

# **341 Introduction to Bioinformatics:**

## **Biological Networks**

Department of Computing, Imperial College London

## **Coursework 2**

(Total 15 marks)

**Due date: March 4, 2010**

Download several biological network data sets (no more than 5) from the databases that we introduced in the class, or from the literature.

**(1)** (5 marks) Compute global network parameters of the selected networks. Compare and contrast the network topologies based on the computed network parameters.

**(2)** (5 marks) Compute some local network properties of the selected networks. Compare and contrast them over the networks. Provide some biological or topological justification for your findings. You may use any specialized freely available packages such as "mfinder" (see <http://www.weizmann.ac.il/mcb/UriAlon/>) or GraphCrunch (<http://www.ics.uci.edu/~bio-nets/graphcrunch/>) to compute these properties. Of course, feel free to write your own code, if you wish, but you are not required to do so.

**(3)** (5 marks) Choose a random graph model (e.g. Erdos-Renyi, scale-free, small-world, geometric, etc.) and use freely available software or implement a program that generates it. Use it to generate several random graphs (up to 10) from the model that correspond to one biological network selected in part (1) above. Compute some network properties (of your choice, from parts (1) and/or (2) above) for these model graphs and compute their statistics (averages, standard deviations, and such). Compare the computed properties of the model networks to the properties of the selected biological networks.

You may use any software of your choice to complete the assignment, including any specialized packages such as those mentioned above. Try to use visual displays (graphs/plots generated in a software of your choice, e.g. gnuplot) for a clear presentation.

Submit your code and results on paper and electronically at the beginning of March 4 class.