

Here is a bibliography of references for further reading about comparative genomics, transcriptional networks, and bayesian methods.

1. **Aerts, S., G. Thijs, B. Coessens, M. Staes, Y. Moreau, and B. De Moor.** 2003. Toucan: deciphering the cis-regulatory logic of coregulated genes. *Nucleic Acids Res* **31**:1753-64.
2. **Aerts, S., P. Van Loo, Y. Moreau, and B. De Moor.** 2004. A genetic algorithm for the detection of new cis-regulatory modules in sets of coregulated genes. *Bioinformatics* **20**:1974-6.
3. **Aerts, S., P. Van Loo, G. Thijs, Y. Moreau, and B. De Moor.** 2003. Computational detection of cis -regulatory modules. *Bioinformatics* **19 Suppl 2**:II5-II14.
4. **Beer, M. A., and S. Tavazoie.** 2004. Predicting gene expression from sequence. *Cell* **117**:185-98.
5. **Bernstein, B. E., M. Kamal, K. Lindblad-Toh, S. Bekiranov, D. K. Bailey, D. J. Huebert, S. McMahan, E. K. Karlsson, E. J. Kulbokas, 3rd, T. R. Gingeras, S. L. Schreiber, and E. S. Lander.** 2005. Genomic maps and comparative analysis of histone modifications in human and mouse. *Cell* **120**:169-81.
6. **Boyd, K. E., and P. J. Farnham.** 1999. Coexamination of site-specific transcription factor binding and promoter activity in living cells. *Mol Cell Biol* **19**:8393-9.
7. **Boyd, K. E., J. Wells, J. Gutman, S. M. Bartley, and P. J. Farnham.** 1998. c-Myc target gene specificity is determined by a post-DNA binding mechanism. *Proc Natl Acad Sci U S A* **95**:13887-92.
8. **Donaldson, I. J., M. Chapman, and B. Gottgens.** 2005. TFBScluster: a resource for the characterisation of transcriptional regulatory networks. *Bioinformatics*.
9. **Fickett, J. W., and W. W. Wasserman.** 2000. Discovery and modeling of transcriptional regulatory regions. *Curr Opin Biotechnol* **11**:19-24.
10. **Flint, J., C. Tufarelli, J. Peden, K. Clark, R. J. Daniels, R. Hardison, W. Miller, S. Philipsen, K. C. Tan-Un, T. McMorro, J. Frampton, B. P. Alter, A. M. Frischauf, and D. R. Higgs.** 2001. Comparative genome analysis delimits a chromosomal domain and identifies key regulatory elements in the alpha globin cluster. *Hum Mol Genet* **10**:371-82.
11. **Ghaemmaghami, S., W. K. Huh, K. Bower, R. W. Howson, A. Belle, N. Dephoure, E. K. O'Shea, and J. S. Weissman.** 2003. Global analysis of protein expression in yeast. *Nature* **425**:737-41.
12. **Harbison, C. T., D. B. Gordon, T. I. Lee, N. J. Rinaldi, K. D. Macisaac, T. W. Danford, N. M. Hannett, J. B. Tagne, D. B. Reynolds, J. Yoo, E. G. Jennings, J. Zeitlinger, D. K. Pokholok, M. Kellis, P. A. Rolfe, K. T. Takusagawa, E. S. Lander, D. K. Gifford, E. Fraenkel, and R. A. Young.** 2004. Transcriptional regulatory code of a eukaryotic genome. *Nature* **431**:99-104.
13. **Hardison, R. C., J. Oeltjen, and W. Miller.** 1997. Long human-mouse sequence alignments reveal novel regulatory elements: a reason to sequence the mouse genome. *Genome Res* **7**:959-66.
14. **Ishwaran, H., and J. S. Rao.** 2003. Detecting Differentially Expressed Genes in Microarrays Using Bayesian Model Selection. *J Am Stat Assoc* **98**:438-455.
15. **Ishwaran, H., and J. S. Rao.** 2005. Spike and slab gene selection for multigroup microarray data. *Journal of the American Statistical Association* **In press**.
16. **Ishwaran, H., and J. S. Rao.** 2005. Spike and slab variable selection: frequentist and Bayesian strategies. *Annals of Statistics* **33**.
17. **Kankainen, M., and L. Holm.** 2004. POBO, transcription factor binding site verification with bootstrapping. *Nucleic Acids Res* **32**:W222-9.
18. **Karanam, S., and C. S. Moreno.** 2004. CONFAC: Automated Application of Comparative Genomic Promoter Analysis to DNA Microarray Datasets. *Nucleic Acids Res* **32**:W475-84.
19. **Lenhard, B., A. Sandelin, L. Mendoza, P. Engstrom, N. Jareborg, and W. W. Wasserman.** 2003. Identification of conserved regulatory elements by comparative genome analysis. *J Biol* **2**:13.

20. **Loots, G. G., and I. Ovcharenko.** 2004. rVISTA 2.0: evolutionary analysis of transcription factor binding sites. *Nucleic Acids Res* **32**:W217-21.
21. **Loots, G. G., I. Ovcharenko, L. Pachter, I. Dubchak, and E. M. Rubin.** 2002. rVista for comparative sequence-based discovery of functional transcription factor binding sites. *Genome Res* **12**:832-9.
22. **Oeltjen, J. C., T. M. Malley, D. M. Muzny, W. Miller, R. A. Gibbs, and J. W. Belmont.** 1997. Large-scale comparative sequence analysis of the human and murine Bruton's tyrosine kinase loci reveals conserved regulatory domains. *Genome Res* **7**:315-29.
23. **Quandt, K., K. Frech, H. Karas, E. Wingender, and T. Werner.** 1995. MatInd and MatInspector: new fast and versatile tools for detection of consensus matches in nucleotide sequence data. *Nucleic Acids Res* **23**:4878-84.
24. **Roven, C., and H. J. Bussemaker.** 2003. REDUCE: an online tool for inferring cis-regulatory elements and transcriptional module activities from microarray data. *Nucleic Acids Res* **31**:3487-90.
25. **Sharan, R., A. Ben-Hur, G. G. Loots, and I. Ovcharenko.** 2004. CREME: Cis-Regulatory Module Explorer for the human genome. *Nucleic Acids Res* **32**:W253-6.
26. **Sharan, R., I. Ovcharenko, A. Ben-Hur, and R. M. Karp.** 2003. CREME: a framework for identifying cis-regulatory modules in human-mouse conserved segments. *Bioinformatics* **19 Suppl 1**:I283-I291.
27. **Tavazoie, S., J. D. Hughes, M. J. Campbell, R. J. Cho, and G. M. Church.** 1999. Systematic determination of genetic network architecture. *Nat Genet* **22**:281-5.
28. **Vega, V. B., D. K. Bangarusamy, L. D. Miller, E. T. Liu, and C. Y. Lin.** 2004. BEARR: Batch Extraction and Analysis of cis-Regulatory Regions. *Nucleic Acids Res* **32**:W257-60.
29. **Wasserman, W. W., and J. W. Fickett.** 1998. Identification of regulatory regions which confer muscle-specific gene expression. *J Mol Biol* **278**:167-81.
30. **Wasserman, W. W., M. Palumbo, W. Thompson, J. W. Fickett, and C. E. Lawrence.** 2000. Human-mouse genome comparisons to locate regulatory sites. *Nat Genet* **26**:225-8.
31. **Xie, X., J. Lu, E. J. Kulbokas, T. R. Golub, V. Mootha, K. Lindblad-Toh, E. S. Lander, and M. Kellis.** 2005. Systematic discovery of regulatory motifs in human promoters and 3' UTRs by comparison of several mammals. *Nature* **434**:338-45.