Statistical Analysis of Genetic Data Math 155, Spring 2008 Jo Hardin HW #1

Due Thursday, Jan 31 (please type responses)

Taken from Discovering Genomics, Proteomics, and Bioinformatics by Campbell & Heyer website: http://wps.aw.com/bc_campbell_genomics_2/43/11232/2875502.cw/index.html See chapter 6, "Basic Research with DNA Microarrays"

- 1. Why is there a dark center in the middle of each spot of figure 6.4 on the website?
- 2. Do you foresee any problems with spotting the entire gene on the chip instead of just part of it?
- 3. Choose two genes from figure 6.6 on the website and draw a graph to represent the change in transcription over time.
- 4. Look at figure 4.7 in the handout from *DGPB*, which depicts the loss of oxygen over time and the transcriptional response of three genes. These data are the ratios of transcription for genes X, Y, and Z during the depletion of oxygen.
 - (a) What is the fold change for each gene at each time point?
 - (b) Were any of the genes in figure 4.7b transcribed similarly?
- 5. In general, why would most spots be yellow at the first time point?
- 6. Given rule #1 on page 109, what color would you see on a DNA chip when cells had their repressor gene *Tup1* deleted?
- 7. What color spots would you expect to see on the chip when the transcription factor Yap1p is overexpressed?
- 8. Let's imagine the green dye labeling of the cDNA did not work as well as it normally does. To compensate, you adjust the scanner so that it brightens the signal from the green channel. Does this present any problems with the data interpretation? Explain.
- 9. What advantages are there for using oligonucleotides instead of cDNA?
- 10. Which form of data (protein or mRNA) gives you the best understanding of genomic responses to an external inducement?