Network Science
PHYS 5116, Fall 2019

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Assignment 3, due by Nov. 25th, 6pm.

You are only allowed to hand in a single file containing all your work, either a PDF or a stapled paper copy. If you attempt to hand in more than one file, we will grade only one of the files, selected at random. Please name your single file as LASTNAME.pdf, *e.g.* Towlson.pdf

1. *Modularity Maximum.* Show that the maximum value of modularity M defined in (9.12) cannot exceed one.

2. *Epidemics on Networks.* Calculate the characteristic time τ and the epidemic threshold λ_c of the SI, SIS and SIR models for networks with:

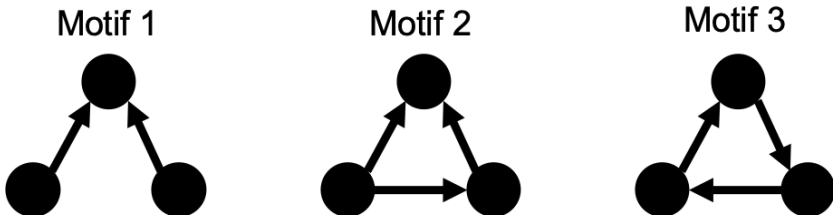
(a) Exponential degree distribution.

(b) Stretched exponential degree distribution.

(c) Delta distribution (all nodes have the same degree)

Assume that the networks are uncorrelated and infinite. Refer to Table 4.2 for the functional form of the distribution and the corresponding first and second moments.

3. *Motifs in networks.* Using the network data provided in the form of an adjacency list at `https://www.dropbox.com/s/qf2cchs3dpmsxj9/Question4.adjlist?dl=0`, read the network into networkx and count the number of appearances of Motifs 1, 2, and 3 (shown below). Note that you should be sure to read in the network as a directed graph as the motifs are directed. The motifs are all on groups of 3 nodes, so you will have to find a way to select groups of 3 nodes (perhaps look at the itertools package in python) to check if they have the given motif. Also, nx.is_isomorphic will check if two subgraphs are isomorphic (meaning there is a direct correspondence between the nodes).



4. *Stochastic epidemics on networks.* Actual epidemics involve discrete events of infection and recovery. In this exercise we will simulate these discrete events and compare the results with the theoretical results summarized on Box 10.7 which are obtained using a continuous approximation.

(a) Generate a random network (ER) with average degree $\bar{k} = 5$ and at least $N = 1000$ nodes. Limit the network to its largest connected component.

(b) Fix the recovery rate at $\mu = 0.1$. At the epidemic threshold, the infection rate has a specific value β_c. Find β_c.

(c) For 10 values of β from $0.5\beta_c$ to $1.5\beta_c$ simulate the SIS model stochastically:

i. Initialize the system with $N_s = 0.1N$ seed nodes infected and the rest susceptible.

ii. For each time-step, sweep through the network. For infected nodes, switch them to susceptible with probability μ. For susceptible nodes, check their neighbors. For each neighbor that is infected, switch the susceptible node to infected with probability β. (Note that susceptible node i gets up to k_i chances to become infected). Record the network state after each time-step/sweep. End the simulation if there are no more infected nodes (absorbing state) or t reaches t_{max} which should be no less than 500 in your simulation. $t = t_{max}$ means the

pandemic state has been reached. Execute no less than $M = 50$ trials for each value of β, re-initializing at random each time.

iii. For each value of β, plot the number of infected nodes at each time step. You should have M curves per plot.

iv. Plot the lifetimes of the epidemics as a function of β. For every value of β you will have at least 50 lifetimes (according to the number of trials you ran). Plot the average lifetime as a function of beta. Add a vertical line at $\beta = \beta_c$. What happens at β_c? How is this result different than what you obtained with the continuous models described in the book?