Answer to Assignment 1 a

According to the principle of base complementary pairs, oligos fixed on the glass as arrays will bond with the matching fragments of target genes.

After fully sequencing a genome, we are capable of designing unique oligos that can match specific fragments of protein expressing genes, which means if these specially designed oligos are all bonded with the specific target fragments that make this condition unique, then the assumption will be proved true or false. Therefore, the expected gene expression should be testified.

Thereafter, labeled and paired cDNA will show fluorescence under the scanner and therefore with the fluorescence intensity the outcome of expressed genes can be quantified.

The reason why microarrays only address the true positives not the false positives is that oligos are designed to bond with the predicted target. If a target is out of prediction, none of these oligos tend to pair with it (except for some low possibility accident)

Answer to Assignment 2

Sensitivity and Specificity of a Microarray

Sensitivity	Sn = |TP|/(|TP|+|FN|)
Specificity	Sp = |TN|/(|TN|+|FP|)

TP: True Positive TN: True Negative FP: False Positive FN: False Negative

In a whole human genome microarray, "Sn" should be:

"quantity of predicted and hit targets" / "the sum of hit targets", while "Sp" should be "quantity of not predicted and not hit target" / "the sum of not hit targets"

Now define "quantity of predicted and hit targets" as "Q_p", "the sum of hit targets" as "Q_h", "quantity of not predicted and not hit target" as "Q_n", "the sum of not hit targets" as "Q_{nh}". We may get a chart down below.

Sensitivity and Specificity of a Microarray of a whole human genome

Sensitivity	Sn = Q_p/ Q_h
Specificity	Sp = Q_n/ Q_{nh}