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Final Project code summary and results

Program structure:

The program consists of five main parts: a main file, a person class implementation file, a population class implementation file, and a header file for both the person and the population class.

The person class is the smallest unit in the program, which is then used to create a population (essentially a vector of persons) for the population class.

Note: A brief description of the methods for each class are found in the README file

Results:

Program for single person:

> The output was as expected, the person would be susceptible to the disease for a random number of days and then be infected with the disease for 5 days.

Program for a population without contagion:

> The output for this program was only one person getting infected(which was expected),but each run that person varied.

Program for a population with contagion and inoculation:

> The general trend was that the higher the probability of transfer and the lower the percentage of inoculation, the more people get sick. However, once the inoculation rate increased to more than 50% no matter how much the probability of transfer increased the number of people sick would not be that high. The reason was that if the infected person was between two inoculated people the disease would not spread, reducing the number of people getting infected.

Program for a population with random spreading:

> In this case, the trend was also the same. As the probability of transfer increased and the percentage of inoculation decreased the more people got sick. However, in this case even if the inoculation rate was high there would still be a lot of people infected.

contagion model			
Population size: 10			
Probability of transfer	percentage innoculated	days ran	total people sick
0.3	0.3	6	1
0.5	0.3	7	3
0.8	0.3	12	7
0.3	0.5	7	2
0.5	0.5	7	2
0.8	0.5	6	1
0.3	0.8	8	3
0.5	0.8	9	4
0.8	0.8	6	1

contagion model			
Population size: 50			
Probability of transfer	percentage innoculated	days ran	total people sick
0.3	0.3	8	3
0.5	0.3	8	3
0.8	0.3	7	2
0.3	0.5	6	1
0.5	0.5	9	3
0.8	0.5	7	2
0.3	0.8	11	4
0.5	0.8	6	1
0.8	0.8	7	3

contagion model			
Population size: 100			
Probability of transfer	percentage innoculated	days ran	total people sick
0.3	0.3	8	2
0.5	0.3	7	3
0.8	0.3	11	9
0.3	0.5	6	1
0.5	0.5	6	1
0.8	0.5	6	1
0.3	0.8	7	2
0.5	0.8	6	1
0.8	0.8	8	3

contagion model			
Population size: 1000			
Probability of transfer	percentage innoculated	days ran	total people sick
0.3	0.3	15	6
0.5	0.3	10	4
0.8	0.3	11	6
0.3	0.5	8	3
0.5	0.5	6	1
0.8	0.5	8	2
0.3	0.8	13	6
0.5	0.8	6	1
0.8	0.8	6	1

Spreading model			
Population size: 10			
Probability of transfer	percentage innoculated	days ran	total people sick
0.3	0.3	10	5
0.5	0.3	10	6
0.8	0.3	11	8
0.3	0.5	6	1
0.5	0.5	10	6
0.8	0.5	9	6
0.3	0.8	6	1
0.5	0.8	7	2
0.8	0.8	6	1

Spreading model			
Population size: 50			
Probability of transfer	percentage innoculated	days ran	total people sick
0.3	0.3	6	1
0.5	0.3	12	24
0.8	0.3	12	35
0.3	0.5	9	6
0.5	0.5	12	26
0.8	0.5	10	31
0.3	0.8	6	1
0.5	0.8	13	12
0.8	0.8	12	18

Spreading model			
Population size: 100			
Probability of transfer	percentage innoculated	days ran	total people sick
0.3	0.3	6	1
0.5	0.3	14	54
0.8	0.3	12	73
0.3	0.5	12	12
0.5	0.5	12	41
0.8	0.5	13	51
0.3	0.8	6	1
0.5	0.8	11	8
0.8	0.8	13	27

Spreading model			
Population size: 1000			
Probability of transfer	percentage innoculated	days ran	total people sick
0.3	0.3	15	39
0.5	0.3	17	565
0.8	0.3	14	723
0.3	0.5	12	23
0.5	0.5	10	9
0.8	0.5	13	536
0.3	0.8	6	1
0.5	0.8	14	73
0.8	0.8	15	253

Contagion
Poulation size: 10

transfer rate   inoculated   total sick

Contagion
Population: 50

transfer rate   inoculation   total sick

Contagion
Population size: 100

transfer rate   inoculation   total sick

Contagion
Population size: 1000

- transfer rate
- inoculation
- total sick

Spreading
Population size: 10

- transfer rate
- inoculation
- total sick

Spreading
Population size: 50

- transfer rate
- inoculation
- total sick

Spreading
Population size: 100

transfer rate inoculation total sick

Spreading
Population size: 1000

transfer rate inoculation total sick