soComp - Ex 2

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June 14, 2015

3.1 Basic Reproductive Number

3.1.1

Using the notation of P_{SI}, P_{IR}, P_{RS} and setting $P_{RS} = 1$, examine the following setting: two conected nodes where the first is infected and the second isn't. The probability that the second node will move from susceptible to infected on the k_{th} turn is:

$$P\left(\text{Infected in the k turn}\right) = \left(1 - P_{SI}\right)^{k-1} P_{SI} \left(1 - P_{IR}\right)^{k}$$

and the total probability of the node being infected before the first is cured is:

$$\begin{aligned}
P &= \sum_{k=1}^{\infty} \left(1 - P_{SI}\right)^{k-1} P_{SI} \left(1 - P_{IR}\right)^{k} \\
&= \sum_{k=1}^{\infty} \left[\left(1 - P_{SI}\right)\left(1 - P_{IR}\right)\right]^{k-1} P_{SI} \left(1 - P_{IR}\right) \\
&= P_{SI} \left(1 - P_{IR}\right) \sum_{k=1}^{\infty} \left[\left(1 - P_{SI}\right)\left(1 - P_{IR}\right)\right]^{k-1} \\
&= P_{SI} \left(1 - P_{IR}\right) \sum_{k=0}^{\infty} \left[\left(1 - P_{SI}\right)\left(1 - P_{IR}\right)\right]^{k} \\
&= P_{SI} \left(1 - P_{IR}\right) \cdot \frac{1}{1 - \left(1 - P_{SI}\right)\left(1 - P_{IR}\right)} \\
&= P_{SI} \left(1 - P_{IR}\right) \cdot \frac{1}{P_{SI} + P_{IR} - P_{SI}P_{IR}}
\end{aligned}$$

3.1.2 Expected Infected Neighbours

Treating each neighbour as an independent bernoulli trial with probability of success being the result from 1.1, and given we have d neighbours then the infected vertex will infect

$$P_{SI} \left(1 - P_{IR}\right) \cdot \frac{d}{P_{SI} + P_{IR} - P_{SI}P_{IR}}$$

vertices on average.

3.1.3 Empiric Epidemic Spread With Infection Expectancy 2

Taking the expectating and plugging in $d = 4$ then equating to the desired expectation of 2 we get the relation:

$$P_{SI} = \frac{P_{IR}}{(1 - P_{IR})}$$

Indeed, using values that hold this relation cause the epidemics to grow more often than not
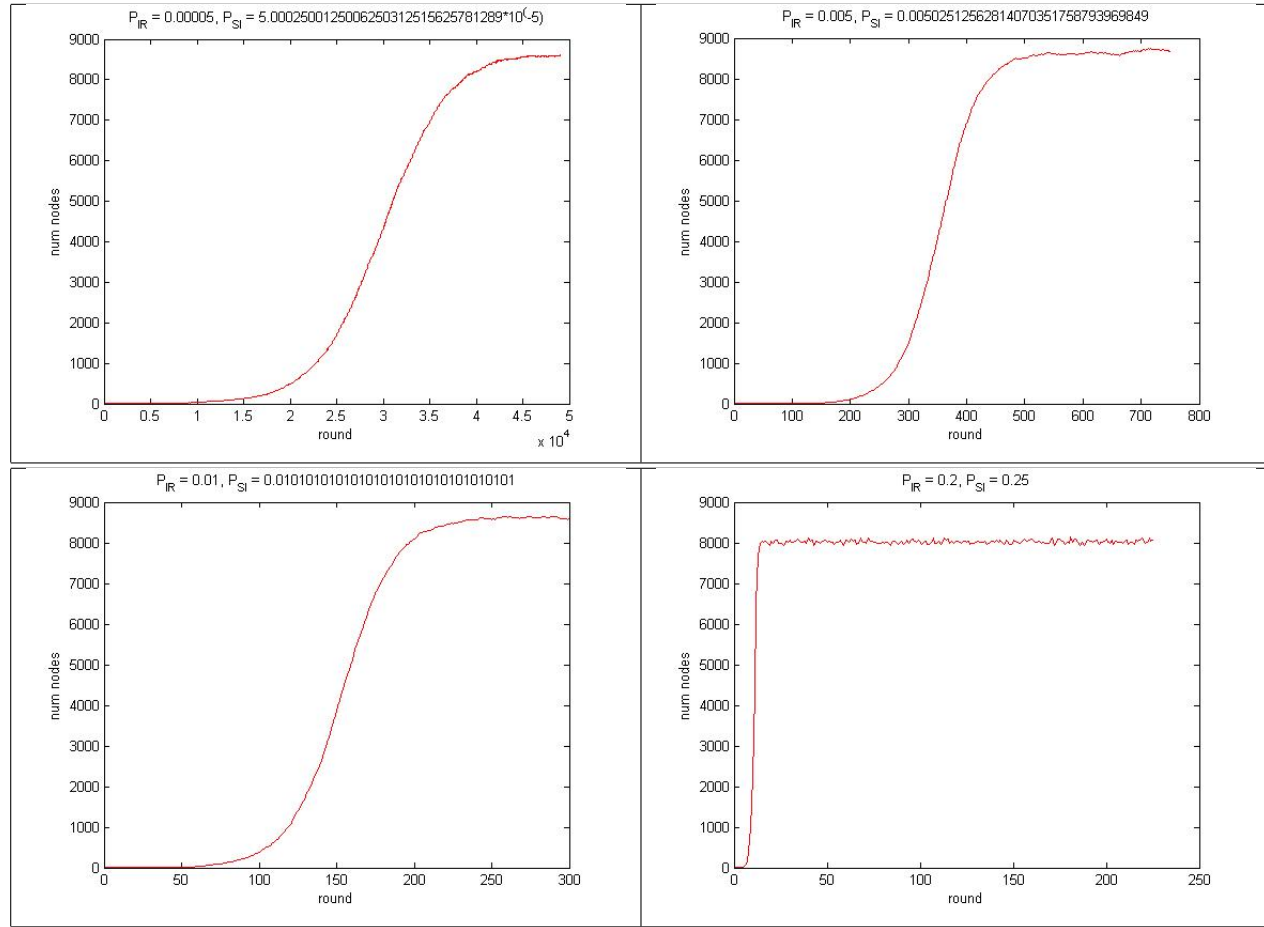

Figure 1: Expectation 2

3.1.4

Here, we get

$$P_{SI} = \frac{P_{IR}}{7\left(1 - P_{IR}\right)}$$

Simulating using the new relation yields that in most cases epidemics will die out. Rarely we saw partial slow spread epidemic that had fluctuations between infected and susceptible like in the last figure
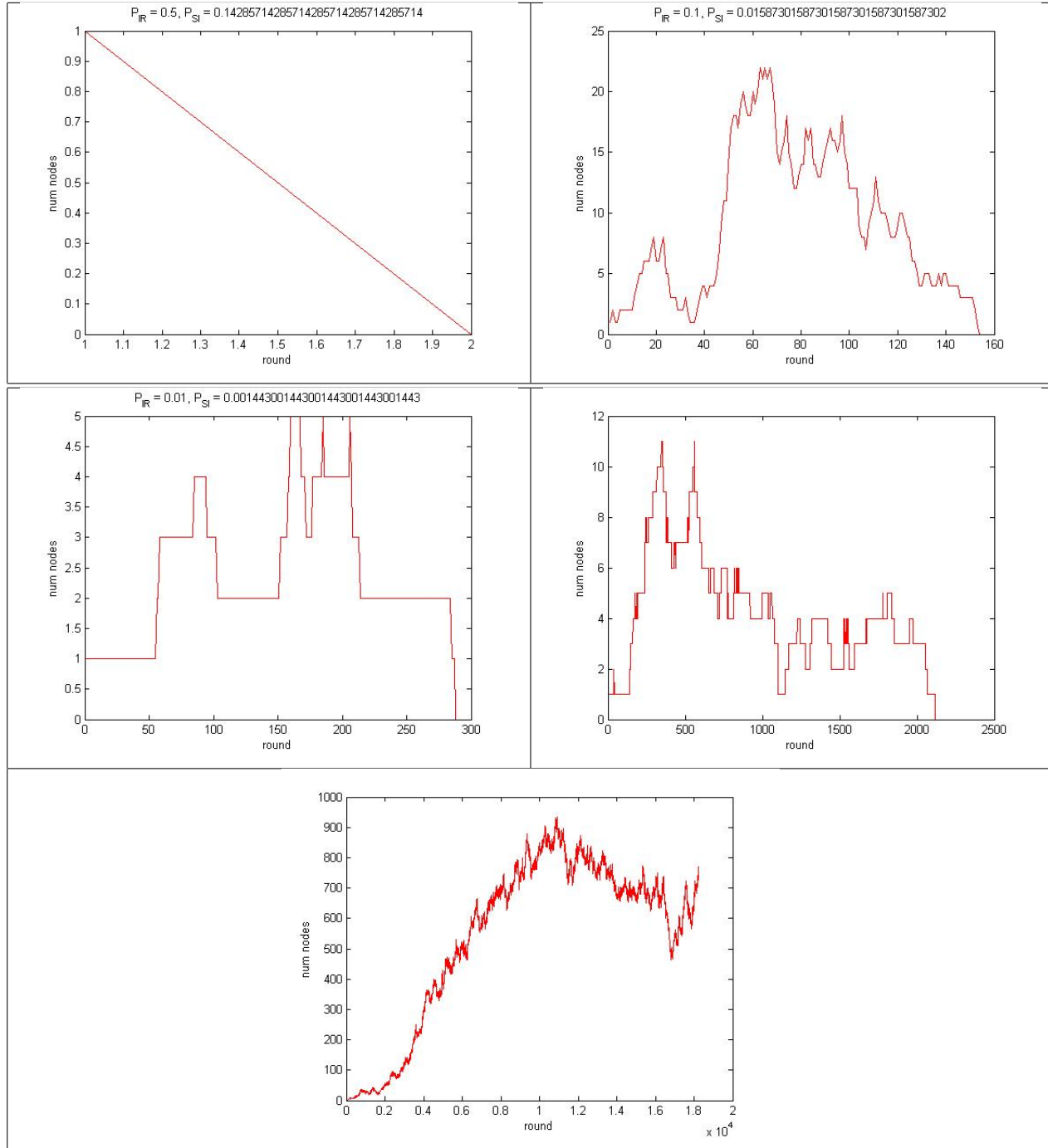
Figure 2: Expectation 0.5

3.2 Scale Free Networks

Simulating free scale graphs with the same parameters as in uniform select showed us many times fast spread with a limit in the number of infested nodes
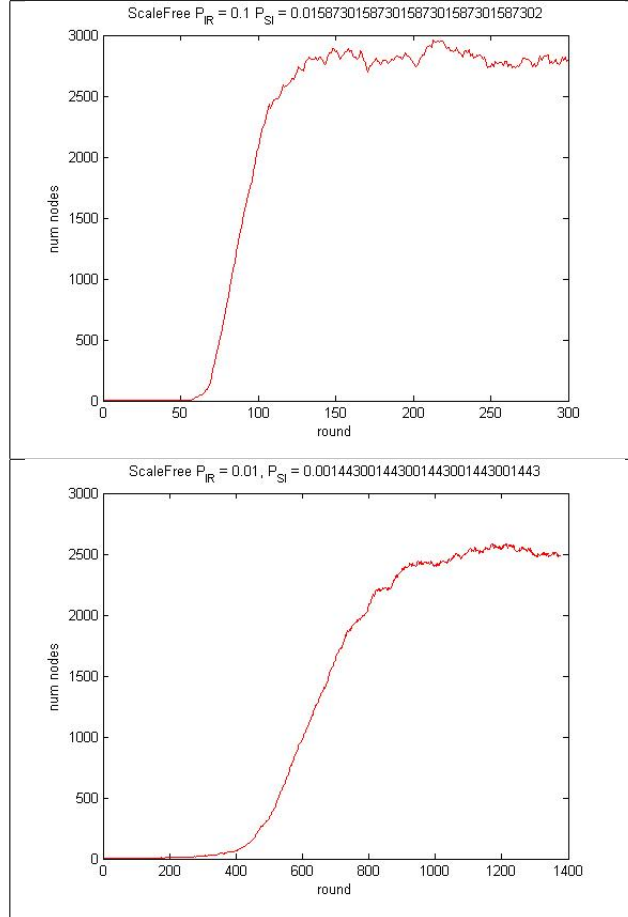

Figure 3: Scale Free

3.3 Small World

3.3.1

Now

$$P_{SI} = 0.08, P_{IR} = 0.15, P_{RS} = 0.005$$

$$N = 300, P_{rewire} = 0$$

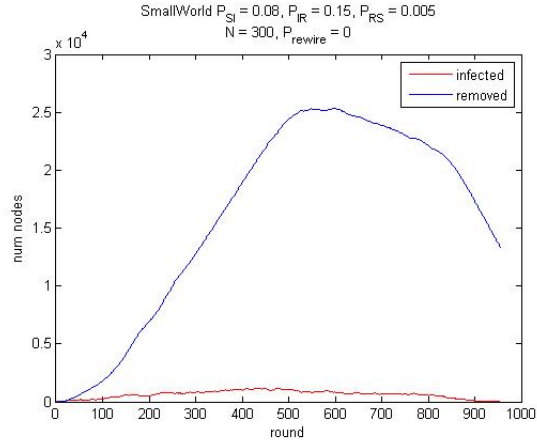Figure 4: No rewire

The epidemic spread fast but didn't last too long because without rewiring, the disease didn't infest again in visited areas.

3.3.2

Now taking

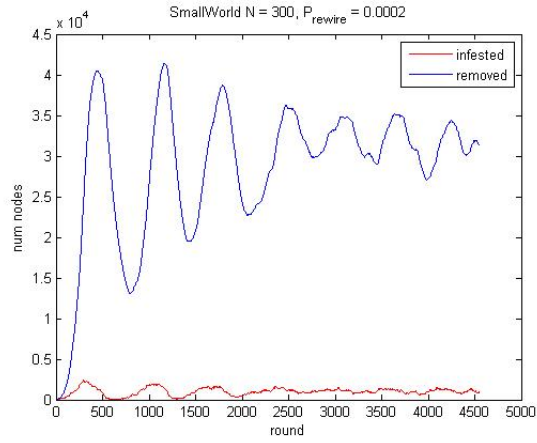$$N = 300, P_{rewire} = 0.0002$$

Figure 5: Rewire 0.0002

As we can see, now the epidemic last much longer than without rewiring and the number of infected individuals is fluctuating greatly. The reason is that without rewiring the epidemic is not infecting again where it already passes,

while in this case the rewiring allows it to infect again visited areas using a long distance link.

3.3.3
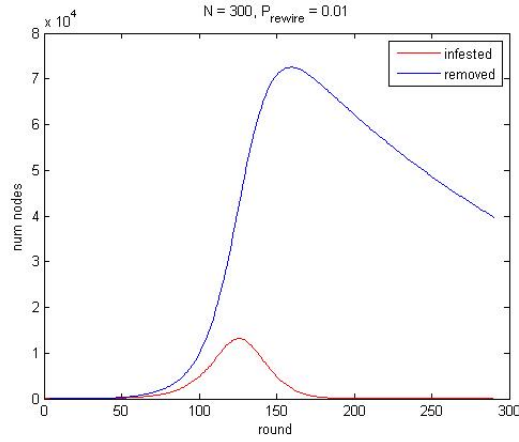
Finally

$$N = 300, P_{rewire} = 0.01$$

Figure 6: Rewire 0.01

Now, the epidemic spread much faster using long distance links, that can be found in higher probability, but fades faster as well. The reason is that the graph is not wide enough, the epidemic spread very fast and the nodes are in remove state, so the epidemic still can't infest them again, so it's fades.

Reproduce Results:

We ran our simulations using the code supplied in *SampleSim.m*. The only modification we've made between runs are the probability variables, and which function to generate the graph with (e.g. SimpleWorld or ScaleFree or Uniform-Select