BBSI: Fundamentals of Microarrays

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Problem Set/Questions 1: 7/19/06

You have discovered a new species of primates, *wookie starwarius*. This species is prone to extreme hair growth and you want to study the mechanisms of this in the hope of discovering a new treatment for baldness in humans. After reading several reviews on DNA microarray technology, you decide that performing microarray studies on skin biopsies from *wookie starwarius* would be your method of choice for this work. However, these studies pose certain technical and theoretical problems:

1) Being a new species, *wookie starwarius* gene structure and expression has not been studied at all. How would you propose conducting microarray studies on a new primate species? Name two alternate approaches.

2) Describe the pros and cons of using spotted cDNA arrays vs. short oligonucleotide microarrays for your studies on *wookie starwarius*.

3) Using the dataset provided (BBSIarraydata7_06.xls), explore your primary data. Using scattergram analysis (to be demonstrated in class), determine if any of the arrays appear "abnormal". What are you looking for in such a quality control step? Similarly, compare results of the two different primary analysis methods that are provided (MAS5 vs. PDNN). Does either appear superior? Why?

4) The goal of these studies is to identify gene expression patterns that might be relevant for treatment of human baldness. There might be many gene expression differences between wookies and humans using the microarray platform utilized. Some (most?) of these may be unrelated to hair growth. Describe an experimental design that might help identify those genes most closely related to hair growth.