

NATIONAL INSTITUTE OF TECHNOLOGY SILCHAR

Cachar, Assam

B.Tech. VIth Sem

Subject Code: CS-321

Subject Name: Social Network Analysis Lab

Submitted By:

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Branch : CSE – B

AIM: TO ANALYSE THE INFORMATION DIFFUSION BY INCORPORATING THE FOLLOWING EPIDEMIC MODELS AND DETERMINE THE BEST SUITABLE MODEL FOR REAL-EORLD SCENARIOS: EPIDEMIC MODELS: SUSCEPTIBLE INFECTED (SI), SUSCEPTIBLE INFECTED RECOVERED (SIR), AND SUSCEPTIBLE INFECTED SUSCEPTIBLE (SIS) AND LINEAR CASCADES (LC).

THEORY:

1. **Susceptible Infected (SI):** In SI model, during the course of an epidemics, a node is allowed to change its status only from Susceptible (S) to Infected (I). SI assumes that if, during a generic iteration, a susceptible node comes into contact with an infected one, it becomes infected with probability β : once a node becomes infected, it stays infected (the only transition allowed is S→I).
2. **Susceptible Infected Recovered (SIR):** In this model, during the course of an epidemics, a node is allowed to change its status from Susceptible (S) to Infected (I), then to Removed (R). SIR assumes that if, during a generic iteration, a susceptible node comes into contact with an infected one, it becomes infected with probability beta, then it can be switch to removed with probability gamma (the only transition allowed are S→I→R).
3. **Susceptible Infected Susceptible (SIS):** n this model, during the course of an epidemics, a node is allowed to change its status from Susceptible (S) to Infected (I). SIS assumes that if, during a generic iteration, a susceptible node comes into contact with an infected one, it becomes infected with probability beta, then it can be switch again to susceptible with probability lambda (the only transition allowed are S→I→S).

$$\text{Susceptible Equation, } \frac{ds}{dt} = -b s(t) i(t)$$

$$\text{Recovered Equation, } \frac{dr}{dt} = k i(t)$$

$$\text{Infected Equation, } \frac{di}{dt} = b s(t) i(t) - k i(t)$$

DATASETS: Football Club, Karate Club, Dolphin Network, Barabasi-Albert Network.

CODE:

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import networkx as nx
from bokeh.io import show
import ndlib.models.ModelConfig as mc
import ndlib.models.epidemics as ep
from ndlib.viz.bokeh.DiffusionTrend import DiffusionTrend

def SImodel (graph):
    print ("SI model")
    SI = ep.SIModel (graph)
    cfg = mc.Configuration ()
    cfg.add_model_parameter ('beta', 0.01)
    cfg.add_model_parameter ("percentage_infected", 0.05)
    SI.set_initial_status (cfg)
    iterations = SI.iteration_bunch (200, node_status = True)
    trends = SI.build_trends (iterations)
    viz = DiffusionTrend (SI, trends)
    show (viz.plot (width = 1000), new = "tab")

def SIRmodel (graph):
    print ("SIR model")
    SIR = ep.SIRModel (graph)
    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)
    SIR.set_initial_status (config)
    iterations = SIR.iteration_bunch (200, node_status = True)
    trends = SIR.build_trends (iterations)
    viz = DiffusionTrend (SIR, trends)
    show (viz.plot (width = 1000), new = "tab")

def SISmodel (graph):
    print ("SIS model")
    SIS = ep.SISMModel (graph)
    config = mc.Configuration ()
    config.add_model_parameter ('beta', 0.01)
    config.add_model_parameter ('lambda', 0.005)
    config.add_model_parameter ('fraction_infected', 0.05)
    SIS.set_initial_status (config)
    iterations = SIS.iteration_bunch (200, node_status = True)
    trends = SIS.build_trends (iterations)
    viz = DiffusionTrend (SIS, trends)
    show (viz.plot (width = 1000), new = "tab")

# NOTE: Sometimes, it may so happen that SI model gets overwritten by either
# SIR model or SIS model in output.

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# In such cases, simply comment SISmodel (graph) and SIRmodel (graph) and run
models individually.

print ("Karate Club")
graph = nx.read_gml ("karate.gml")
SImodel (graph)
SIRmodel (graph)
SISmodel (graph)

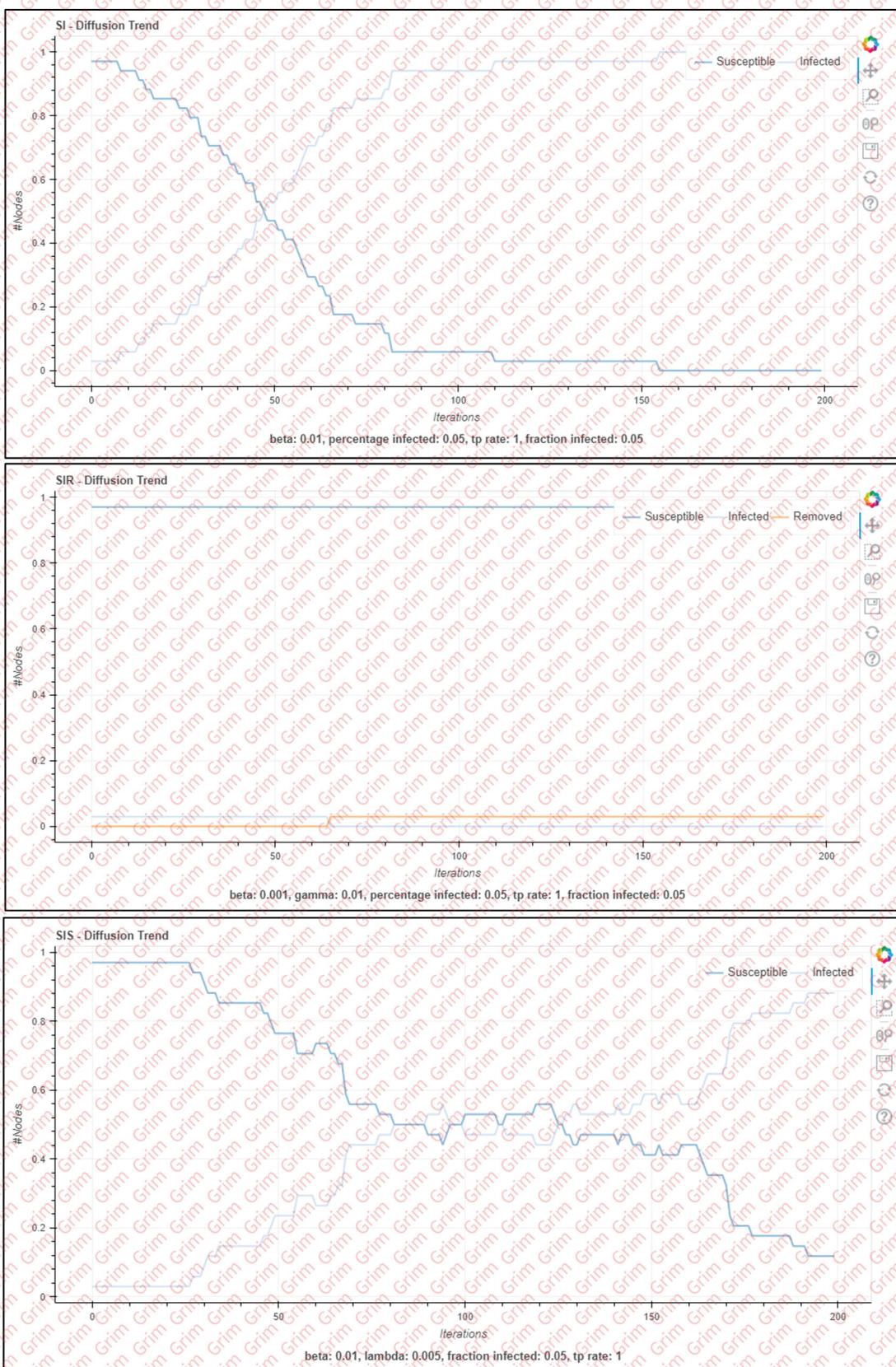
# print ("Football Club")
# graph = nx.read_gml ("football.gml")
# SImodel (graph)
# SIRmodel (graph)
# SISmodel (graph)

# print ("Dolphin Network")
# graph = nx.read_gml ("dolphins.gml")
# SImodel (graph)
# SISmodel (graph)
# SIRmodel (graph)

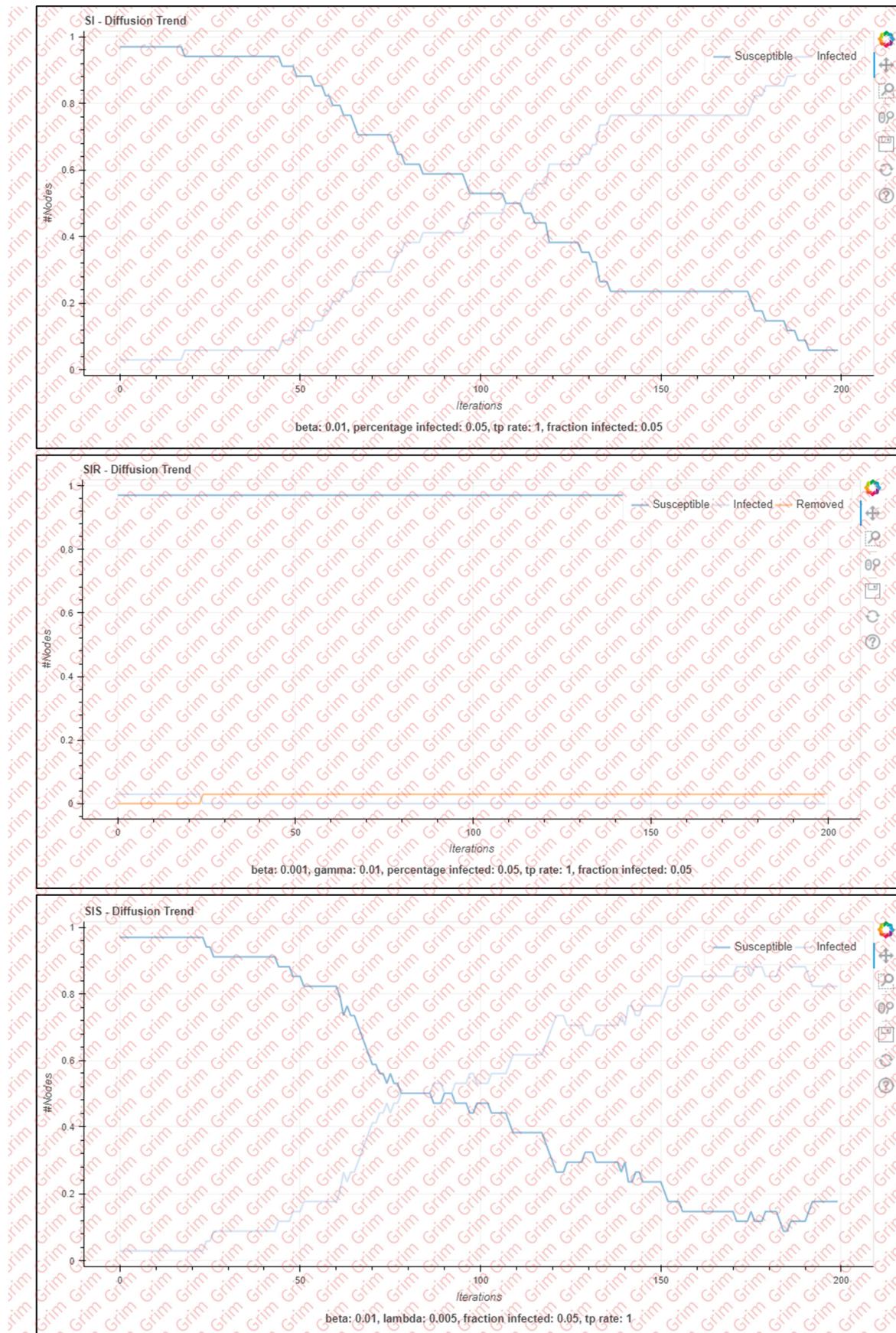
# print ("Albert Barabasi Network")
# graph = nx.barabasi_albert_graph (100, 15)
# SImodel (graph)
# SISmodel (graph)
# SIRmodel (graph)
```

OUTPUT AND OBSERVATIONS:

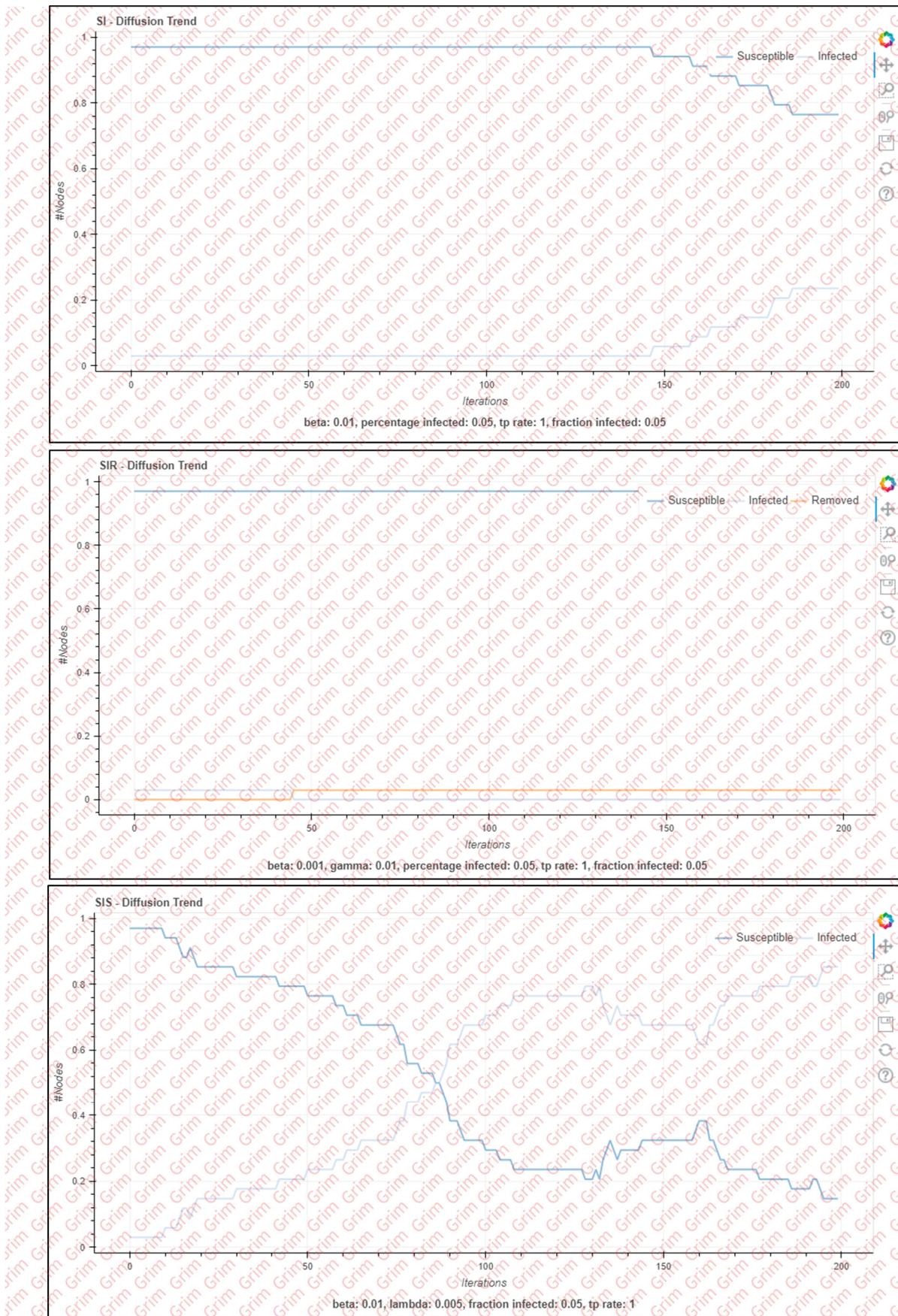
// KARATE CLUB



// FOOTBALL CLUB



// DOLPHINS NETWORK



// BARABASI-ALBERT GRAPH

