## **BBSI:** Fundamentals of Microarrays

Michael F. Miles, M.D., Ph.D. Professor Depts. of Pharmacology/Toxicology and Neurology and The Center for Study of Biological Complexity Virginia Commonwealth University e-mail: <u>mfmiles@vcu.edu</u> phone: 804-225-4054

## Problem Set/Questions 2: 7/7/05

A t-test is a simple statistical measure of significance. It basically asks how likely a given experimental result is expected to occur just by chance. The datasheet contains a column where t-test values have been calculated for human vs. wookie PDNN results. Filter the genes for a t-test value ("p-value")  $\leq 0.01$  (1/100 liklihood of occurring by chance). This is a set of genes that have significant expression differences between wookies and humans. Using the database resources provided (see URL links for 7/6 lecture), explore whether these genes contain information about a coherent biological function:

1) You want to first determine whether this list of "wookie genes" might contain an unexpected number of genes related to a specific biological function (e.g. genes involved in glucose metabolism). Copy the "Accession numbers" for the wookie genes and paste these into the Fatigo gene list window (http://www.fatigo.org/). Be sure to select the "GenBank" button under "database" and then choose either "molecular function" under Ontology. Leave the other options at defaults and then click on GO button in lower right corner.

Play with the data a bit. Try comparing your list of wookie genes to e.g. a random list of accession numbers from the chip (using the "compare two lists" function). Anything interesting about the categories that are significant for the wookie genes? Can you formulate a hypothesis to explain the result? How would you test your hypothesis that this biological function category has something to do with hair growth? How might you design a drug to alter how growth, given these results?

2) Take the 5 most positive genes (lowest p-values on the t-test) from the wookie gene list and explore their relationships using the "ACC link" to derive quick info on chromosomal location, function. Also submit the probeset Ids or ACC numbers for these genes to PubGene, the UCSC genome browser and WebQTL (to be demonstrated in class – but explore on your own first!!). Are there any new conclusions to be drawn from your list of wookie genes?