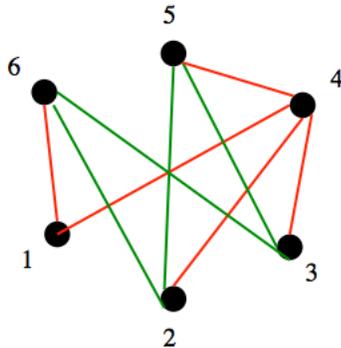


Problem Set 3 for CaSB 186
Due February 17, 2017 in Lab section
(Late problem sets will lose 10 points per day)

1. Find a monochromatic clustering (all clusters/groups/collection of nodes interacts with other clusters/groups/collection of nodes with only the same color links/edges). Do not use the trivial cases that each node is its own cluster or that the whole network is a single cluster. Try to make the cluster sizes as large as possible without grouping everything into a single node.



2. Consider the simplest SIR model form class but now allow Recovered individuals, R , to have some mortality rate, Z , so that even after they recover, the individual is in a weakened state and more likely to die from other infections or problems. Then our equations become

$$\dot{S} = -\beta IS \equiv f(I, S, R)$$

$$\dot{I} = \beta IS - \gamma I \equiv g(I, S, R)$$

$$\dot{R} = \gamma I - ZR \equiv h(I, S, R)$$

Recall that I is number of infected individuals, S is the number of susceptible individuals, β is the infection rate and γ is the recovery rate.

- a. Write down an equation for the rate of change in the total population size, N .
- b. What are the fixed points for these equations?
- c. Can we calculate the eigenvalue of our interaction matrix, A , to find the likelihood of infection and compute our parameter R_0 ?
- d. Compute the standard Jacobian matrix for these equations for early stages in an infection where you perturb off the case of no infected individuals, I , and the whole population is susceptible $S=N$ as we did in class for the regular SIR model.
- e. Using software or by hand compute eigenvalues for this matrix. Is this system stable? Describe what you think will happen with the dynamics of the system. From these equations, once the epidemics dies out, what will the equation for the number of recovered individuals, R , reduce to? Can you solve this and say whether there will be many recovered individuals R a long time after the epidemic is over?

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3. If you have a reaction that involves 2 enzymes of type E , where this variable represents the concentration of that enzyme, and two different proteins of type P_1 and P_2 , also representing concentrations, to come together and interact, and you need to write down a differential equation model for this, how should multiply together these variables for the terms that represent the interaction in the equation.