# Complex Networks: Quiz #13

Due on Jan 30th, 2019

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## Problem 1

Do simulations with same parameters (number of nodes, beta, gamma, percentage infected) but with different network structures such as:

- 1. complete graph (clique)
- 2. star graph
- 3. cycle graph
- 4. barbell graph
- 5. lollipop graph

#### Answer 1

```
!pip install -q ndlib
!pip install -q bokeh
import networkx as nx
import matplotlib.pyplot as plt
import numpy as np
import ndlib.models.epidemics.SIRModel as sir
# Network Definition
g1 = nx.complete_graph(1000)
g2 = nx.star_graph(999)
g3 = nx.cycle_graph(1000)
g4 = nx.barbell_graph(499, 2)
g5 = nx.lollipop_graph(998,2)
# Model Selection
model1 = sir.SIRModel(g1)
model2 = sir.SIRModel(g2)
model3 = sir.SIRModel(g3)
model4 = sir.SIRModel(g4)
model5 = sir.SIRModel(g5)
import ndlib.models.ModelConfig as mc
# Model Configuration
config = mc.Configuration()
config.add_model_parameter('beta', 0.001)
config.add_model_parameter('gamma', 0.01)
config.add_model_parameter("percentage_infected", 0.05)
model1.set_initial_status(config)
model2.set_initial_status(config)
model3.set_initial_status(config)
model4.set_initial_status(config)
model5.set_initial_status(config)
# Simulation
iterations1 = model1.iteration_bunch(200)
trends1 = model1.build_trends(iterations1)
iterations2 = model2.iteration_bunch(200)
trends2 = model2.build_trends(iterations2)
```

```
iterations3 = model3.iteration_bunch(200)
trends3 = model3.build_trends(iterations3)
iterations4 = model4.iteration_bunch(200)
trends4 = model4.build_trends(iterations4)
iterations5 = model5.iteration_bunch(200)
trends5 = model5.build_trends(iterations5)
# Visualization
from bokeh.io import output_notebook, show
output_notebook() # there will be no output without this
from ndlib.viz.bokeh.DiffusionTrend import DiffusionTrend
from ndlib.viz.bokeh.DiffusionPrevalence import DiffusionPrevalence
print("complete graph\n", nx.info(g1))
# Diffusion trend
viz1 = DiffusionTrend(model1, trends1)
p1 = viz1.plot(width=400, height=400)
show(p1)
# Prevalence plot
viz1 = DiffusionPrevalence(model1, trends1)
p1 = viz1.plot(width=400, height=400)
show(p1)
print("star graph\n", nx.info(g2))
viz2 = DiffusionTrend(model2, trends2)
p2 = viz2.plot(width=400, height=400)
show(p2)
viz2 = DiffusionPrevalence(model2, trends2)
p2 = viz2.plot(width=400, height=400)
show(p2)
print("cycle graph\n", nx.info(g3))
viz3 = DiffusionTrend(model3, trends3)
p3 = viz3.plot(width=400, height=400)
show(p3)
viz3 = DiffusionPrevalence(model3, trends3)
p3 = viz3.plot(width=400, height=400)
show(p3)
print("barbell graph\n", nx.info(g4))
viz4 = DiffusionTrend(model4, trends4)
p4 = viz4.plot(width=400, height=400)
show(p4)
viz4 = DiffusionPrevalence(model4, trends4)
p4 = viz4.plot(width=400, height=400)
show(p4)
```

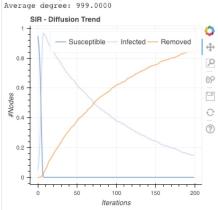
```
print("lollipop\n", nx.info(g5))
viz5 = DiffusionTrend(model5, trends5)
p5 = viz5.plot(width=400, height=400)
show(p5)

viz5 = DiffusionPrevalence(model5, trends5)
p5 = viz5.plot(width=400, height=400)
show(p5)

## Multiple plot
#from ndlib.viz.bokeh.MultiPlot import MultiPlot
#vm = MultiPlot()
#vm.add_plot(p)
#vm.add_plot(p2)
#m = vm.plot()
#show(m)
```

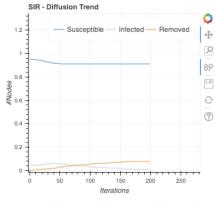
#### The result is:

complete graph
Name:
Type: Graph
Number of nodes: 1000
Number of edges: 499500
Average degree: 999.0000

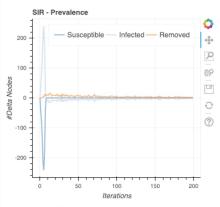


beta: 0.001, gamma: 0.01, percentage infected: 0.05

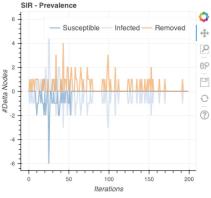
star graph
Name:
Type: Graph
Number of nodes: 1000
Number of edges: 999
Average degree: 1.9980



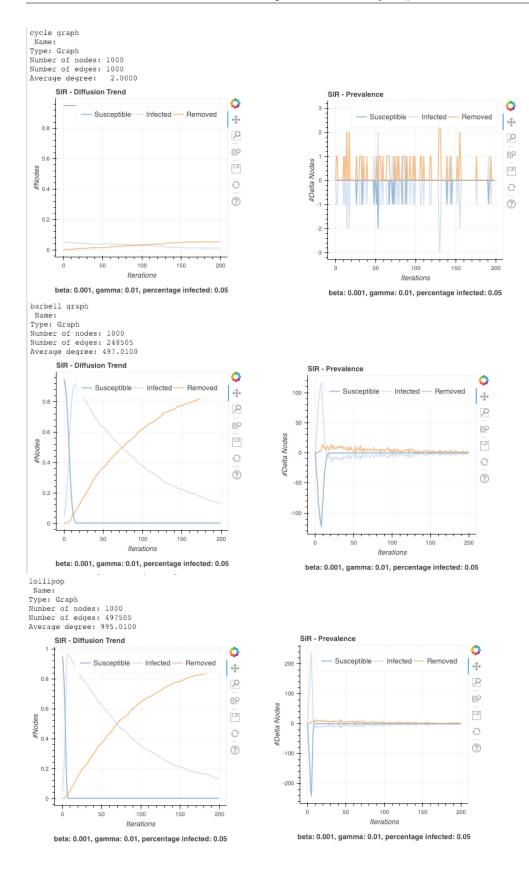
beta: 0.001, gamma: 0.01, percentage infected: 0.05



beta: 0.001, gamma: 0.01, percentage infected: 0.05



beta: 0.001, gamma: 0.01, percentage infected: 0.05



# Problem 2

Show an example of Diffusion Trend which is quite different from that of Erdos-Renyi network (together with used network structure).

### Answer 2

From the images above, we can find that the Diffusion Trend of star graph and cycle graph is quite different from Erdos-Renyi network. From the images we can see that the infected people increase much slower than the infected in Erdos-Renyi. In 200 interations, there are less than 200 infected in 1000 people, which is because the edge between nodes are less so that the disease is difficult for spreading.