on the data structures that Chin came up with. After outputting the results, Chin organized the main structure and presented it in the slide. Eventually, Ting divided those functions into two different source file, `model.c` and `network.c`. Both of them were connected to the main function via the makefile.
- Ting Liao: network functions, print functions, some suggestions for the iteration function and the makefile steps
- Chin Wang: model functions, most code of the iteration function and the output for the slides.
- All in all, we both contributed great efforts on the Epidemic Network Model program. We appreciate that TA Darby gave us a hand on handling the bug while dividing functions into different source files.