Spread of Viruses on a Computer Network

New Mexico Supercomputing Challenge

Final Report

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1.0: Executive Summary

Computer viruses are a major issue to government, business, and individual people today. We have been trying to better understand how viruses infect computer networks by simulating the spread of viruses in networks of different structure. We want to determine how the structure of the network affects the time in which the virus infection dies out. Specifically, we measure how the diameter and the spectral radius of the network impacts the speed of infection spread and disappearance. We used NetLogo for our simulations and one of models in its library as a basis for our codes. In that model, computers and connections are represented by nodes and links. There are 3 types of nodes: infected, susceptible, and resistant, where the type of node can change during the simulation based on the types of its neighbors and random variables. We encoded four network types for our experiments: star, complete, random and power law networks. For each network type, we ran the simulation for five sizes: 200, 400, 600, 800, and 1000 nodes. For each network type and size we ran 10 simulations and recorded the time and the number of ticks. We then computed the average for each network type and size and analyzed the results. We observed that when a network has a larger diameter, it does not take longer for the virus to disappear. However, when the spectral radius is larger, the speed in which the virus gets eliminated does increase. Hence, the spectral radius can be used to determine which network structures are more resistant to virus spread.

2.0 Problem Statement

Viruses spread by moving from one infected node to another along links.Hence, the pattern of the links of the network, also called the structure or the topology of the network, determines how fast the viruses spread. If there are more links in a network, then it seems more likely that the virus will spread quicker and take a longer time to eliminate, but if there are fewer links it shouldn't take very long for the virus to die out. The problem we are considering in this project is to study how different layouts for the nodes and links in a computer network affect the speed in which viruses spread. We want to model different network layouts for the nodes and links and simulate the spread of viruses.

3.0 Background Information

A computer virus is a small program that spreads from one computer to another and causes malfunction or data loss. A virus is usually spread by email or when a user downloads an infected file from the Internet. The virus replicates itself by automatically sending itself to all of its neighbors. Studying computer viruses is important because they cause billions of dollars of economic damage. So, tools were made to discover and remove viruses from the computers [KEG]. Many people have worked on detecting and removing viruses and there is a whole field of computer science dealing with viruses and malware that is called cybersecurity [SF]. Some of the research includes detecting viruses with anti-virus software. Other researchers study the traffic between computers on a network to discover anomalies that may indicate virus activity. We are going to study viruses by using computer simulation.

4.0 Methodology

We used NetLogo as a language to use for simulating the spread of viruses in a network. We chose NetLogo because it is a convenient language for doing computer simulations and it has a library of models that we can use while developing our codes. We based our simulation code on one such existing model called *Viruses on a Network* in the NetLogo library, which we updated with additional functionality. We modified the model by allowing different network types as input. While the original code worked with random geometric networks only, we modified it so that it can generate, display, and simulate with different network types. With each network structure, we simulated the spread of viruses in networks of different sizes and recorded the number of ticks and the time it took for the virus to be extinguished. (*Tick* is a term used in NetLogo to describe the current number of time-steps of the simulation.) We analyzed the data in order to discover some relationship between the network structure and the number of ticks until the virus is eliminated.

4.1 Our hypothesis

In this project, we want to find out how fast the virus is eliminated depending on the graph's structure. We conjecture that it depends on the diameter of the network and/or the size of its spectral radius, namely, that greater the diameter/spectral radius, the longer it will take for the virus to be extinguished. The *diameter* of the network is the maximum distance between two nodes. It is relevant to know the diameter because the larger it is, the longer it takes for the virus to spread. The *spectral radius of a graph* is the spectral radius of its adjacency matrix. The *spectral radius of a matrix* is the largest eigenvalue by the absolute value. As with the diameter, we think that the larger the spectral radius, the longer it will take for the virus to be eliminated, because the longer it will take for information to go from one side of the network to the other. Moreover, in [GMT], a condition for the speed of virus die-out was found that relates the spectral radius and infection rate with whether the duration of the virus infection is “short” or “long.” In that paper [GMT], “short” means logarithmic and “long” means exponential. Hence, their result cannot be used to predict which of two network types is more resistant to a virus spread, but suggests that the spectral radius might be a relevant characteristic. We are going to check to see if that is true or not.

4.2 Modeling the virus infection

To find out how the layout of the nodes and links affect the speed that the viruses spread, we coded different models. We used Virus in A Network model from the NetLogo library, which simulates the spread of viruses through a network. Each node represents a computer, and we are modeling the progress of a computer virus through this network. The links in the networks represent the connection between computers and their neighbors. Each node may be one of these three states: susceptible, infected, or resistant. *Infected* nodes are the ones that currently have the virus. They try to send it to all their neighbors who are susceptible. Infected nodes have a recovery chance and can either become susceptible again or resistant. A node can become resistant by a resistance probability that is set in the model. The *susceptible* nodes are the nodes that are vulnerable to the virus. When a neighbor of a susceptible node is infected, it can get infected too depending on the virus spread probability, which is a parameter specified in the model. When an infected node becomes *resistant*, it stays resistant, and it is not possible for the virus to spread through its links.

4.3 Test networks

We will be using four different network types in our project; star network, complete network, random network, and power law network.

4.3.1 Star Network

The first model we will use is the star network, which is a network that has one node connected to every other node and there are no direct connections between the other nodes. The node that is connected to all other nodes is called the *central node.* We are interested in studying this network because it is one of the simplest kinds of connected networks. It is simple because all the nodes except for the central node have one neighbor. Star networks can help when analyzing more complex networks. For instance, it is easier to understand the power law network because it is made up of several star networks. Each one of these star networks consists of node a degree more than one and all of its neighbors. Understanding the properties of each star network in the power law network helps us understand it as a whole [GMT].

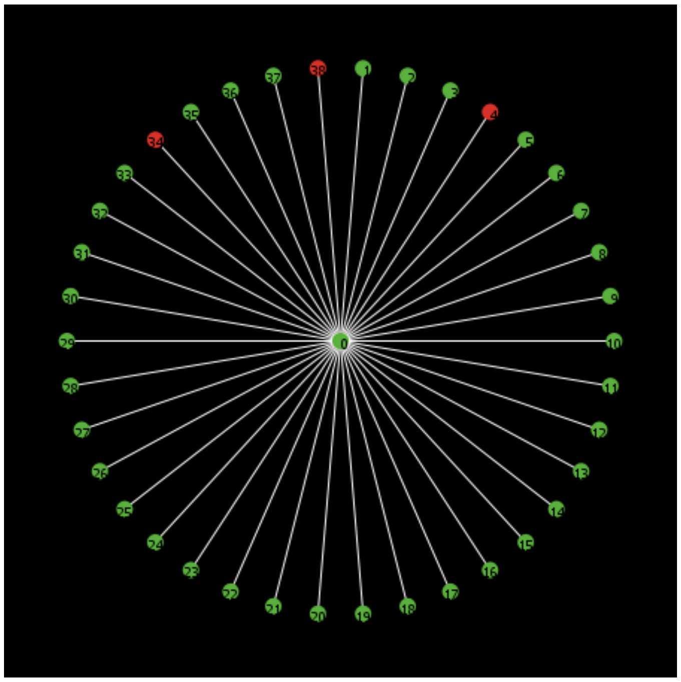

Figure 1. A star network.

4.3.2 Complete Network

In the complete network each node is linked with every other node. Complete networks are important because they are used in practice, For instance, large Border Gateway Protocol (BGP) servers form a complete network [GMT]. BGP is a standard protocol for exchanging information [EGC]. Also, complete networks are interesting to study because they have the maximum possible number of links.

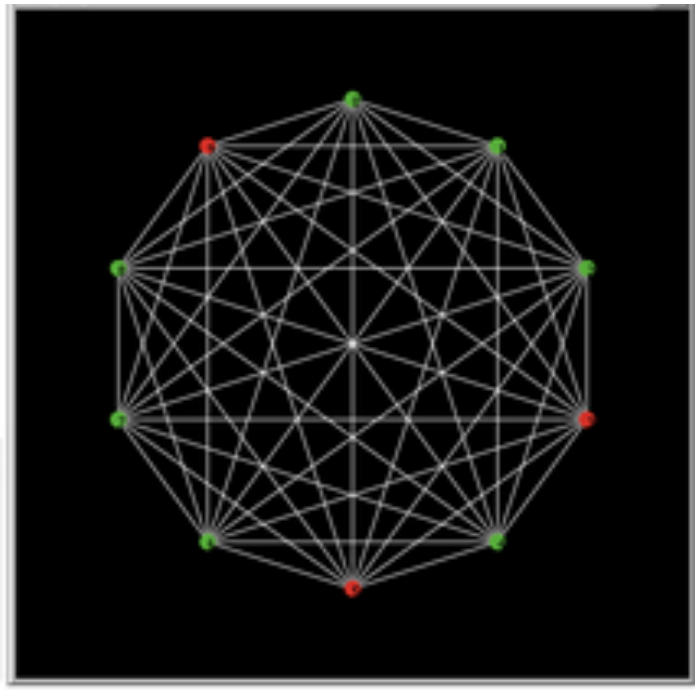

Figure 2. A complete graph

4.3.3 Random Network

In a random network, the nodes and links are randomly placed. There are several ways to generate a random network. In the model that we used, we have parameters n and m, number of nodes and links as input. We create n nodes without links between them. We choose a random pair of vertices. If there is no link between them, we create a link. If there is already a link, we don’t do anything. We repeat, until m links are created. Random networks are interesting for our project because they are an important class of networks that have been studied very often. Also, we want to compare them with the power law networks that are important for the practice.

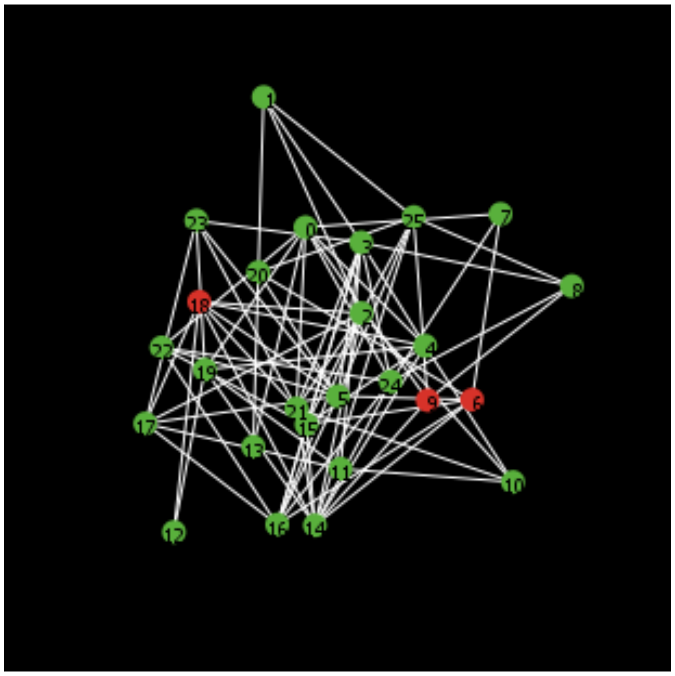

Figure 3. Random graph.

4.3.4 Power Law Network

Finally, we have a power law network, also known as scale free network [RPS]. These networks have degrees of the nodes that satisfy the power law. To be more specific, in a power law network the fraction *f*(*k*) of nodes that have *k* neighbors is

$$f(k) = k^{-\gamma}$$

for some positive number γ.

We find power law networks interesting to study because the Internet AS-level graph is shown to be of this type [GMT]. Also, many real life networks such as social networks are known to be power law networks. We generate the power law network by using the preferential attachment model [BA]. In this model, we start with two nodes and a link between them. We add a new node link it to one of the existing nodes with probabilities proportional to their degrees. We continue until the required number of nodes are created.

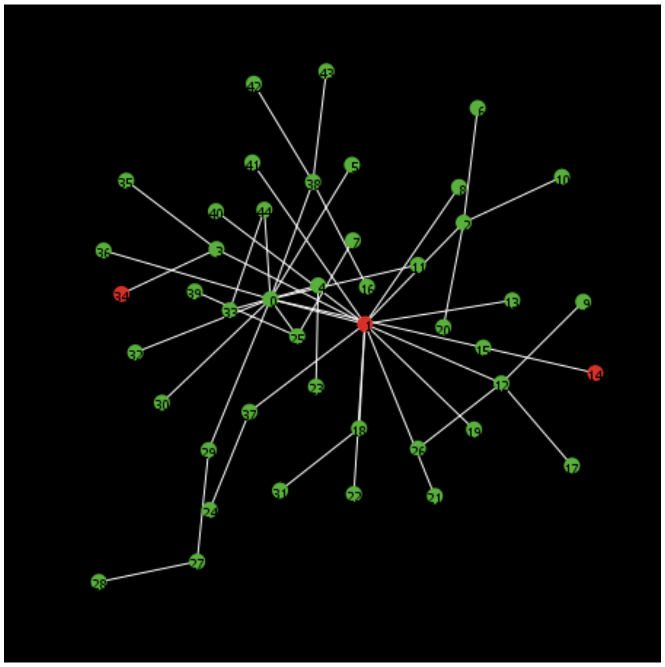

Figure 4. Power law graph.

5.0 Results

We performed several experiments in order to measure the time and the number of ticks for each network type and size. For each network type we generated and did simulations with network of size 200, 400, 600, 800, and 1,000 nodes since there is randomness in how the virus will spread in a given network (because of the probabilities used to determine if a node will get infected and when and whether it will become resistant) and since some networks are random (the random and power law networks), the simulation times may be quite different even for networks of the same size and type. For that reason, we tested with each case 10 times. After getting the data from all experiment, we computed the averages for each network type and put them in a graph. We also made a graph that includes averages of all network types. The results presented in Figures 5-9.

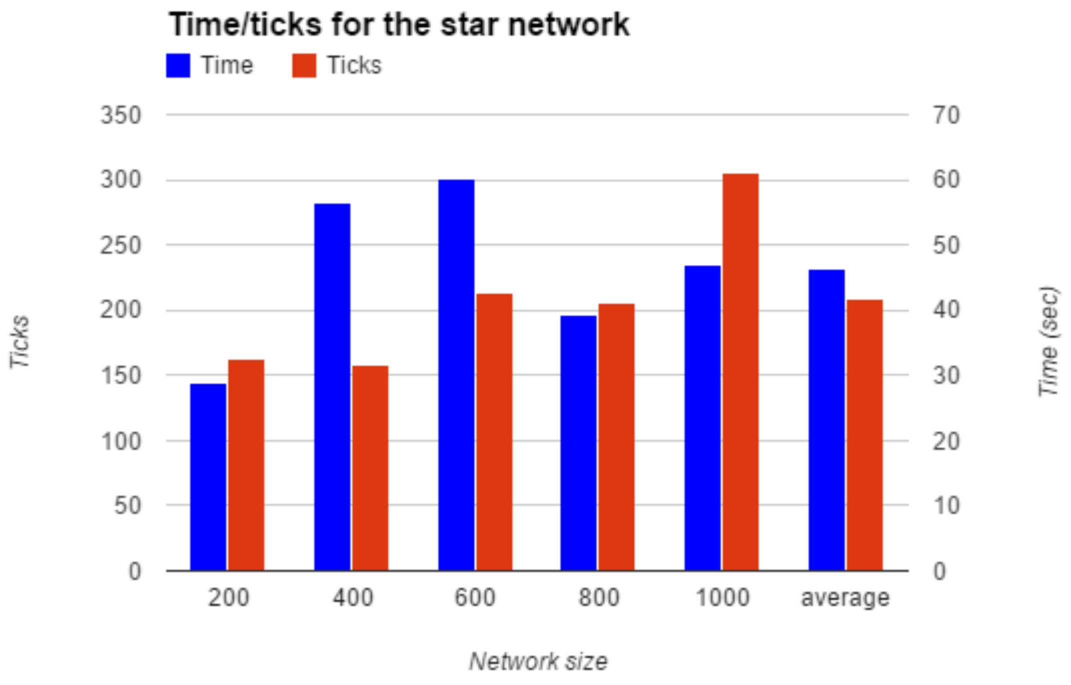

Figure 5. Experimental results for the star network

Figure 5 shows the results for the star network. We observe that the running times and the number of ticks are not correlated to each other, and they are not correlated with the size of the network. Both of those results were unexpected for us.

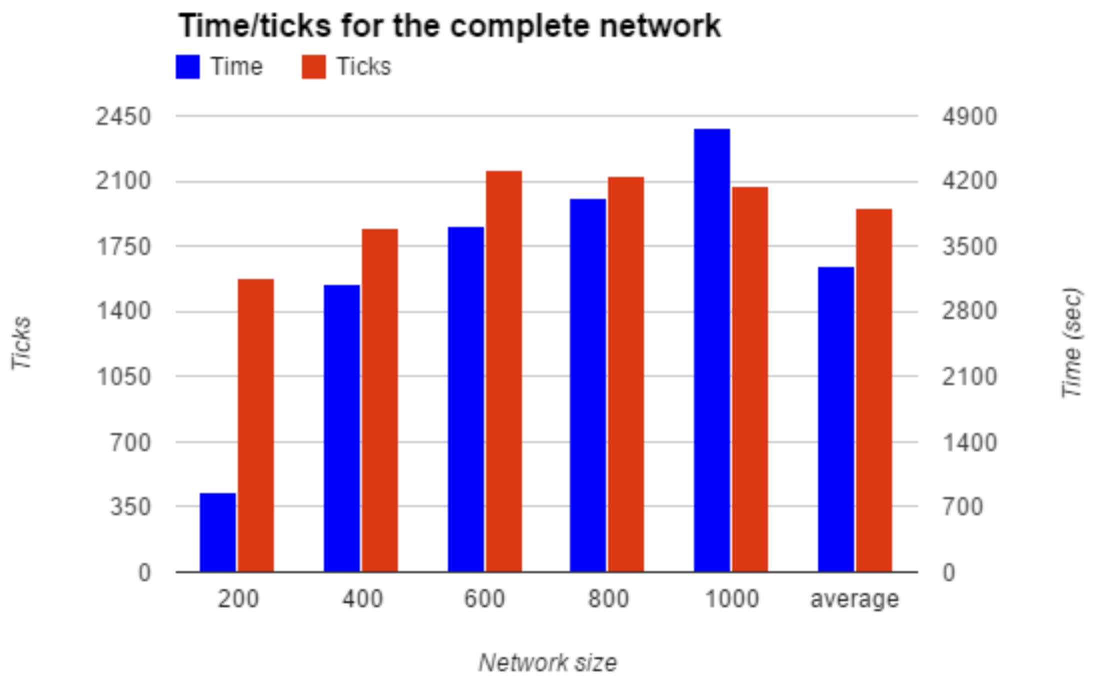

Figure 6. Experimental results for the complete network

The results for the complete networks are given in Figure 6. We observe that the time and ticks grow large as the network size gets bigger and they are much bigger than the corresponding values for the star network.

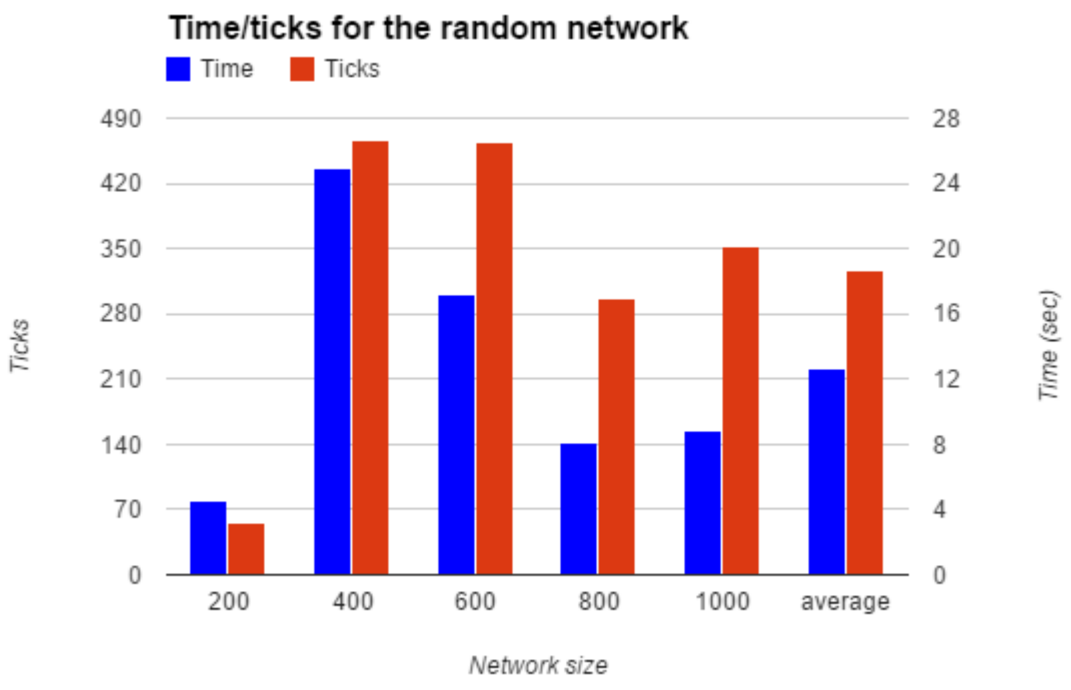

Figure 7. Experimental results for the random network

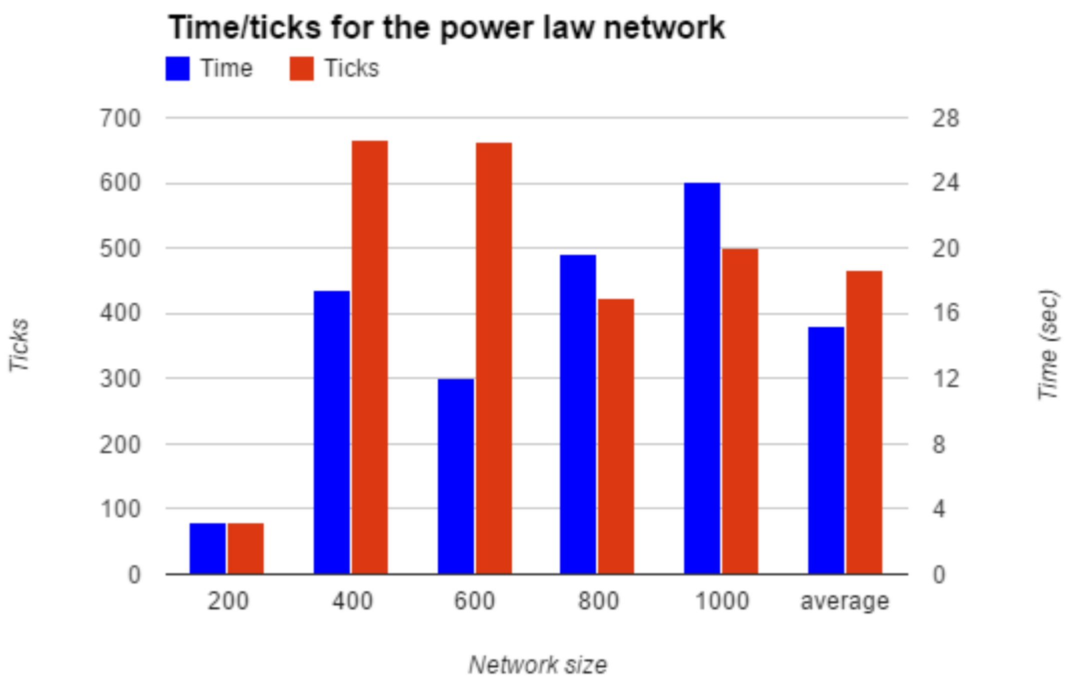

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Figure 8. Experimental results for the power law network

Figures 7 and 8 show the results for the random and the power law network. We notice that the values are very similar. This is surprising because the networks are very different from each other. The time and the ticks don't seem to increase with the network size. Surprisingly,, for both networks, the network size of 400 and 600 node take much longer than any of the other sizes. We have also noticed that the 200 average is much smaller than the rest of the sizes. We suppose that this unexpected behavior cannot be explained by the simulation model or the structure of the networks, but by the NetLogo implementation.

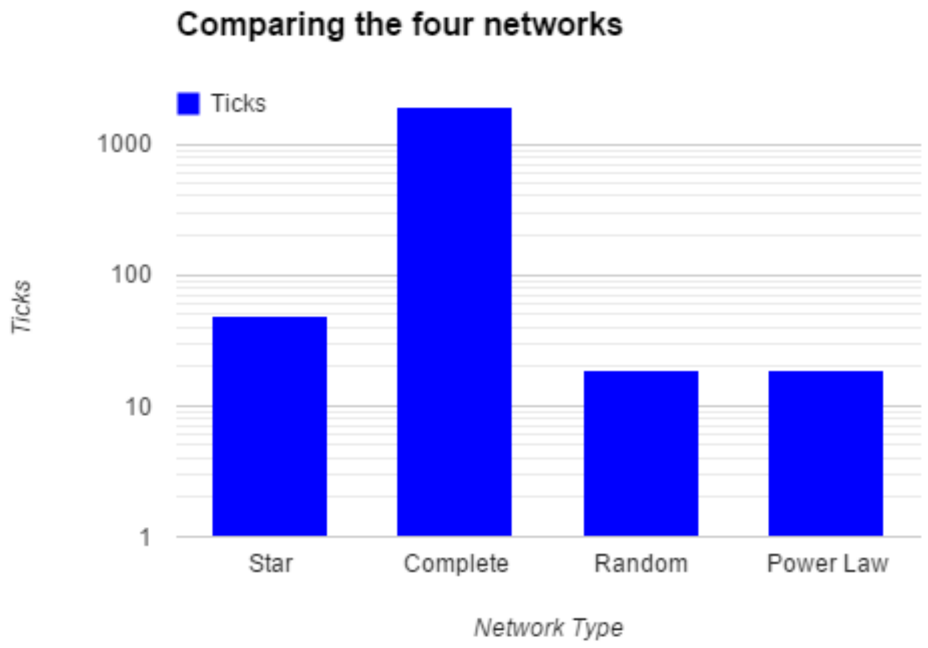

Figure 9. Comparison of the number of ticks for all networks

Finally, Figure 9 compares the average number of ticks (number of time steps) that it takes for the virus to die out for each network type. Clearly, the complete network takes longest, followed by the star network, and the random and power law network. The values for the random and power law network look indistinguishable, but this is not because of the logarithmic scale used; in fact they are extremely close to each other: 18.664 for the random and 18.656 for the power law.

In order to test our hypothesis, that the times for virus die out depend on the diameter and the spectral radius of the graph of the corresponding network, we put the relevant information about the four types of network in Table 1. The diameters of the star and the complete graph we found by direct analysis of the networks, for the diameter of the random graph we used [HI], and for the diameter of the power law graph we used [BR]. This data does not support the our conjecture that smaller diameters mean that the virus spread will take longer. So our first hypothesis is not confirmed. To get the spectral radii of the star network, the complete network, and the random network we used [GMT]. We notice that the spectral radius of the complete graph is bigger than the spectral radius of the star network, which is bigger than the spectral radius of the random graph. Comparing this with Figure 9, we observe the same ordering: the largest number of ticks is recorded for the complete network, followed by the star network, and the random network. For the power law network we did not find a formula for the spectral radius, but we expect that it is similar as for the random network. While we did not expect that the random and the power law network have so similar virus die out times, this data is consistent with the data for the star network (Figure 5). We can think of the random and the power law network as consisting of stars, each star centered at a different node and containing also all neighbors of this node. While in the random network all stars will be of sizes that are almost the same, in the power law network they will be different. But Figure 5 shows that the sizes of the stars do not matter for the time for virus die out, so we can expect that the random and the power law network will have similar behaviors.

	Star	**Complete**	**Random**	**Power Law**
Diameter	$\mathbf{2}$	$\mathbf{1}$	$\boldsymbol{log\ n}$	$\boldsymbol{log\ n}$
Spectral radius	$\boldsymbol{\sqrt{n}}$	$\boldsymbol{n-1}$	$\boldsymbol{d}$	$-$

Table 1: Diameter and spectral radius of the 4 networks, where d is the average degree. Our random networks have average degree of nodes 4.

6.0 Conclusion

In conclusion, our experiment have shown that our hypothesis that the spectral radius is a good indicator for the time it takes to extinguish a virus from the network, with greater radius corresponding to longer times, while the diameter is not. We also observed that the simulation codes are scalable for the star, random, and power law networks, but not for the complete network, where a network of 1000 nodes takes roughly an hour to simulate. NetLogo is very convenient language for such type of simulations as it is very powerful and has nice tools that help running experiments, but the drawback is that the code may not be very efficient.

7.0 Original Achievements

Our original achievement was to determine whether the diameter and the spectral radius affect the speed in which the virus dies out. In our best knowledge, nobody has studied such model for virus spread as ours and on these network types.

We found that NetLogo is very convenient language for this type of simulations, both because of the language features and tools, as well as the library of models that is available. NetLogo was fast enough to let us check our hypothesis, although for running simulations on very large networks it may not be fast enough.

During our work on this project we have learned many things that we did not know before. One thing we have found is that each run is different, even if the network is the same, and we have to ran the experiment for each network type and number of nodes multiple times and then take the average of the results.

8.0 Future Work

Although we have accomplished our achievements, much can still be done with this project. Experimenting with various alternative network structures to see how the behavior of the virus differs with other networks such as real-life network. Also, we can extend this model by trying to model both the spread of viruses and countermeasures by cyber defenders, like making certain nodes resistant.

9.0 Work Cited

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10.0 Appendix

10.1 Acknowledgements

I would like to thank the organizers of the New Mexico Supercomputing challenge for all their assistance. I would also like to thank my mentors and the NetLogo models library for their codes and information.

10.2 Program Code

```
;;=================================================

;; Virus spread for Star networks in NetLogo

;; Adapted from Virus on a Network in the Models Library

;; Modified by Christie Djidjev

;; March 2015

;;=================================================


turtles-own
[
    infected?           ;; if true, the turtle is infectious
  resistant?            ;; if true, the turtle can't be infected
  virus-check-timer     ;; number of ticks since this turtle's last virus-check

]

to setup
  clear-all
  setup-nodes
  ; setup-spatially-clustered-network
  ask n-of initial-outbreak-size turtles
    [ become-infected ]
  ask links [ set color white ]
  layout-radial turtles links (turtle 0)
  reset-ticks
  reset-timer
end


to setup-nodes
```

```
  set-default-shape turtles "circle"
  cro number-of-nodes
  [
    set label who
    set label-color black
    fd 15
    become-susceptible
    set virus-check-timer random virus-check-frequency
  ]
  make-star number-of-nodes
end

to make-star [num-nodes]
  let counter1 0
    let counter2 (counter1 + 1)
    while [counter2 < number-of-nodes]
    [
      ask (turtle counter1) [create-link-with (turtle counter2)]
      set counter2 (counter2 + 1)
    ]
  set counter1 (counter1 + 1)
end

to go
  if all? turtles [not infected?]
    [
        type count turtles type "," type ticks type "," print timer
        stop
    ]
  ask turtles
  [
     set virus-check-timer virus-check-timer + 1
     if virus-check-timer >= virus-check-frequency
```

```
          [ set virus-check-timer 0 ]
    ]
    spread-virus
    do-virus-checks
    tick
end

to become-infected    ;; turtle procedure
    set infected? true
    set resistant? false
    set color red
end

to become-susceptible    ;; turtle procedure
    set infected? false
    set resistant? false
    set color green
end

to become-resistant    ;; turtle procedure
    set infected? false
    set resistant? true
    set color gray
    ask my-links [ set color gray - 2 ]
end

to spread-virus
    ask turtles with [infected?]
        [ ask link-neighbors with [not resistant?]
                [ if random-float 100 < virus-spread-chance
                        [ become-infected ] ] ]
end
```

```
to do-virus-checks
   ask turtles with [infected? and virus-check-timer = 0]
   [
      if random 100 < recovery-chance
      [
         ifelse random 100 < gain-resistance-chance
            [ become-resistant ]
            [ become-susceptible ]
      ]
   ]
end


;;=============================================

;; Virus spread for the complete networks

;; Adapted from Virus on a Network in the Models Library

;; Modified by Christie Djidjev

;; March 2015

;;=============================================

turtles-own

[
   infected?             ;; if true, the turtle is infectious
   resistant?            ;; if true, the turtle can't be infected
   virus-check-timer     ;; number of ticks since this turtle's last virus-check
]

to setup
   clear-all
   setup-nodes
   ; setup-spatially-clustered-network
   ask n-of initial-outbreak-size turtles
      [ become-infected ]
   ask links [ set color white ]
   reset-ticks
   reset-timer
end

to setup-nodes
   set-default-shape turtles "circle"
   cro number-of-nodes
   [
      set label who
      set label-color black
      fd 15
      become-susceptible
      set virus-check-timer random virus-check-frequency
   ]
   make-mesh number-of-nodes
end

to make-mesh [num-nodes]
   let counter1 0
   while [counter1 < number-of-nodes]
   [
      let counter2 (counter1 + 1)
      while [counter2 < number-of-nodes]
      [
         ask (turtle counter1) [create-link-with (turtle counter2)]
         set counter2 (counter2 + 1)
      ]
   set counter1 (counter1 + 1)
   ]
end
```

```
to go
   if all? turtles [not infected?]
      [
            type count turtles type "," type ticks type "," print timer
            stop
      ]
   ask turtles
   [
       set virus-check-timer virus-check-timer + 1
       if virus-check-timer >= virus-check-frequency
          [ set virus-check-timer 0 ]
   ]
   spread-virus
   do-virus-checks
   tick
end

to become-infected    ;; turtle procedure
   set infected? true
   set resistant? false
   set color red
end

to become-susceptible    ;; turtle procedure
   set infected? false
   set resistant? false
   set color green
end

to become-resistant    ;; turtle procedure
   set infected? false
   set resistant? true
```

```
  set color gray
  ask my-links [ set color gray - 2 ]
end

to spread-virus
  ask turtles with [infected?]
    [ ask link-neighbors with [not resistant?]
        [ if random-float 100 < virus-spread-chance
            [ become-infected ] ] ]
end

to do-virus-checks
  ask turtles with [infected? and virus-check-timer = 0]
  [
    if random 100 < recovery-chance
    [
      ifelse random 100 < gain-resistance-chance
        [ become-resistant ]
        [ become-susceptible ]
    ]
  ]
end

;;================================================

;; Virus spread for the random networks

;; Adapted from Virus on a Network in the Models Library

;; Modified by Christie Djidjev

;; March 2015

;;================================================

turtles-own
[
  infected?             ;; if true, the turtle is infectious
  resistant?            ;; if true, the turtle can't be infected
  virus-check-timer     ;; number of ticks since this turtle's last virus-check

]

to setup
  clear-all
  setup-nodes
  ; setup-spatially-clustered-network
  ask n-of initial-outbreak-size turtles
    [ become-infected ]
  ask links [ set color white ]
   repeat 50
  [
    layout-spring turtles links 0.7(world-width / (sqrt number-of-nodes)) 1
  ]
  reset-ticks
  reset-timer
end


to setup-nodes
  set-default-shape turtles "circle"
  cro number-of-nodes
  [
    set label who
    set label-color black
    fd 15
    become-susceptible
    set virus-check-timer random virus-check-frequency
  ]
  make-random number-of-nodes
```

```
end

to make-random [num-nodes]
   repeat 3 * num-nodes
   [
      add-edge
   ]
end

to add-edge
   let node1 one-of turtles
   let node2 one-of turtles
   ask node1 [
      ifelse link-neighbor? node2 or node1 = node2
      ;; if there's already an edge there, then go back
      ;; and pick new turtles
      [ add-edge ]
      ;; else, go ahead and make it
      [ create-link-with node2 ]
   ]
end

to go
   if all? turtles [not infected?]
      [
            type count turtles type "," type ticks type "," print timer
            stop
      ]
   ask turtles
   [
       set virus-check-timer virus-check-timer + 1
       if virus-check-timer >= virus-check-frequency
          [ set virus-check-timer 0 ]
   ]
   spread-virus
   do-virus-checks
   tick
end

to become-infected    ;; turtle procedure
   set infected? true
   set resistant? false
   set color red
end

to become-susceptible    ;; turtle procedure
   set infected? false
   set resistant? false
   set color green
end

to become-resistant    ;; turtle procedure
   set infected? false
   set resistant? true
   set color gray
   ask my-links [ set color gray - 2 ]
end

to spread-virus
   ask turtles with [infected?]
      [ ask link-neighbors with [not resistant?]
            [ if random-float 100 < virus-spread-chance
                  [ become-infected ] ] ]
end

to do-virus-checks
```

```
   ask turtles with [infected? and virus-check-timer = 0]
   [
      if random 100 < recovery-chance
      [
         ifelse random 100 < gain-resistance-chance
            [ become-resistant ]
            [ become-susceptible ]
      ]
   ]
end

;;==============================================

;; Virus spread for the power law networks

;; Adapted from Virus on a Network in the Models Library

;; Modified by Christie Djidjev

;; March 2015

;;==============================================


turtles-own
[
   infected?            ;; if true, the turtle is infectious
   resistant?           ;; if true, the turtle can't be infected
   virus-check-timer    ;; number of ticks since this turtle's last virus-check

]

to setup
   clear-all
   setup-nodes
   ; setup-spatially-clustered-network
   ask n-of initial-outbreak-size turtles
```

```
      [ become-infected ]
   ask links [ set color white ]
    repeat 50
   [
      layout-spring turtles links 0.3 (world-width / (sqrt number-of-nodes)) 1
   ]
   reset-ticks
   reset-timer
end


to setup-nodes
   set-default-shape turtles "circle"
   cro 1
   [
      set-attributes
   ]
   cro 1
   [
      set-attributes
      create-link-with turtle 0
   ]

   cro number-of-nodes - 2
   [
      set-attributes
      create-link-with find-partner
   ]
end

to set-attributes
   set label who
   set label-color black
   fd 15
   become-susceptible
   set virus-check-timer random virus-check-frequency
end

to-report find-partner
   report [one-of both-ends] of one-of links
end

to go
   if all? turtles [not infected?]
      [
         type count turtles type "," type ticks type "," print timer
         stop
      ]
   ask turtles
   [
       set virus-check-timer virus-check-timer + 1
       if virus-check-timer >= virus-check-frequency
          [ set virus-check-timer 0 ]
   ]
   spread-virus
   do-virus-checks
   tick
end

to become-infected    ;; turtle procedure
   set infected? true
   set resistant? false
   set color red
end

to become-susceptible    ;; turtle procedure
```

```
   set infected? false
   set resistant? false
   set color green
end

to become-resistant    ;; turtle procedure
   set infected? false
   set resistant? true
   set color gray
   ask my-links [ set color gray - 2 ]
end

to spread-virus
   ask turtles with [infected?]
      [ ask link-neighbors with [not resistant?]
            [ if random-float 100 < virus-spread-chance
                  [ become-infected ] ] ]
end

to do-virus-checks
   ask turtles with [infected? and virus-check-timer = 0]
   [
      if random 100 < recovery-chance
      [
         ifelse random 100 < gain-resistance-chance
            [ become-resistant ]
            [ become-susceptible ]
      ]
   ]
end
```