

# Analyzing spread of disease in networks

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July 14, 2020

## 1 The Premise

We make use of python's EON module to run SIR simulations on different networks, such as random networks and small world networks. Throughout the analysis, we will take graphs of order:  $|V| = 1000$ , unless stated otherwise. The order of the graph will serve as our population size,  $N$ . For the SIR simulation, we will take  $\tau$  (transmission rate per edge) = 0.33 and  $\gamma$  (recovery rate per node) = 10. We will change the probability of rewiring,  $p$ , and calculate the average peak values of infection and average time taken to reach that value over a course of 100 iterations.

## 2 Random Graphs

We made use of the erdos renyi random graphs to run the simulation, with different  $p$  values. Below is a snapshot of the spread of disease in the network at different time intervals when  $p = 0.3$ .

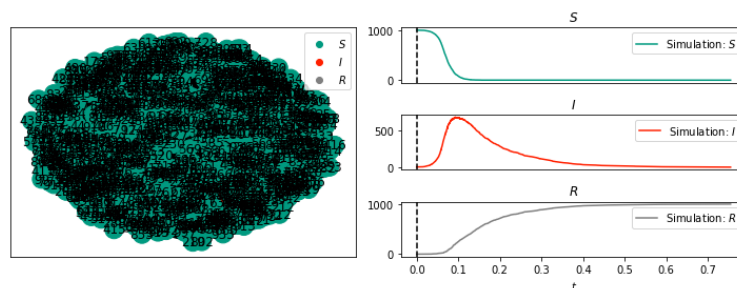


Figure 1: Random Network at  $t=0$

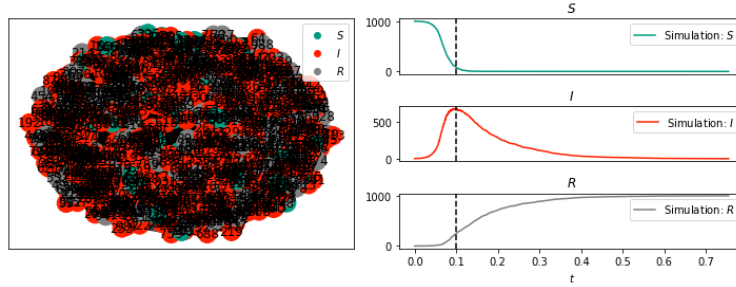


Figure 2: Random Network at peak infections

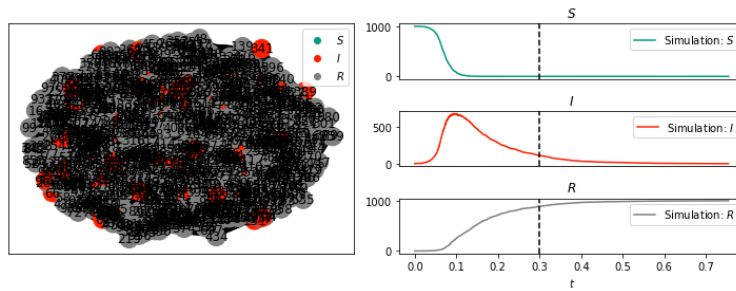


Figure 3: Random Network when the infection has died out

## 2.1 Plots for the Random Graph

p	avg edges	avg peak	avg time
0.0	00.00	1.00	0.000
0.1	50.15	263.86	0.270
0.2	100.06	456.87	0.130
0.3	150.22	619.69	0.100
0.4	99.93	668.66	0.076
0.5	249.74	744.71	0.064
0.6	299.86	764.77	0.055
0.7	349.80	792.45	0.046
0.8	399.73	801.35	0.040
0.9	449.39	805.03	0.035
1.0	499.50	851.96	0.034

The graph of average edges against  $p$  is almost linear. That is because we start with a fixed number of edges and  $p$  presents the probability of choosing them. As  $p$  increases, the probability of choosing the total number of edges also increases hence we see a linear increase in average number of edges wrt  $p$ .

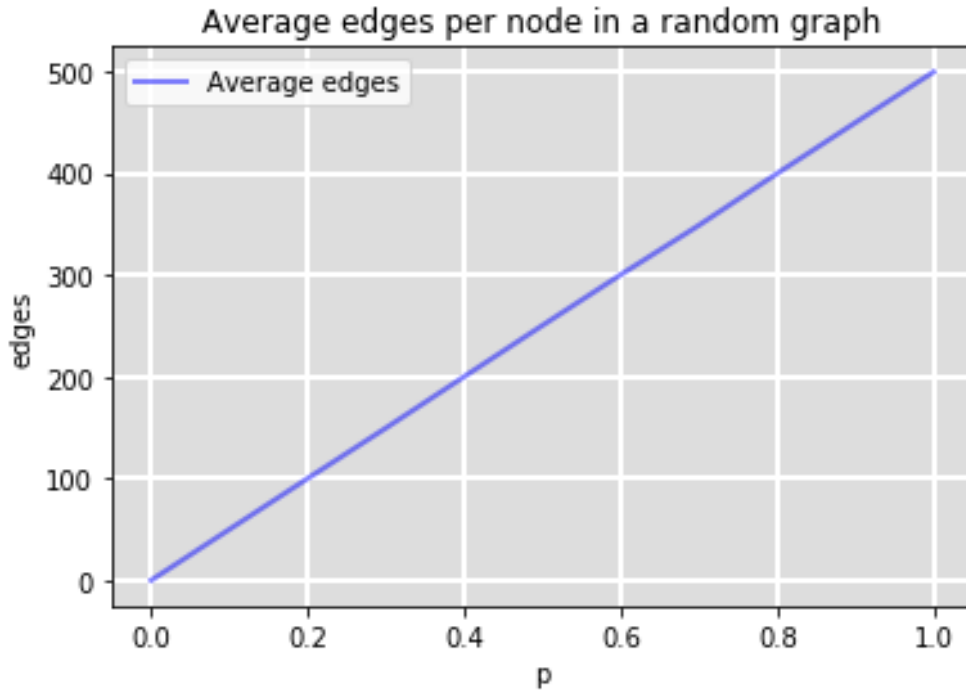


Figure 4: Average peak value and p

Let's take a look at the graph of peak values against p.

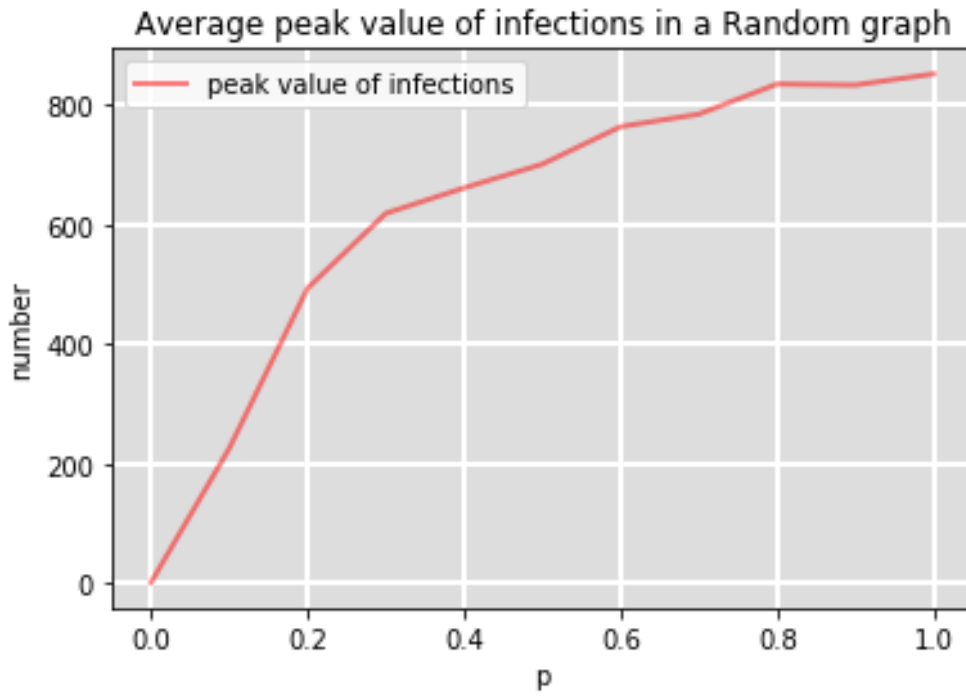


Figure 5: Average peak value and p

The plot shows a clear positive relationship between average peak value of infections and

probability of rewiring edges,  $p$ . As  $p$  increases, we increase the average number of edges per node and thus there is a higher probability that someone will get infected, leading to higher peak values.

Naturally, we would expect the average time taken to reach peak value to follow a negative relationship with  $p$ , as  $p$  increases the time taken decreases. That is exactly what we find.

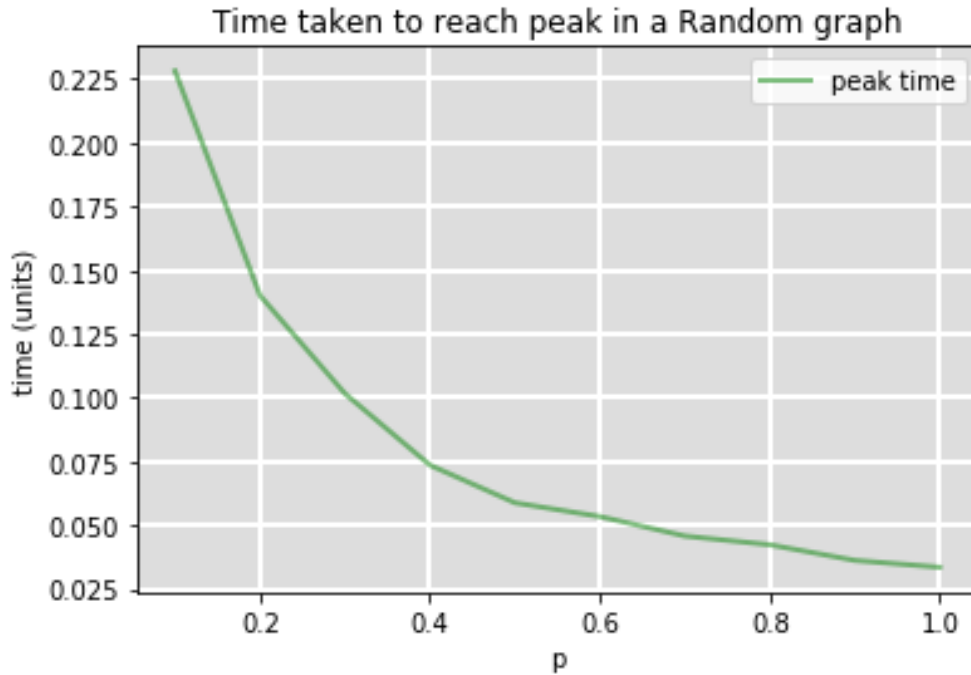
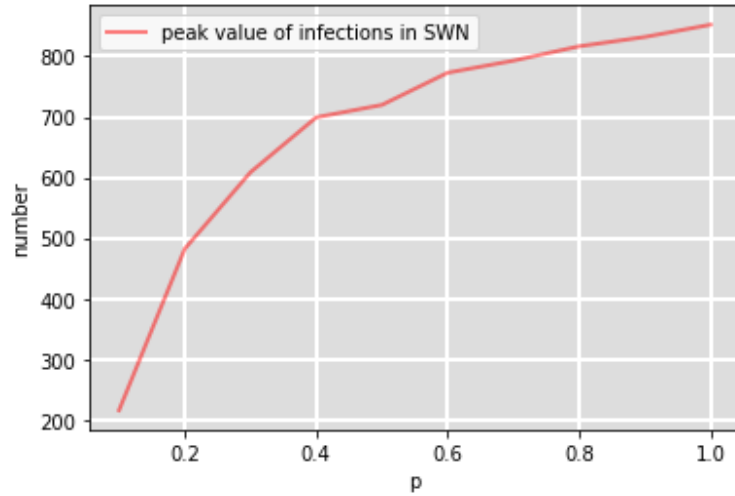


Figure 6: Average peak time and  $p$

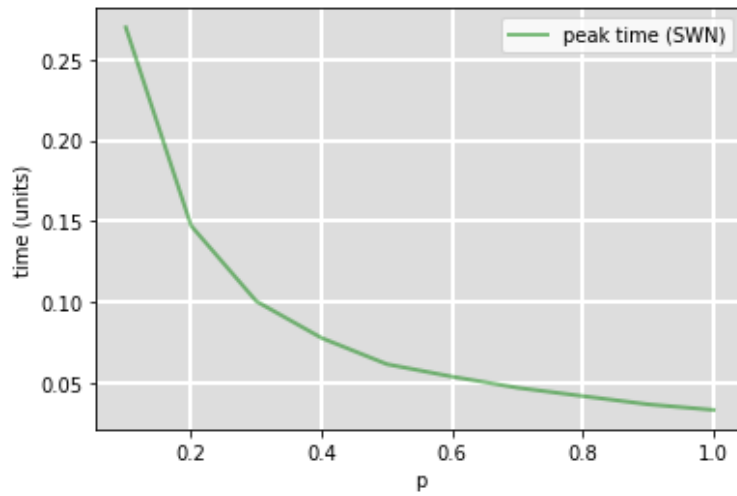
As  $p$  increases, we moves towards a more disordered network where there is a higher likelihood of clusters forming. Such clusters connect such nodes that may be too far away, thus making the network more susceptible to attacks and the causing the disease to spread faster. The graph here is in agreement with what Watts and Strogatz proposed in their original paper.

### 3 Small World Networks

We will use the watts-strogatz SWN to analyze the spread of disease in terms of peak value and peak time. We will keep all the parameters the same as before.



(a) Avg Peak value



(b) Avg Peak time

Figure 7: Plots for a Small World Network

Since we kept the average number of edges the same for both the SWN and random networks, we do not see much difference between the two. In fact, the two plots above show that the spread is almost identical as the spread in the random graph.