Solutions to Problem 2

Shashank Sule

December 20, 2020

1 Problem 1

We have that $T_c = \frac{\sum_{k=1}^{\infty} kp_k}{\sum_{k=1}^{\infty} k(k-1)p_k} = \frac{\sum_{k=1}^{\infty} kp_k}{\sum_{k=1}^{\infty} k^2 p_k - \sum_{k=1}^{\infty} kp_k} = \frac{\langle k \rangle}{\langle k^2 \rangle - \langle k \rangle} = \frac{1}{\frac{\langle k^2 \rangle}{\langle k \rangle} - 1} = \frac{1}{\kappa_0 - 1}$. Assuming that vaccination prevents an individual from either catching or spreading the disease, vaccinating with probability v is equivalent to percolating with probability v; as a consequence the critical probability of having a giant component (i.e an epidemic) is $v_c = 1 - \frac{1}{\kappa_0 - 1} = 1 - T_c$. Consequently if $v > v_c$ then we lose the giant component (so there is no epidemic) and if $v < v_c$ we have a giant component (there is an epidemic).

2 Problem 2

a) Setting $\alpha = 2.2$ we find the solution to $u = G_1(u) = \mathrm{Li}_{\alpha-1}(u)/u\mathrm{Li}_{\alpha-1}(1)$. The proportion of vertices in the giant component is:

```
Out[59]: 0.8037364752242915
```

b) Setting $T = 0.4$, the proportion of vertices affected by the epidemic is computed by solving $u = G_1(1 - T + Tu)$ (part (a) is just the case $T = 1$).

```
Out[37]: 0.7117217936756421
```

Thus about 71% of the people are affected by the epidemic.

c) Note that $\alpha < 3$ so $T_c = 0$ so there will always be an epidemic. As a consequence of part (a) we have that $v_c = 1.0$. So everybody will have to be vaccinated! Unfortunately, the probability of vaccinating a person these days is the probability that a vaccine is given to them times the probability that they will take the vaccine and the latter isn't always 1...

3 Problem 3

a) Number of vertices in the giant component:

```
Out[75]: 8172
```

Note that it provides us a check on the theoretical estimate derived in part (a) of Problem 2.

b) The transmission graph also contains a giant component. The number of affected vertices:

```
In [86]: DFSTree = GraphTraversals.my_dfs(Sick_Graph);
         sizes = get_prop(DFSTree, :cc_sizes);
         maximum(sizes)

Out[86]: 5640
```

c) Note that $T_c = 1/G_1'(1)$ i.e the reciprocal of the average number of second neighbours.

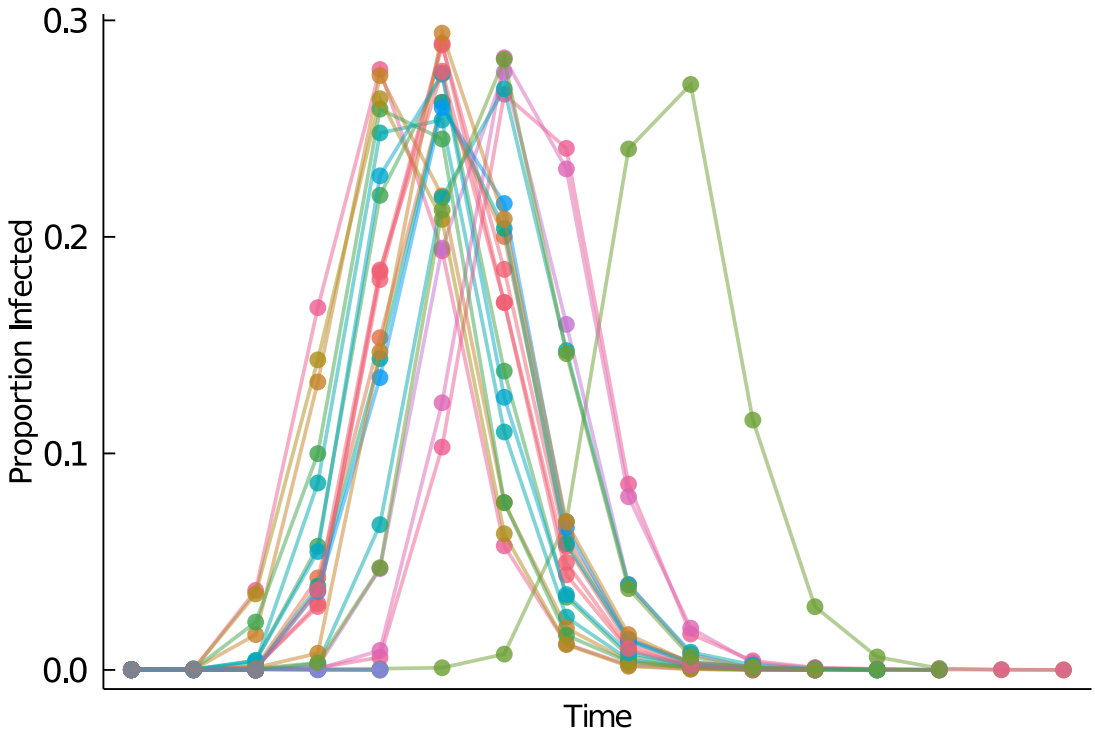
```
T_c = 0.004839685420447671
```

d) Since $v_c = 1 - \frac{1}{\kappa - 1}$ we compute the κ for the graph with epidemic and then its v_c.

```
v_c = 0.9800564643003383
```

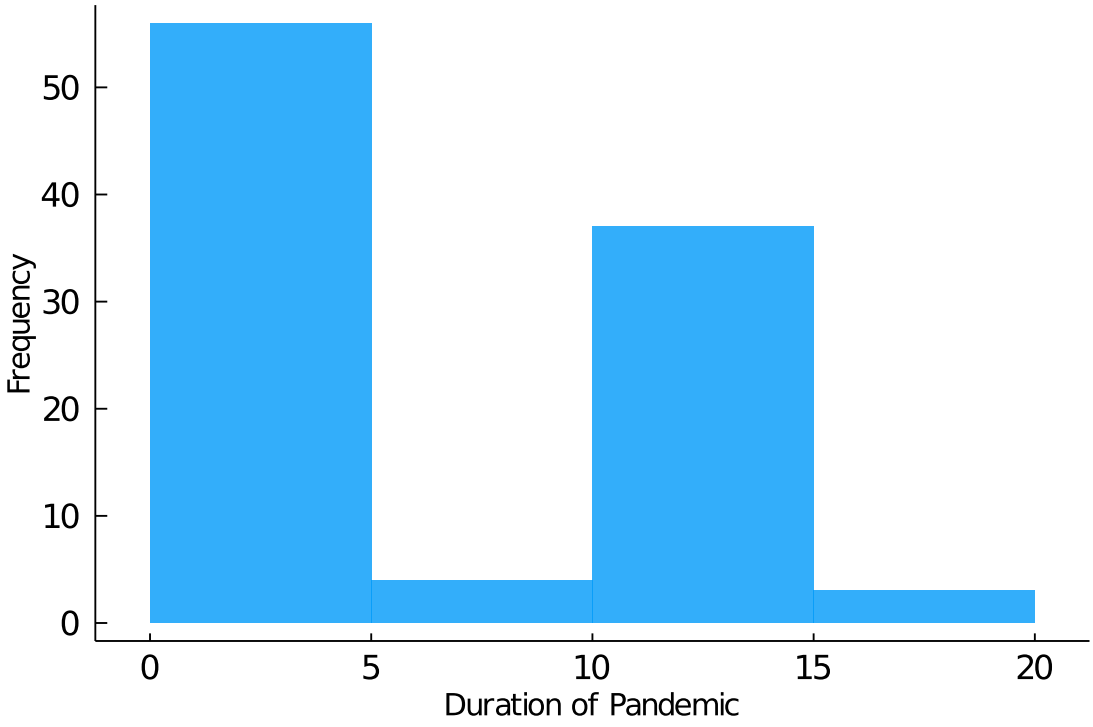
4 Problem 4

We simulate the SIR model as follows: An initial node is infected at time $t = 1$; for all subsequent times t, each susceptible node to an infected node is infected with probability 0.4. An infected node flips to a recovered node after one time period of infection. Over a 100 trials, we found that most widespread infections infected about 30% of the population, so there was no epidemic.



Furthermore, most infections lasted for less than 5 time periods but about 40% (the ones that produced the most widespread infections) lasted for between 10 and 15 time periods. In the short spreads, the initial vertex was usually in the small components of the graph. The long spreads correspond to the initial vertex being in the giant component.

Out[257]:



The relationship between BFS and SIR is as follows: Set $T = 1$. Then in the second time period, the initial node infects all of its neighbours. In the third one, all these neighbours infect their neighbours except for the ones already infected, and so on. In other words, at time t, the infection spreads to all the susceptible (i.e. undiscovered) neighbours of the currently infected (discovered and active). Moreover, the chain of individuals to patient zero is at most t persons long at time t, because at one time only the immediate neighbours of an infected vertex are infected (i.e explored). This process is exactly the Breadth First Search. Introducing $T < 1.0$ is essentially doing a Breadth First Search with "mistakes."