Fall 2002 Genomics Final Mega-Problem Set (#3)
Proteomics, Circuits and Systems Biology

There is no time limit on this mega-problem set (MPS), though I have tried to design one that you should be able to complete within 6 hours, except for typing and web searches. There are 3 pages for this MPS, including this cover sheet. This MPS also includes two PDF files. You have 1 week to complete this MPS (December 11 – 18).You are not allowed discuss the MPS with anyone until all MPSs are turned in at 2 pm on Wednesday December 18. **PROBLEM SETS ARE DUE AT 2 PM ON WEDNESDAY DECEMBER 18**. You may use a calculator, your notes, the book, old MPSs and the internet. This is a challenging MPS, so do NOT put it off too long. You may take it in as many blocks of time as you need. Remember I will be gone Dec. 13 – 18 until about 9 am.

The **answers to the questions must be typed on a separate sheet of paper** unless the question specifically says to write the answer in the space provided. If you do not write your answers in the appropriate location, I may not find them. You might want capture screen images as a part of your answers which you may do without seeking permission since your test answers will not be in the public domain. If you are asked to print out any pages, you do not have to print in color, unless stated otherwise. Please bind your printouts near your typed answers and label which printouts go with which questions.

-3 pts if you do not follow this direction.
Please do not write or type your name on any page other than this cover page.
Staple all your pages (INCLUDING THE MPS PAGES) together when finished with the MPS.

Name (please print):

Write out the full pledge and sign:

How long did this MPS take you to complete (excluding typing)?

32 pts.

1) Look at figure 9.1b in the textbook. Then answer these questions:

a) Use SGD and DIP to document the interactions indicated in the circuit diagram in figure 9.1. [Note: SGD has a new look and some new features.] You may print or use screen shots to document your findings. Please make sure any screen shots are legible. Explain in words what you found and where you found it.

b) Focus for now on the SGD database of interactions "PathCalling" that is accessible through SGD. Enter the protein name "HBS1". Follow the resulting links to uncover a potential source for misunderstanding that is present in the PathCalling database. The problem stems from PathCalling's standard way of presenting the data that could lead to a misunderstanding. We did not discuss this standard in class but you should uncover it when you analyze the data for this question. Describe the source for potential misunderstanding this standard presents. Support your answer with screen shots or printouts.

c) Now open the PDF file called "Idekernetwork.pdf". Analyze this figure and compare it to the data you have uncovered in part A. Evaluate any apparent inconsistencies if you know that Ideker used the PathCalling database for his source of protein interactions.

d) Can you resolve the apparent inconsistency from part C is you use other sources instead of PathCalling? Explain your answer and support it with data.

15 pts.

2) Go to PDB and find some structures to answer these questions:

a) First, view 1D66. Now view 1AW6. If you know that1AW6 is one half of the dimer you saw in 1D66, tell me what you are seeing in 1AW6. Given what we have studied this semester, what is the value of 1AW6?

b) Find structures for oxy-myoglobin and deoxy-myoglobin. Show in images and describe in words the differences between these two structures. Be sure to illustrate these differences with printouts or screen shots. Be sure the key points are legible.

The remaining questions are based on the paper by Milo *et al.* (Science. Vol. 298: 824-827. 2002.) which I have attached to your email.

15 pts.

3) a) Interpret figure 2. Explain what was done to generate both panels A and B and what was learned from these figures.

b) What caveat did the authors acknowledge as a potential weakness to their research?

22 pts.

4) This is a wide open question with four major parts.

a) Give hypothetical/stereotypical examples for each network motif in

i) gene regulation (2 examples total)

ii) neurons (3 examples total)

iii) food webs (2 examples total)

b) For gene regulation (or protein interactions), find one real example for the feed-forward loop or one real example of the bi-fan. You may use any gene/protein circuit we have covered in *this* class, including any web sites, PDF files associated with any of the ~~exams~~ megaproblem sets, or the textbook.

c) Using your example from part b, show how your chosen network motif is regulated at the transcription level. You must use a database for this answer and support your answer with screen shots or **color** printouts.

d) What is the critical difference between a food web and a cell web when examining network motifs? Don't just quote the paper back to me; use your own words and give real examples to support your answer. Your examples can be drawn from *any* course and/or your personal experiences. If you choose an example that I may not be familiar with, give me enough information (i.e. a good citation) so I can verify your example. The authors provide one answer but you may not agree with them. You may think of a better answer than the one they discuss.

16 pts.

5) Your final genomics question is designed to give you an opportunity to think about the future. Tell me how the paper by Milo *et al*. could be utilized for future research. There are probably many good answers to this question so don't try to come up with *the* right answer. I want to see what you think the next step would be from here.