

## Readings for Module 4: Differentially Expressed Genes

- Dudoit, S., Yang, Y. H, Speed, T. P., and Callow, M. J. (2002). Statistical methods for identifying differentially expressed genes in replicated cDNA microarray experiments. *Statistica Sinica* 12(1),111-139. Available at: <http://128.32.135.2/~sandrine/research.html>
- Dudoit S., Shaffer J.P., and Boldrick J.C. (2003). Multiple hypothesis testing in microarray experiments. *Statistical Science* 18(1), 71-103. Available at: <http://128.32.135.2/~sandrine/research.html> (a very nice paper to learn more and gather references on methods for multiple comparisons)
- Tusher, V. G., Tibshirani, R., and Chu, G. (2001). Significance analysis of microarrays applied to the ionizing radiation response. *PNAS* 98, 5116-5121. Preprint: <http://www-stat.stanford.edu/~tibs/lab/publications.html>
- Efron B., Tibshirani, R., Storey J. D., and Tusher V. (2001). Empirical Bayes analysis of a microarray experiment. *Journal of the American Statistical Association* 96, 1151-1160.
- Storey, J. D., and Tibshirani, R. (2002), Statistical methods for detecting differential gene expression, *Journal of Molecular Biology* (special issue).
- Efron B., Tibshirani R. (2002). Empirical bayes methods and false discovery rates for microarrays. *Genetic Epidemiology* 23(1), 70-86.
- Pan W. (2002), "A comparative review of statistical methods for discovering differentially expressed genes in replicated microarray experiments", *Bioinformatics* 18, 536-545. U of MN tech report: <http://www.biostat.umn.edu/~weip/ge.html>
- Pan, W., Lin, J. and Le, C. (2001) A mixture model approach to detecting differentially expressed genes with microarray data. *Biostatistics*. U. of MN tech report: <http://www.biostat.umn.edu/~weip/ge.html>
- Pan, W., Lin, J., Le C. (2002). How many replicates of arrays are required to detect gene expression changes in microarray experiments? A mixture model approach. *Genome Biology*.
- Ideker T., Thorsson V., Siegel A.F., and Hood L. (2000). Testing for differentially-expressed genes by maximum-likelihood analysis of microarray data. *Journal of Computational Biology* 7 (6), 805-817.
- Sapir M. and Churchill G. A. (2000). Estimating the posterior probability of differential gene expression from microarray data. JAX preprint: <http://www.jax.org/research/churchill/pubs/marina.pdf>
- Cui X. and Churchill G.A. (2003). Statistical tests for differential expression in cDNA microarray experiments. *Genome Biology* 4(4), 210.
- Chiligrarian A., Gevorgyan N., Vardanyan A., Jones D., Szabo A. (2002). Multivariate approach or selecting sets of differentially expressed genes. *Mathematical Biosciences* 176 (1), 59-69.
- Park T., Yi S.G., Lee S., Lee S.Y., Yoo D.H., Ahn J.I and Lee Y.S. (2003). Statistical tests for identifying differentially expressed genes in time-course microarray experiments. *Bioinformatics* 19(6): 694-703.