

Bibliography

- B Alberts, A Johnson, J Lewis, M Raff, K Roberts, and P Walter. *Molecular biology of the cell*. Garland Science, New York, 4th edition, 2002.
- U Alon. Biological networks: the tinkerer as an engineer. *Science*, 301(5641):1866–7, 2003.
- CA Ball, IAB Awad, J Demeter, J Gollub, JM Hebert, T Hernandez-Boussard, H Jin, JC Matese, M Nitzberg, F Wymore, ZK Zachariah, PO Brown, and G Sherlock. The stanford microarray database accommodates additional microarray platforms and data formats. *Nucl. Acids Res.*, 33(suppl_1):D580–582, 2005.
- N Banerjee and MQ Zhang. Identifying cooperativity among transcription factors controlling the cell cycle in yeast. *Nucl. Acids Res.*, 31(23):7024–7031, 2003.
- Z Bar-Joseph, GK Gerber, TI Lee, NJ Rinaldi, JY Yoo, F Robert, DB Gordon, E Fraenkel, TS. Jaakkola, RA Young, and DK Gifford. Computational discovery of gene modules and regulatory networks. *Nat Biotechnol*, 21(11):1337–42, 2003.
- S Barbaric, M Munsterkotter, J Svaren, and W Horz. The homeodomain protein pho2 and the basic-helix-loop-helix protein pho4 bind dna cooperatively at the yeast pho5 promoter. *Nucl. Acids Res.*, 24(22):4479–4486, 1996.
- T Barrett, DB Troup, SE Wilhite, P Ledoux, D Rudnev, C Evangelista, IF Kim, A Soboleva, M Tomashevsky, and R Edgar. Ncbi geo: mining tens of millions

BIBLIOGRAPHY

- of expression profiles—database and tools update. *Nucl. Acids Res.*, 35(suppl_1):D760–765, 2007.
- AR Borneman, TA Gianoulis, ZD Zhang, H Yu, J Rozowsky, MR Seringhaus, LY Wang, M Gerstein, and M Snyder. Divergence of transcription factor binding sites across related yeast species. *Science*, 317(5839):815–819, 2007.
- ML Bulyk. Dna microarray technologies for measuring protein-dna interactions. *Current Opinion in Biotechnology*, 17(4):422–430, 2006.
- O Carmel-Harel, R Stearman, AP Gasch, D Botstein, PO Brown, and G Storz. Role of thioredoxin reductase in the yap1p-dependent response to oxidative stress in *saccharomyces cerevisiae*. *Molecular Microbiology*, 39(3):595–605, 2001.
- P Cliften, P Sudarsanam, A Desikan, L Fulton, B Fulton, J Majors, R Waterston, BA Cohen, and M Johnston. Finding functional features in *saccharomyces* genomes by phylogenetic footprinting. *Science*, 301(5629):71–76, 2003.
- The Gene Ontology Consortium. The gene ontology project in 2008. *Nucl. Acids Res.*, 36(suppl_1):D440–444, 2008.
- M Das and H-K Dai. A survey of dna motif finding algorithms. *BMC Bioinformatics*, 8(Suppl 7):S21, 2007.
- J Demeter, C Beauheim, J Gollub, T Hernandez-Boussard, H Jin, D Maier, JC Matese, M Nitzberg, F Wymore, ZK Zachariah, PO Brown, G Sherlock, and CA Ball. The stanford microarray database: implementation of new analysis tools and open source release of software. *Nucl. Acids Res.*, 35(suppl_1):D766–770, 2007.
- P D’haeseleer. How does dna sequence motif discovery work? 24(8):959–961, 2006.

BIBLIOGRAPHY

- SW Doniger, J Huh, and JC Fay. Identification of functional transcription factor binding sites using closely related *saccharomyces* species. *Genome Res.*, 15(5):701–709, 2005.
- F Gao, BC Foat, and HJ Bussemaker. Defining transcriptional networks through integrative modeling of mrna expression and transcription factor binding data. *BMC Bioinformatics*, 5:31, 2004.
- AP Gasch, PT Spellman, CM Kao, O Carmel-Harel, MB Eisen, G Storz, D Botstein, and PO Brown. Genomic expression programs in the response of yeast cells to environmental changes. *Mol Biol Cell*, 11:4241 – 4257, 2000.
- AC Gavin, P Aloy, P Grandi, R Krause, M Boesche, M Marzioch, C Rau, LJ Jensen, S Bastuck, and B Dumpelfeld. Proteome survey reveals modularity of the yeast cell machinery. *Nature*, 440:631 – 636, 2006.
- G Gibson. Microarray analysis. *PLoS Biology*, 1(1):e15, 2003.
- D Greenbaum, R Jansen, and M Gerstein. Analysis of mrna expression and protein abundance data: an approach for the comparison of the enrichment of features in the cellular population of proteins and transcripts. *Bioinformatics*, 18(4):585–96, 2002.
- D GuhaThakurta and GD Stormo. Identifying target sites for cooperatively binding factors. *Bioinformatics*, 17(7):608–621, 2001.
- JD Han, N Bertin, T Hao, DS Goldberg, GF Berizzi, LV Zhang, D Dupuy, AJ Walhout, ME Cusick, FP Roth, and M Vidal. Evidence for dynamically organized modularity in the yeast protein-protein interaction network. *Nature*, 430:88 – 93, 2004.
- CT Harbison, DB Gordon, TI Lee, NJ Rinaldi, KD Macisaac, TW Danford, NM Hannett, JB Tagne, DB Reynolds, J. Yoo, EG Jennings, J Zeitlinger, DK Pokholok, M Kellis, PA Rolfe, KT Takusagawa, ES Lander, DK Gifford, E Fraenkel, and

BIBLIOGRAPHY

- RA Young. Transcriptional regulatory code of a eukaryotic genome. *Nature*, 431(7004):99–104, 2004.
- JS Hardwick, FG Kuruvilla, JK Tong, AF Shamji, and SL Schreiber. Rapamycin-modulated transcription defines the subset of nutrient-sensitive signaling pathways directly controlled by the tor proteins. *PNAS*, 96(26):14866–14870, 1999.
- LH Hartwell, JJ Hopfield, S Leibler, and AW Murray. From molecular to modular cell biology. *Nature*, 402(6761 Suppl):C47–52, 1999.
- RD Hawkins and B Ren. Genome-wide location analysis: insights on transcriptional regulation. *Hum. Mol. Genet.*, 15(suppl_1):R1–7, 2006.
- MJ Heller. Dna microarray technology: Devices, systems, and applications. *Annual Review of Biomedical Engineering*, 4(1):129–153, 2002.
- JD Hoheisel. Microarray technology: beyond transcript profiling and genotype analysis. *7(3):200–210*, 2006.
- T Hubbard, D Andrews, M Caccamo, G Cameron, Y Chen, M Clamp, L Clarke, G Coates, T Cox, F Cunningham, V Curwen, T Cutts, T Down, R Durbin, XM Fernandez-Suarez, J Gilbert, M Hammond, J Herrero, H Hotz, K Howe, V Iyer, K Jekosch, A Kahari, A Kasprzyk, D Keefe, S Keenan, F Kokocinski, D London, I Longden, G McVicker, C Melsopp, P Meidl, S Potter, M Proctor, G.and Rae, D Rios, M Schuster, S Searle, J Severin, G Slater, D Smedley, J Smith, W Spooner, A Stabenau, J Stalker, R Storey, S Trevanion, A Ureta-Vidal, J Vogel, S White, C Woodwark, and E Birney. Ensembl 2005. *Nucleic Acids Res*, 33(Database issue):D447–53, 2005.
- TR Hughes, MJ Marton, AR Jones, CJ Roberts, R Stoughton, CD Armour, HA Bennett, E Coffey, H Dai, YD He, MJ Kidd, AM King, MR Meyer, D Slade, PY Lum,

BIBLIOGRAPHY

- SB Stepaniants, DD Shoemaker, D Gachotte, K Chakraburty, J Simon, M Bard, and SH Friend. Functional discovery via a compendium of expression profiles. *Cell*, 102(1):109–26, 2000.
- J Ihmels, G Friedlander, S Bergmann, O Sarig, Y Ziv, and N Barkai. Revealing modular organization in the yeast transcriptional network. *Nat Genet*, 31(4):370–7, 2002.
- S Istrail and EH Davidson. Logic functions of the genomic cis-regulatory code. *Proc Natl Acad Sci U S A*, 102(14):4954–9, 2005.
- T Ito, T Chiba, R Ozawa, M Yoshida, M Hattori, and Y Sakaki. A comprehensive two-hybrid analysis to explore the yeast protein interactome. *Proc Natl Acad Sci USA*, 98:4569 – 4574, 2001.
- VR Iyer, CE Horak, CS Scafe, D Botstein, M Snyder, and PO Brown. Genomic binding sites of the yeast cell-cycle transcription factors sbf and mbf. *Nature*, 409(6819):533–538, 2001.
- M Kato, N Hata, N Banerjee, B Futcher, and MQ Zhang. Identifying combinatorial regulation of transcription factors and binding motifs. *Genome Biol*, 5(8):R56, 2004.
- M Kellis, N Patterson, M Endrizzi, B Birren, and ES Lander. Sequencing and comparison of yeast species to identify genes and regulatory elements. *Nature*, 423:241 – 254, 2003.
- H Kitano. Computational systems biology. *Nature*, 420(6912):206–10, 2002a.
- H Kitano. Systems biology: a brief overview. *Science*, 295(5560):1662–4, 2002b.
- M Koranda, A Schleiffer, L Endler, and G Ammerer. Forkhead-like transcription factors recruit ndd1 to the chromatin of g2/m-specific promoters. *406(6791):94–98*, 2000.

BIBLIOGRAPHY

- NJ Krogan, G Cagney, H Yu, G Zhong, X Guo, A Ignatchenko, J Li, S Pu, N Datta, and AP Tikuisis. Global landscape of protein complexes in the yeast *saccharomyces cerevisiae*. *Nature*, 440:637 – 643, 2006.
- L Kruglyak and DL Stern. Evolution: An embarrassment of switches. *Science*, 317 (5839):758–759, 2007.
- H-J Lee, T Manke, R Bringas, and M Vingron. Prioritization of gene regulatory interactions from large-scale modules in yeast. *BMC Bioinformatics*, 9(1):32, 2008.
- TI Lee, NJ Rinaldi, F Robert, DT Odom, Z Bar-Joseph, GK Gerber, NM Hannett, CT Harbison, CM Thompson, I Simon, J Zeitlinger, EG Jennings, HL Murray, DB Gordon, B Ren, JJ Wyrick, JB Tagne, TL Volkert, E Fraenkel, DK Gifford, and RA Young. Transcriptional regulatory networks in *saccharomyces cerevisiae*. *Science*, 298(5594):799–804, 2002.
- K Lemmens, T Dhollander, T De Bie, P Monsieurs, K Engelen, B Smets, J Winderickx, B De Moor, and K Marchal. Inferring transcriptional modules from chip-chip, motif and microarray data. *Genome Biology*, 7(5):R37, 2006.
- G Lesage and H Bussey. Cell wall assembly in *saccharomyces cerevisiae*. *Microbiol. Mol. Biol. Rev.*, 70(2):317–343, 2006.
- RJ Lipshutz, SPA Fodor, TR Gingeras, and DJ Lockhart. High density synthetic oligonucleotide arrays. *Nature Genetics*, 21:20–24, 1999. TY - JOUR.
- NM Luscombe, MM Babu, H Yu, M Snyder, SA Teichmann, and M Gerstein. Genomic analysis of regulatory network dynamics reveals large topological changes. *Nature*, 431(7006):308–12, 2004.
- K MacIsaac, T Wang, DB Gordon, D Gifford, G Stormo, and E Fraenkel. An improved

BIBLIOGRAPHY

- map of conserved regulatory sites for *saccharomyces cerevisiae*. *BMC Bioinformatics*, 7(1):113, 2006.
- T Manke, R Bringas, and M Vingron. Correlating protein-dna and protein-protein interaction networks. *J Mol Biol*, 333(1):75–85, 2003.
- DE Martin, A Soulard, and MN Hall. Tor regulates ribosomal protein gene expression via pka and the forkhead transcription factor fhl1. *Cell*, 119(7):969–979, 2004.
- V Matys, E Fricke, R Geffers, E Gossling, M Haubrock, R. Hehl, K Hornischer, D Karas, AE Kel, OV Kel-Margoulis, DU Kloos, S Land, B Lewicki-Potapov, H Michael, R Munch, I Reuter, S Rotert, H Saxel, M Scheer, S Thiele, and E Wingender. Transfac: transcriptional regulation, from patterns to profiles. *Nucleic Acids Res*, 31(1):374–8, 2003.
- V Matys, OV Kel-Margoulis, E Fricke, I Liebich, S Land, A Barre-Dirrie, I Reuter, D Chekmenev, M Krull, K Hornischer, N Voss, P Stegmaier, B Lewicki-Potapov, H Saxel, AE Kel, and E Wingender. Transfac(r) and its module transcompel(r): transcriptional gene regulation in eukaryotes. *Nucl. Acids Res.*, 34(suppl_1):D108–110, 2006.
- HW Mewes, C Amid, R Arnold, D Frishman, U Guldener, G Mannhaupt, M Munsterkotter, P Pagel, N Strack, V Stumpflen, J Warfsmann, and A Ruepp. Mips: analysis and annotation of proteins from whole genomes. *Nucleic Acids Res*, 32 (Database issue):D41–4, 2004.
- HW Mewes, S Dietmann, D Frishman, R Gregory, G Mannhaupt, KFX Mayer, M Munsterkotter, A Ruepp, M Spannagl, V Stumpflen, and T Rattei. Mips: analysis and annotation of genome information in 2007. *Nucl. Acids Res.*, 36(suppl_1):D196–201, 2008.

BIBLIOGRAPHY

- R Milo, S Shen-Orr, S Itzkovitz, N Kashtan, D Chklovskii, and U Alon. Network motifs: Simple building blocks of complex networks. *Science*, 298(5594):824–7, 2002.
- LL Newcomb, JA Diderich, MG Slattery, and W Heideman. Glucose regulation of *saccharomyces cerevisiae* cell cycle genes. *Eukaryotic Cell*, 2(1):143–149, 2003.
- DT Odom, RD Dowell, ES Jacobsen, W Gordon, TW Danford, KD MacIsaac, PA Rolfe, CM Conboy, DK Gifford, and E Fraenkel. Tissue-specific transcriptional regulation has diverged significantly between human and mouse. *39(6):730–732*, 2007.
- K Ogata, K Sato, and T Tahirov. Eukaryotic transcriptional regulatory complexes: cooperativity from near and afar. *Current Opinion in Structural Biology*, 13(1):40–48, 2003.
- H Parkinson, U Sarkans, M Shojatalab, N Abeygunawardena, S Contrino, R Coulson, A Farne, GG Lara, E Holloway, M Kapushesky, P Lilja, G Mukherjee, A Oezcimen, T Rayner, P Rocca-Serra, A Sharma, S Sansone, and A Brazma. Arrayexpress—a public repository for microarray gene expression data at the ebi. *Nucleic Acids Res*, 33(Database issue):D553–5, 2005.
- H Parkinson, M Kapushesky, M Shojatalab, N Abeygunawardena, R Coulson, A Farne, E Holloway, N Kolesnykov, P Lilja, M Lukk, R Mani, T Rayner, A Sharma, E William, U Sarkans, and A Brazma. Arrayexpress—a public database of microarray experiments and gene expression profiles. *Nucl. Acids Res.*, 35(suppl_1):D747–750, 2007.
- A Patil and H Nakamura. Filtering high-throughput protein-protein interaction data using a combination of genomic features. *BMC Bioinformatics*, 6(1):100, 2005.

BIBLIOGRAPHY

- Y Pilpel, P Sudarsanam, and GM Church. Identifying regulatory networks by combinatorial analysis of promoter elements. *Nat Genet*, 29(2):153–9, 2001.
- P Prochasson, L Florens, SK Swanson, MP Washburn, and JL Workman. The hir corepressor complex binds to nucleosomes generating a distinct protein/dna complex resistant to remodeling by swi/snf. *Genes Dev.*, 19(21):2534–2539, 2005.
- S Rahmann, T Muller, and M Vingron. On the power of profiles for transcription factor binding site detection. *Stat. Appl. Genet. Mol. Biol.*, 2(1):Article 7, 2003.
- T Reguly, A Breitkreutz, L Boucher, B-J Breitkreutz, G Hon, C Myers, A Parsons, H Friesen, R Oughtred, A Tong, C Stark, Y Ho, D Botstein, B Andrews, C Boone, O Troyanskya, T Ideker, K Dolinski, N Batada, and M Tyers. Comprehensive curation and analysis of global interaction networks in saccharomyces cerevisiae. *Journal of Biology*, 5(4):11, 2006.
- B Ren, F Robert, JJ Wyrick, O Aparicio, EG Jennings, I Simon, J Zeitlinger, J Schreiber, N Hannett, E Kanin, TL Volkert, CJ Wilson, SP Bell, and RA Young. Genome-wide location and function of dna binding proteins. *Science*, 290(5500):2306–2309, 2000.
- CJ Roberts, B Nelson, MJ Marton, R Stoughton, MR Meyer, HA Bennett, YD He, H Dai, WL Walker, TR Hughes, M Tyers, C Boone, and SH Friend. Signaling and circuitry of multiple mapk pathways revealed by a matrix of global gene expression profiles. *Science*, 287(5454):873–80, 2000.
- F Rolland, J Winderickx, and JM Thevelein. Glucose-sensing and -signalling mechanisms in yeast. *FEMS Yeast Research*, 2(2):183–201, 2002.
- T Schlitt and A Brazma. Current approaches to gene regulatory network modelling. *BMC Bioinformatics*, 8(Suppl 6):S9, 2007.

BIBLIOGRAPHY

- E Schweizer and J Hofmann. Microbial type i fatty acid synthases (fas): Major players in a network of cellular fas systems. *Microbiol. Mol. Biol. Rev.*, 68(3):501–517, 2004.
- E Segal, M Shapira, A Regev, D Pe’er, D Botstein, D Koller, and N Friedman. Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. *Nat Genet*, 34(2):166–76, 2003.
- G Sherlock. Analysis of large-scale gene expression data. *Brief Bioinform*, 2(4):350–362, 2001.
- R Siddharthan, ED Siggia, and E van Nimwegen. Phylogibbs: A gibbs sampling motif finder that incorporates phylogeny. *PLoS Computational Biology*, 1(7):e67, 2005.
- D Sikder and T Kodadek. Genomic studies of transcription factor-dna interactions. *Current Opinion in Chemical Biology*, 9(1):38–45, 2005.
- I Simon, J Barnett, N Hannett, CT Harbison, NJ Rinaldi, TL Volkert, JJ Wyrick, J Zeitlinger, DK Gifford, TS Jaakkola, and RA Young. Serial regulation of transcriptional regulators in the yeast cell cycle. *Cell*, 106(6):697–708, 2001.
- PT Spellman, G Sherlock, MQ Zhang, VR Iyer, K Anders, MB Eisen, PO Brown, D Botstein, and B Futcher. Comprehensive identification of cell cycle-regulated genes of the yeast saccharomyces cerevisiae by microarray hybridization. *Mol Biol Cell*, 9(12):3273–97, 1998.
- LD Stein. Integrating biological databases. *4(5):337–345*, 2003.
- JD Storey and R Tibshirani. Statistical significance for genomewide studies. *PNAS*, 100(16):9440–9445, 2003.
- JM Stuart, E Segal, D Koller, and SK Kim. A gene-coexpression network for global discovery of conserved genetic modules. *Science*, 302(5643):249–55, 2003.

BIBLIOGRAPHY

- A Tanay, R Sharan, M Kupiec, and R Shamir. Revealing modularity and organization in the yeast molecular network by integrated analysis of highly heterogeneous genomewide data. *Proc Natl Acad Sci U S A*, 101(9):2981–6, 2004.
- A Tanay, A Regev, and R Shamir. Conservation and evolvability in regulatory networks: the evolution of ribosomal regulation in yeast. *Proc Natl Acad Sci U S A*, 102(20):7203–8, 2005.
- S Tavazoie, JD Hughes, MJ Campbell, RJ Cho, and GM Church. Systematic determination of genetic network architecture. *Nat Genet*, 22(3):281–5, 1999.
- M Tompa, N Li, TL Bailey, GM Church, B De Moor, E Eskin, AV Favorov, MC Frith, Y Fu, WJ Kent, VJ Makeev, AA Mironov, WS Noble, G Pavese, G Pesole, M Regnier, N Simonis, S Sinha, G Thijs, J van Helden, M Vandenbogaert, Z Weng, C Workman, C Ye, and Z Zhu. Assessing computational tools for the discovery of transcription factor binding sites. *Nat Biotechnol*, 23(1):137–44, 2005.
- H-K Tsai, HH-S Lu, and W-H Li. Statistical methods for identifying yeast cell cycle transcription factors. *Proceedings of the National Academy of Sciences*, 102(38):13532–13537, 2005.
- P Uetz, L Giot, G Cagney, TA Mansfield, RS Judson, JR Knight, D Lockshon, V Narayan, M Srinivasan, P Pochart, A Qureshi-Emili, Y Li, B Godwin, D Conover, T Kalbfleisch, G Vijayadamodar, M Yang, M Johnston, S Fields, and JM Rothberg. A comprehensive analysis of protein-protein interactions in *saccharomyces cerevisiae*. *Nature*, 403(6770):623–7, 2000.
- V van Noort, B Snel, and MA Huynen. Predicting gene function by conserved co-expression. *Trends in Genetics*, 19(5):238–242, 2003.
- W-S Wu, W-H Li, and B-S Chen. Computational reconstruction of transcriptional regulatory modules of the yeast cell cycle. *BMC Bioinformatics*, 7(1):421, 2006.

BIBLIOGRAPHY

- X Xu, L Wang, and D Ding. Learning module networks from genome-wide location and expression data. *FEBS Lett*, 578(3):297–304, 2004.
- I Yanai, JO Korbel, S Boue, SK McWeeney, P Bork, and MJ Lercher. Similar gene expression profiles do not imply similar tissue functions. *Trends in Genetics*, 22(3):132–138, 2006.
- T Yu and KC Li. Inference of transcriptional regulatory network by two-stage constrained space factor analysis. *Bioinformatics*, 21(21):4033–8, 2005.
- J Zeitlinger, I Simon, CT Harbison, NM Hannett, TL Volkert, GR Fink, and RA Young. Program-specific distribution of a transcription factor dependent on partner transcription factor and mapk signaling. *Cell*, 113(3):395–404, 2003.
- N Zhang, DC Gardner, SG Oliver, and LI Stateva. Down-regulation of the expression of *pkc1* and *srp1/psa1/vig9*, two genes involved in cell wall integrity in *Saccharomyces cerevisiae*, causes flocculation. *Microbiology*, 145(2):309–316, 1999.