Useful References and Web Links

**Talk 1: Plotting the path from RNA to microarray: the importance of experimental planning and methods**


**Talk 2: Microarray Analysis Challenges: microarray experimental design**

The following references can be found at [http://www.jax.org/staff/churchill/labsite/pubs/index.html](http://www.jax.org/staff/churchill/labsite/pubs/index.html)


5.) Wu, Kerr and Churchill(2002), MAANOVA: A Software Package for the Analysis of Spotted cDNA Microarray Experiments, Chapter of The analysis of gene expression data: methods and software, in press, Springer (two color figures are here: Color figure 4 and Color figure 6).

Talk 3: I Just Received My Microarray Data, Now What?


The following references (found at http://www.tigr.org/software/tm4/mev.html) describe the clustering algorithms supported by the TIGR MultiExperiment Viewer (MeV):

Hierarchical clustering

k-means clustering

Self-organizing maps

**Principal components analysis**

**Cluster affinity search technique**

**Template matching**

**T-test**

**Significance Analysis of Microarrays (SAM)**

**QT_Clust**

**Support vector machines**

**Gene shaving**
genes with similar expression patterns. Genome Biol. 1:RESEARCH0003.

**Relevance networks**

**Self Organizing Trees (SOTA)**

**Figures of Merit (FOM)**

**Talk 4: Data Normalization and transformation**


I. Statistical tests


7) Dudoit, S., Yang, Y.-H., Callow, M.J. & Speed, T.P. Statistical methods for identifying differentially expressed genes in replicated cDNA microarray experiments. Technical


### III. Class predictions methods


6) Dettling M, Buhlmann P. Supervised clustering of genes. Genome Biol. 2002;3(12)


Talk 5  Gene Clustering and data analysis

1.) [http://www.bioconductor.org/workshop.html](http://www.bioconductor.org/workshop.html)  A series of links to previous talks dealing with microarray data analysis.

2.) The following series of references (found at [http://www-stat.stanford.edu/~tibs/lab/publications.html](http://www-stat.stanford.edu/~tibs/lab/publications.html)) cover methods of statistical data analysis and clustering

Storey JD and Tibshirani R. (2001) Estimating false discovery rates under dependence, with applications to DNA microarrays. [PostScript] [PDF]


3.) The following series of references found at http://www.uc.edu/bioinformatics/#Microarray%20Publications, deal with fundamental aspects of performing microarray experiments, data analysis, and several examples of expression experiments from the literature.


Leikauf G.D., Haffey B.D., Horner M.L., Medvedovic M., Sartor M.A.,
Tomlinson C.R., Henning L.M., Case L.M., Wesselkamper SC, Singer, J.B.,
candidate gene for acute lung injury in mice: Thyroid hormone receptor-

M. Sartor, M. Medvedovic, and B. Aronow. "Microarray data normalization:
the art and science of overcoming technical variance to maximize the

Medvedovic, M., Yeung, K.Y., Bumgarner, R.E. Bayesian mixture model
based clustering of replicated microarray data. Bioinformatics, Feb 2004,
epub.

A. Puga, M. Sartor, M. Huang, J.K. Kerzee, Y. Wei, C. Tomlinson, C.S. Baxter
and M. Medvedovic. Gene expression profiles of mouse aorta and cultured
vascular smooth muscle cells are widely different, yet show common
responses to dioxin exposure. (Submitted) 2004.

Y. Wei, K. Tepperman, M. Huang, M. Sartor and A. Puga. Chromium inhibits
transcription from PAH-inducible promoters by blocking the release of HDAC
and preventing the binding of p300 to chromatin. J. of Biol Chem. 2004;

Karyala, S., J. Guo, M. Sartor, M. Medvedovic, S. Kann, A. Puga, P. Ryan,
benzo[a]pyrene- and dioxin-treated vascular smooth muscle cells of AHR-

Junhai Guo, Maureen Sartor, Saikumar Karyala, Mario Medvedovic, Simone
Kann, Alvaro Puga, Patrick Ryan, and Craig R. Tomlinson. Expression of
genes in the TGF-β signaling pathway is significantly deregulated in smooth
muscle cells from aorta of aryl hydrocarbon receptor knockout mice.


