

## Lab 4B: Microarrays, part II: Cancer and Genomic Microarrays

The diffuse large B-cell lymphoma tissue you saw at the beginning of the cancer lecture results from changes in gene expression in a somatic clone. In this laboratory exercise, we will use microarray data to examine these changes on a genomic scale.

### Objectives

- 1) Review the DLBCL microarray experiments from lecture and learn more about how these experiments were done.
- 2) Apply global measurements of gene expression to breast cancer and to think about how chromosomal mutations could contribute to cancer.

### Introduction

Cancer is a disease of the genome. A single cell accumulates genetic changes that allow it to ignore death signals and to proliferate in the absence of normal growth signals. These genetic changes result in large changes in gene expression in the transformed cell, and are present in all of its cancerous progeny. Often, treatments and prognosis depend on knowing the nature of the progenitor cell and something about which genetic changes have occurred during its transformation. In this lab exercise, we will use microarrays to simultaneously measure the expression of large numbers of genes in normal and cancer cells and then use these expression data to categorize the cancer clones.

You may complete this exercise with a lab partner if you would like. No one should work in a group of more than two people. Answers to the questions in this assignment can be turned in at the end of lab, or Friday 2 April, in lecture at the latest.

### Procedure

Beginning in Chapter 5 of your Campbell and Heyer text, read pages 138 - 140 before coming to class. Note that several of the figures you will need for this section are on the CD-ROM that came with your text. Make sure you view and understand them. Remember to bring the CD to lab. Answer Discovery Questions 1, 5, 6, and 11, and bring them to class with you.

In class, begin by accessing the explore lymphoma website, and answer Discovery Question 4. Remember that the two orange samples are normal GC B-cells. Answer Discovery Questions 7-10. How were the data in the UniGene database generated?

Continue with the breast cancer project. A recent review that discusses some of this data in context has been posted to the course links page. Answer Discovery Questions 14-19 and 21-23. Make sure that all of your answers have complete explanations, for example what is it that you are looking at in question 14. What is the meaning of the diversity?

Finally, read the paper by Ma et al. from the links page. Write a complete analysis of this paper, comparing it to other experiments you have seen. Organize your analysis by explaining the question, putting the question in context with what is already known, explaining the experimental design, the results, and the implications.