

## GENE EXPRESSION & MICROARRAY BACKGROUND INFORMATION SHEET

Your group is responsible for analyzing data on gene expression. Your goal is to determine relationships between proteins that define the cellular network.

One way to determine relationships between proteins is to change the amount of one protein in the cell and see how others are affected. Individual proteins can be removed from the cellular network by “**knocking out**” the gene for that protein. By mutating or removing the gene from the chromosome, the mRNA cannot be transcribed, and the protein will not be made in the cell. Other procedures can be used to make the cell constantly produce a particular protein much more than normal. This is called “**overexpression**.”

We can measure the effects of knocking out or overexpressing particular genes by measuring the changes to the amounts of other proteins compared with the normal strain. The amount of protein transcribed from a gene is called the “**expression**” of the gene.

If the amount of protein is more than normal, it has higher or greater expression. We indicate this affect with a (+). If the amount of protein is less than normal, it has lower expression. We indicate this with a (-). If the amount of protein is the same as normal, it has the same expression. We indicate this with a (0).

Measuring the amount of mRNA often correlates with amount of protein present because the protein is coded by mRNA (remember the Central Dogma: DNA → mRNA → protein). We can measure mRNA using **microarray technology**.

**You may want to view the following animations for more information on microarray technologies:**

**Microarray animation:**

<http://www.bio.davidson.edu/Courses/genomics/chip/chip.html>