

Appendix D: Knowledge Questions

1. You are investigating the changes in gene expression in cancer cells compared to normal cells by labeling of RNA samples. When you look at your entire microarray after performing the scan in both dye channels, you observe spots with several shades of green, but no red spots. Which of the following best explains the data?

- A. the hybridization temperature was too high
- B. poor quality of both starting RNA samples
- C. poor labeling of one of the samples
- D. there is no problem; this is what you expect
- E. I cannot make a reasonable guess.

2. The tiff images of your microarray show a gradient of color intensity, with spots fluorescing more strongly at one end of the microarray than at the other. This phenomenon is probably caused by...

- A. poor mixing of the labeled probe
- B. scanning error due to default settings
- C. analysis software setting needs adjusting
- D. bad probe synthesis and/or labeling
- E. I cannot make a reasonable guess

3. You are designing a negative control spot for a DNA microarray. Which of the following would be the best negative control?

- A. a DNA that is non-homologous to any other DNA spotted
- B. a DNA containing sequences homologous to all spots on the array
- C. a spot of salt only (no nucleic acid)
- D. mitochondrial DNA from your organism
- E. chloroplast DNA from your organism
- F. I cannot make a reasonable guess.

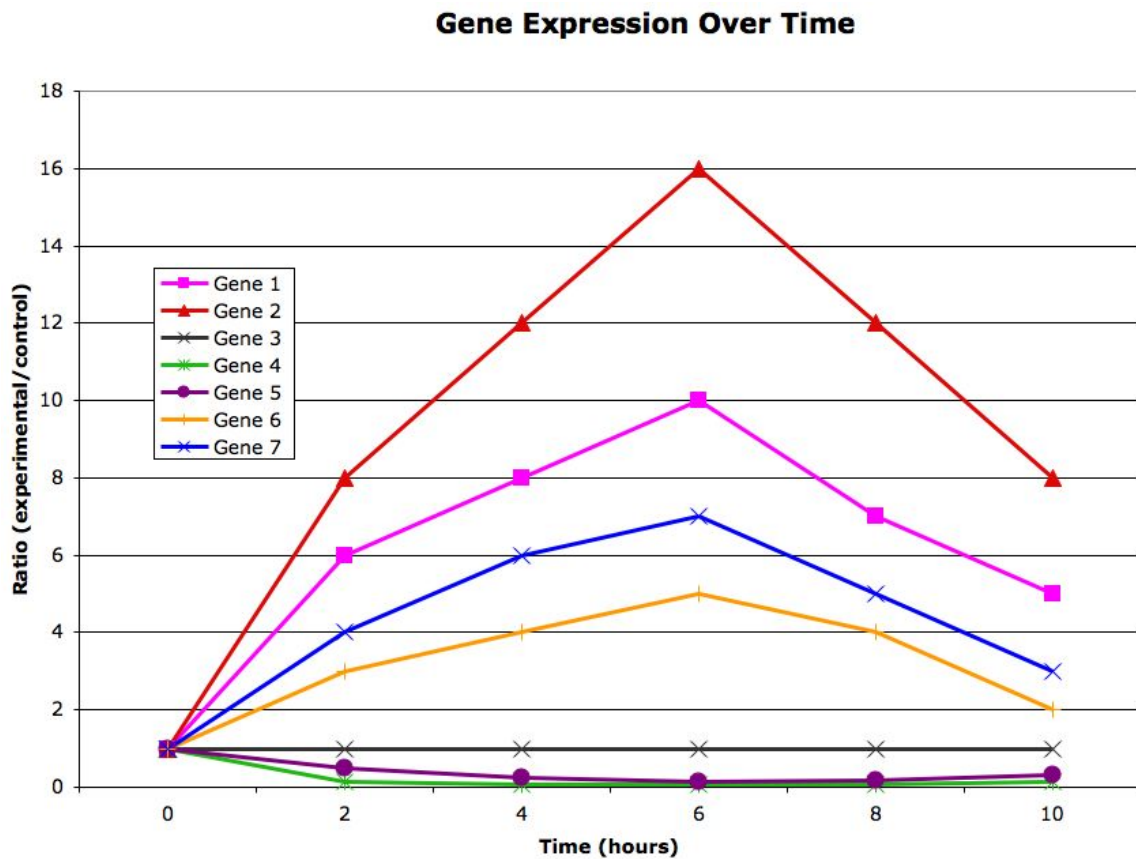
4. You are interested in a bacterium that grows in high temperature conditions. One interesting observation is that it is green when grown at the normal high temperature, but colorless when grown at a temperature that is 20 degrees below the optimal growth temperature. Which of the following would be the best description of the way you could investigate this difference using microarrays?

- A. Isolate genomic DNA from the organism grown at the two temperatures, label it, and hybridize the labeled DNA to the microarray
- B. Isolate total RNA from the organism grown at the two temperatures, and incubate the total RNA with the array.
- C. Isolate total RNA from the organism grown at the two temperatures, reverse transcribe it with dyes to cDNA and incubate with the microarray.

- D. PCR amplify the genes for photosynthesis in the presence of dye-labeled nucleotides and incubate the products with the microarray
- E. Isolate plasmid DNA from the organism, label it, then incubate it with the microarray
- F. I cannot make a reasonable guess.

5. The figure shows the ratio of gene expression at the indicated time to gene expression at time zero for several genes. Gene 2's ratios are represented by the top red line, and Gene 4's ratios by the bottom green line. Looking at these patterns, what can you conclude about the relative change in gene expression over time?

- A. Gene 2 changes more over time than Gene 4.
- B. Gene 4 changes more over time than Gene 2.
- C. Gene 2 and Gene 4 change about the same over time.
- D. Because of the scale, it is difficult to tell whether one gene changes more over time than the other.
- E. I cannot make a reasonable guess.



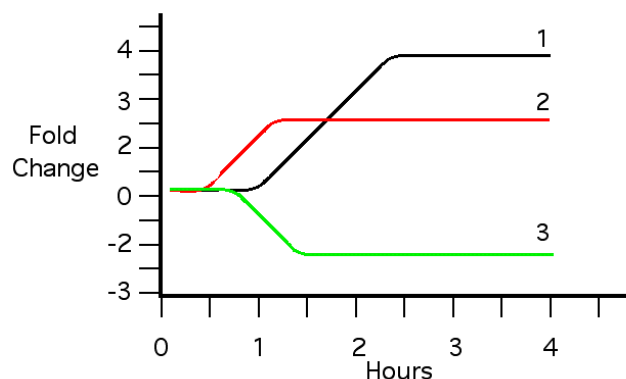
6. In testing whether the expression of 1000 genes differs between a knock-out strain and wild-type, the change in expression level for a particular gene is assigned a p-value of 0.005.

- (a) This result means that this gene was affected by the gene knock-out.
- (b) Just by chance, you would expect 5 of the genes to show this much change in expression level.**
- (c) This probability indicates the gene is probably not of interest due to its low score.
- (d) This result is not significant, meaning that this gene was not affected by the knock-out.
- (e) I cannot make a reasonable guess.

7. Gene expression ratios between treated cells at several time points and untreated cells are clustered using hierarchical clustering. A cluster of ten genes is defined by selecting all genes below a particular node in the dendrogram. Which of the following can you infer about the cluster?

- (a) All the genes in the cluster are in the same biological pathway.
- (b) The clustered genes have highly correlated gene expression patterns.**
- (c) If we repeated the experiment, the same ten genes would be clustered together.
- (d) The clustered genes have significant expression ratios.
- (e) I cannot make a reasonable guess.

8. A well controlled DNA microarray experiment was performed. Fluorescent cDNAs were produced from control and experimental cells. Which of the following statements is most consistent with the data in the figure below?

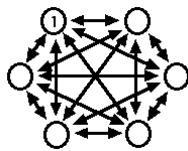


- A. Gene 1 is likely to induce gene 2
- B. Gene 1 is likely to be induced by gene 2**
- C. Gene 1 is likely to be induced by gene 3

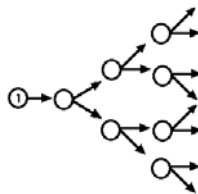
- D. Gene 1 is likely to be repressed by gene 2
- E. Gene 1 is likely to be repressed by gene 3
- F. I cannot make a reasonable guess.

9. You have studied gene 1 in a catabolic pathway of a sugar. Which of the following diagrams represent the most likely relationship of the other genes to gene 1 in wild-type cells? Circles represent proteins and arrows indicate interactions that regulate the activity of the protein at the pointed end of the arrow (choose the best answer).

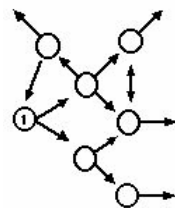
A. Gene 1 will affect the activity of every other gene.



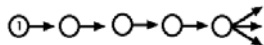
B. Gene 1 will initiate a cascade which continues to grows in size.



C. Gene 1 will regulate some genes and be regulated by some.



D. Gene 1 will initiate a linear pathway of genes identical to the metabolic pathway.



E. I cannot make a reasonable guess.

10. In a hypothetical pathway, gene T encodes a nuclear transcription factor which activates genes A, B and C. The following highly reproducible microarray data were collected under two growth conditions.

Gene	Ratio of gene expression under the two growth conditions – condition 1: condition 2
T	1:1
A	1:7
B	1:6
C	1:8

Which of the following statements are plausible hypotheses to explain these data?

- A. Genes A, B, and C are regulated by gene T.
- B. Genes A, B, and C are regulated by more than just gene T.**
- C. Gene B induces A which induces C.
- D. The mRNA for the transcription factor was degraded under condition 2.
- E. I cannot make a reasonable guess

11. A smoker and a coal miner both have lung cancer. The cancers are histologically identical, but there might be functionally important differences in gene expression in the two cancers that would allow personalized treatment. Which of the experiments is the best approach to determine appropriate treatment for the two lung cancers?

- A. Hybridize labeled cDNA from the two lung cancers to a microarray.
- B. Hybridize labeled lung cancer and muscle cell cDNA to a microarray for each patient.
- C. Hybridize labeled lung cancer and normal lung cell cDNA to a microarray for each patient.**
- D. Compare the karyotype of tumor vs. normal cells for each individual.
- E. I cannot make a reasonable guess.