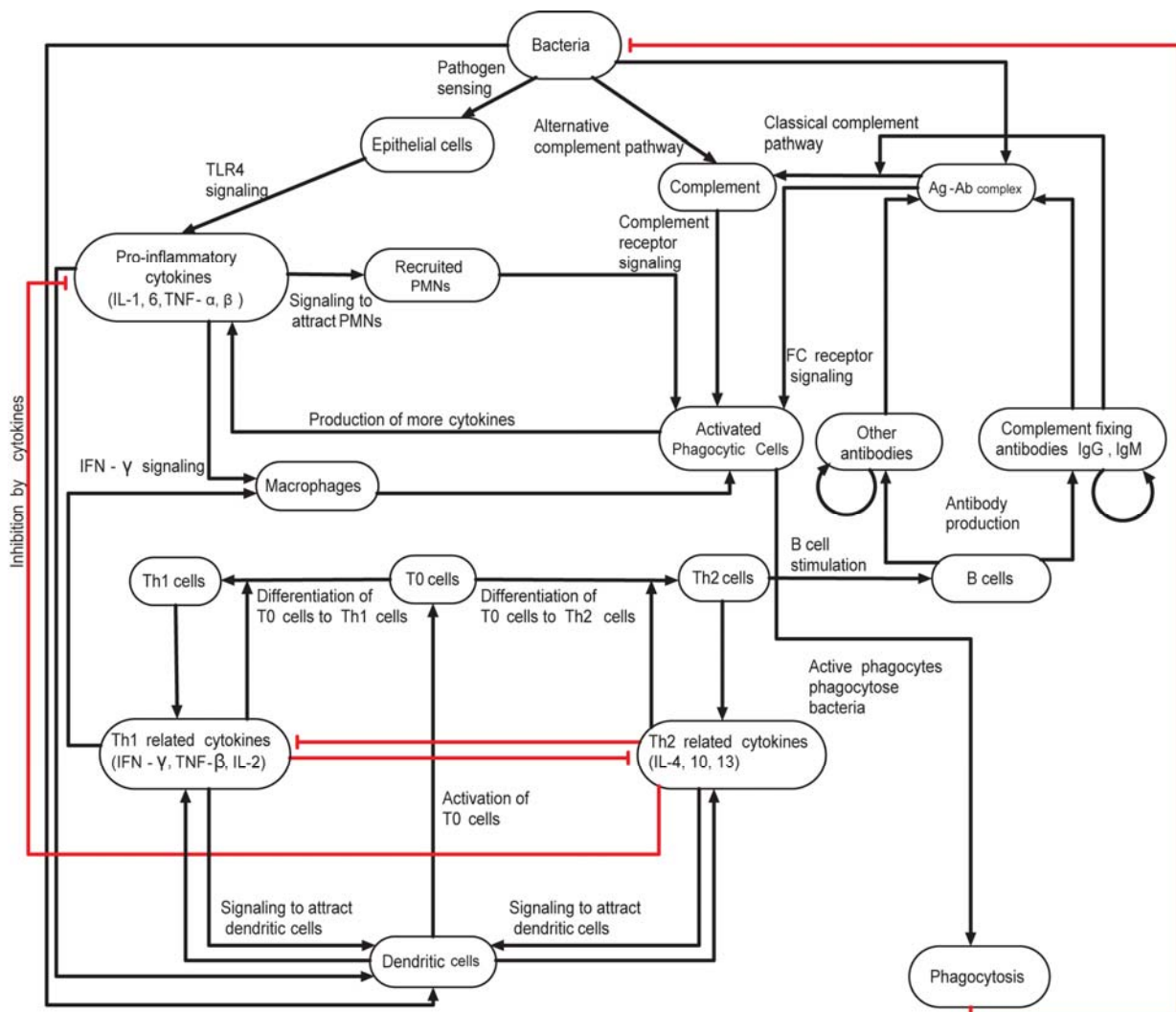


PHYS 597A, CMPSC 497E, Graphs and Networks in Systems Biology

Homework 8, due Tuesday Nov. 3

1. Perform a topological analysis of the network below. Consider that edges terminating in edges are directed toward the endpoint of the edge (e.g. the edge from Th2 related cytokines is directed toward Th2 cells). For points (a)-(c) you can disregard the sign of the edges (but not their direction!) and the two autoregulatory loops.



- (a) What is the in and out-degree distribution of the network?
- (b) Is the network strongly connected? If not, find the largest strongly connected component, and the in/outcomponents of the strongly connected component.
- (c) What is the average distance between the nodes of the largest strongly connected component?
- (d) Give examples of network motifs and interesting subgraphs. Now you can take into account the edge signs.
- (e) In your assessment, which nodes or edges play the most important role in the connectivity of the network?

2. Now turn the topological analysis into a pseudo-dynamic one. Assume that initially only the node Bacteria is active. When a node is active, all its edges are also active. Assume that in order to activate a node at least half of the edges that activate it must be active, but even one active inhibition will inactivate the node regardless of the presence of activation. How will the activity propagate through the network, i.e. which nodes will be active/inactive at one step away from bacteria, two steps away, ... ? At what steps do you need more information to decide what will happen next?

Try to extract as much information from the graph as you can. By doing this you are predicting the extent to which the network topology determines the system's dynamics.

Extra credit: use programming/software for either problem (or both).