

References

- [1] Daniel P. Aalberts, Eric G. Daub, and Jesse W. Dill. Quantifying optimal accuracy of local primary sequence bioinformatics methods. *Bioinformatics*, 21(16):3347–3351, 2005.
- [2] Federico Abascal, Rafael Zardoya, and David Posada. Protttest: Selection of best-fit models of protein evolution. *Bioinformatics*, 21(9):2104–2105, 2005.
- [3] J.C. Abbott, D.M. Aanensen, K. Rutherford, S. Butcher, and B.G. Spratt. Webact — an online companion for the artemis comparison tool. *Bioinformatics*, 21(18):3665–3666, 2005.
- [4] Osman Abul, Reda Alhajj, Faruk Polat, and Ken Barker. Finding differentially expressed genes for pattern generation. *Bioinformatics*, 21(4):445–450, 2005.
- [5] Alexej Abyzov, Mounir Errami, Chesley M. Leslin, and Valentin A. Ilyin. Friend, an integrated analytical front-end application for bioinformatics. *Bioinformatics*, 21(18):3677–3678, 2005.
- [6] Jesús S. Aguilar-Ruiz. Erratum to "shifting and scaling patterns from gene expression data". *Bioinformatics*, 21(23):4317–4317, 2005. Originally in *Bioinformatics*, Vol. 21, 2005, No. 20, 3840-3845.
- [7] Jesús S. Aguilar-Ruiz. Shifting and scaling patterns from gene expression data. *Bioinformatics*, 21(20):3840–3845, 2005. see Erratum in *Bioinformatics*, Vol. 21, 2005, No. 23, 4317-4317.
- [8] Stuart Aitken. Formalizing concepts of species, sex and developmental stage in anatomical ontologies. *Bioinformatics*, 21(11):2773–2779, 2005.
- [9] Stuart Aitken, Roman Korf, Bonnie Webber, and Jonathan Bard. Cobra: A bio-ontology editor. *Bioinformatics*, 21(6):825–826, 2005.
- [10] Fátima Al-Shahrour, Ramón Díaz-Uriarte, and Joaquín Dopazo. Discovering molecular functions significantly related to phenotypes by combining gene expression data and biological information. *Bioinformatics*, 21(13):2988–2993, 2005.

- [11] Mario Albrecht, Carola Huthmacher, Silvio C.E. Tosatto, and Thomas Lengauer. Decomposing protein networks into domain-domain interactions. *Bioinformatics*, 21(S2):220–221, 2005.
- [12] Jonathan E. Allen and Steven L. Salzberg. Jigsaw: Integration of multiple sources of evidence for gene prediction. *Bioinformatics*, 21(18):3596–3603, 2005.
- [13] Gelio Alves and Yi-Kuo Yu. Robust accurate identification of peptides (raid): Deciphering ms^2 data using a structured library search with de novo based statistics. *Bioinformatics*, 21(19):3726–3732, 2005.
- [14] B. Anand, V.S. Gowri, and N. Srinivasan. Use of multiple profiles corresponding to a sequence alignment enables effective detection of remote homologues. *Bioinformatics*, 21(12):2821–2826, 2005.
- [15] Vivek Anantharaman and L. Aravind. Meds and pocr are novel domains with a predicted role in sensing simple hydrocarbon derivatives in prokaryotic signal transduction systems. *Bioinformatics*, 21(12):2805–2811, 2005.
- [16] Christian N.K. Anderson, Uma Ramakrishnan, Yvonne L. Chan, and Elizabeth A. Hadly. Serial simcoal: A population genetics model for data from multiple populations and points in time. *Bioinformatics*, 21(8):1733–1734, 2005.
- [17] Anders Andersson, Rolf Bernander, and Peter Nilsson. Dual-genome primer design for construction of dna microarrays. *Bioinformatics*, 21(3):325–332, 2005.
- [18] S.I. Ao, Kevin Yip, Michael Ng, David Cheung, Pui-Yee Fong, Ian Melhado, and Pak C. Sham. Clustag: Hierarchical clustering and graph methods for selecting tag snps. *Bioinformatics*, 21(8):1735–1736, 2005.
- [19] Kiyoko F. Aoki, Hiroshi Mamitsuka, Tatsuya Akutsu, and Minoru Kanehisa. A score matrix to reveal the hidden links in glycans. *Bioinformatics*, 21(8):1457–1463, 2005.
- [20] Alberto Apostolico, Matteo Comin, and Laxmi Parida. Conservative extraction of over-represented extensible motifs. *Bioinformatics*, 21(S1):9–18, 2005.

- [21] Florence Armand, Philipp Bucher, C. Victor Jongeneel, and Edward E. Farmer. Rapid and selective surveillance of arabidopsis thaliana genome annotations with centrifuge. *Bioinformatics*, 21(12):2906–2908, 2005.
- [22] Vicente Arnau, Sergio Mars, and Ignacio Marín. Iterative cluster analysis of protein interaction data. *Bioinformatics*, 21(3):364–378, 2005.
- [23] Peter F. Arndt and Terence Hwa. Identification and measurement of neighbor-dependent nucleotide substitution processes. *Bioinformatics*, 21(10):2322–2328, 2005.
- [24] Roland Arnold, Thomas Rattei, Patrick Tischler, Minh-Duc Truong, Volker Stümpflen, and Werner Mewes. Simap — the similarity matrix of proteins. *Bioinformatics*, 21(S2):42–46, 2005.
- [25] Irena I. Artamonova, Goar Frishman, Mikhail S. Gelfand, and Dmitriy Frishman. Mining sequence annotation databanks for association patterns. *Bioinformatics*, 21(S3):49–57, 2005.
- [26] Musa H. Asyali and Musa Alci. Reliability analysis of microarray data using fuzzy *c*-means and normal mixture modeling based classification methods. *Bioinformatics*, 21(5):644–649, 2005.
- [27] Volkan Atalay and Rengul Cetin-Atalay. Implicit motif distribution based hybrid computational kernel for sequence classification. *Bioinformatics*, 21(8):1429–1436, 2005.
- [28] A. Selim Aytuna, Attila Gursoy, and Ozlem Keskin. Prediction of protein-protein interactions by combining structure and sequence conservation in protein interfaces. *Bioinformatics*, 21(12):2850–2855, 2005.
- [29] F. Azuaje. Integrative data analysis for functional prediction: A multi-objective optimization approach. *Bioinformatics*, 21(9):2099–2100, 2005.
- [30] Kyoungghwa Bae, Bani K. Mallick, and Christine G. Elsik. Prediction of protein interdomain linker regions by a hidden markov model. *Bioinformatics*, 21(10):2264–2270, 2005.

- [31] David J. Bakewell and Ernst Wit. Weighted analysis of microarray gene expression using maximum-likelihood. *Bioinformatics*, 21(6):723–729, 2005.
- [32] Rajarajeswari Balasubramaniyan, Eyke Hüllermeier, Nils Weskamp, and Jörg Kämper. Clustering of gene expression data using a local shape-based similarity measure. *Bioinformatics*, 21(7):1069–1077, 2005.
- [33] Lei Bao and Yan Cui. Prediction of the phenotypic effects of non-synonymous single nucleotide polymorphisms using structural and evolutionary information. *Bioinformatics*, 21(10):2185–2190, 2005.
- [34] Y. Barash, G. Elidan, T. Kaplan, and N. Friedman. Cis: Compound importance sampling method for protein-dna binding site p -value estimation. *Bioinformatics*, 21(5):596–600, 2005.
- [35] C. Paul Barrett and Martin E.M. Noble. Dynamite extended: Two new services to simplify protein dynamic analysis. *Bioinformatics*, 21(14):3174–3175, 2005.
- [36] J.C. Barrett, B. Fry, J. Maller, and M.J. Daly. Haploview: Analysis and visualization of ld and haplotype maps. *Bioinformatics*, 21(2):263–265, 2005.
- [37] William T. Barry, Andrew B. Nobel, and Fred A. Wright. Significance analysis of functional categories in gene expression studies: A structured permutation approach. *Bioinformatics*, 21(9):1943–1949, 2005.
- [38] Daniela Bartels, Sebastian Kespohl, Stefan Albaum, Tanja Drüke, Alexander Goesmann, Julia Herold, Olaf Kaiser, Alfred Pühler, Friedhelm Pfeiffer, Günter Raddatz, Jens Stoye, Folker Meyer, and Stephan C. Schuster. Baccardi — a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. *Bioinformatics*, 21(7):853–859, 2005.
- [39] Alex Bateman, Matthew T.G. Holden, and Corin Yeats. The g5 domain: A potential n-acetylglucosamine recognition domain involved in biofilm formation. *Bioinformatics*, 21(8):1301–1303, 2005.

- [40] Grégory Batt, Delphine Ropers, Hidde de Jong, Johannes Geiselmann, Radu Mateescu, Michel Page, and Dominique Schneider. Validation of qualitative models of genetic regulatory networks by model checking: Analysis of the nutritional stress response in *escherichia coli*. *Bioinformatics*, 21(S1):19–28, 2005.
- [41] Matthew J. Beal, Francesco Falciani, Zoubin Ghahramani, Claudia Rangel, and David L. Wild. A bayesian approach to reconstructing genetic regulatory networks with hidden factors. *Bioinformatics*, 21(3):349–356, 2005.
- [42] Niko Beerenwinkel, Jörg Rahnenführer, Rolf Kaiser, Daniel Hoffmann, Joachim Selbig, and Thomas Lengauer. Mtreemix: A software package for learning and using mixture models of mutagenetic trees. *Bioinformatics*, 21(9):2106–2107, 2005.
- [43] Niko Beerenwinkel, Tobias Sing, Thomas Lengauer, Jörg Rahnenführer, Kirsten Roomp, Igor Savenkov, Roman Fischer, Daniel Hoffmann, Joachim Selbig, Klaus Korn, Hauke Walter, Thomas Berg, Patrick Braun, Gerd Fätkenheuer, Mark Oette, Jürgen Rockstroh, Bernd Kupfer, Rolf Kaiser, and Martin Däumer. Computational methods for the design of effective therapies against drug resistant hiv strains. *Bioinformatics*, 21(21):3943–3950, 2005.
- [44] Robert G. Beiko, Cheong Xin Chan, and Mark A. Ragan. A word-oriented approach to alignment validation. *Bioinformatics*, 21(10):2230–2239, 2005.
- [45] Tim Beißbarth, Jason A. Tye-Din, Gordon K. Smyth, Terence P. Speed, and Robert P. Anderson. A systematic approach for comprehensive t-cell epitope discovery using peptide libraries. *Bioinformatics*, 21(S1):29–37, 2005.
- [46] Steven L. Bell and Bernhard Ø. Palsson. expa: A program for calculating extreme pathways in biochemical reaction networks. *Bioinformatics*, 21(8):1739–1740, 2005.
- [47] Robert Belshaw and Aris Katzourakis. Blastalign: A program that uses blast to align problematic nucleotide sequences. *Bioinformatics*, 21(1):122–123, 2005.

- [48] I. Ben-Gal, A. Shani, A. Gohr, J. Grau, S. Arviv, A. Shmilovici, S. Posch, and I. Grosse. Identification of transcription factor binding sites with variable-order bayesian networks. *Bioinformatics*, 21(11):2657–2666, 2005.
- [49] Asa Ben-Hur and William Stafford Noble. Kernel methods for predicting protein-protein interactions. *Bioinformatics*, 21(S1):38–46, 2005.
- [50] Yoram Ben-Shaul, Hagai Bergman, and Hermona Soreq. Identifying subtle interrelated changes in functional gene categories using continuous measures of gene expression. *Bioinformatics*, 21(7):1129–1137, 2005.
- [51] Halima Bensmail, Jennifer Golek, Michelle M. Moody, John O. Semmes, and Abdelali Haoudi. A novel approach for clustering proteomics data using bayesian fast fourier transform. *Bioinformatics*, 21(10):2210–2224, 2005.
- [52] Casey M. Bergman, Joseph W. Carlson, and Susan E. Celniker. Drosophila dnase i footprint database: A systematic genome annotation of transcription factor binding sites in the fruitfly, drosophila melanogaster. *Bioinformatics*, 21(8):1747–1749, 2005.
- [53] Søren Besenbacher, Thomas Mailund, Lasse Westh-Nielsen, and Christian N.S. Pedersen. Rbt — a tool for building refined buneman trees. *Bioinformatics*, 21(8):1711–1712, 2005.
- [54] Thijs Beuming, Lucy Skrabanek, Masha Y. Niv, Piali Mukherjee, and Harel Weinstein. Pdzbase: A protein-protein interaction database for pdz-domains. *Bioinformatics*, 21(6):827–828, 2005.
- [55] A. Beyer and T. Wilhelm. Dynamic simulation of protein complex formation on a genomic scale. *Bioinformatics*, 21(8):1610–1616, 2005.
- [56] Robert J. Beynon. A simple tool for drawing proteolytic peptide maps. *Bioinformatics*, 21(5):674–675, 2005.
- [57] Nitin Bhardwaj and Hui Lu. Correlation between gene expression profiles and protein-protein interactions within and across genomes. *Bioinformatics*, 21(11):2730–2738, 2005.

- [58] Kavitha Bhasi, Alan Forrest, and Murali Ramanathan. Splendid: A semi-parametric, model-based method for obtaining transcription rates and gene regulation parameters from genomic and proteomic expression profiles. *Bioinformatics*, 21(20):3873–3879, 2005.
- [59] Manoj Bhasin, Aarti Garg, and G.P.S. Raghava. Pslpred: Prediction of subcellular localization of bacterial proteins. *Bioinformatics*, 21(10):2522–2524, 2005.
- [60] David R. Bickel. Probabilities of spurious connections in gene networks: Application to expression time series. *Bioinformatics*, 21(7):1121–1128, 2005.
- [61] Sven Bilke, Qing-Rong Chen, Craig C. Whiteford, and Javed Khan. Detection of low level genomic alterations by comparative genomic hybridization based on cdna micro-arrays. *Bioinformatics*, 21(7):1138–1145, 2005.
- [62] Fabian Birzele, Jan E. Gewehr, and Ralf Zimmer. Quasar — scoring and ranking of sequence-structure alignments. *Bioinformatics*, 21(24):4425–4426, 2005.
- [63] Åsa K. Björklund, Daniel Soeria-Atmadja, Anna Zorzet, Ulf Hammerling, and Mats G. Gustafsson. Supervised identification of allergen-representative peptides for in silico detection of potentially allergenic proteins. *Bioinformatics*, 21(1):39–50, 2005.
- [64] Jacek Blazewicz, Marta Szachniuk, and Adam Wojtowicz. Rna tertiary structure determination: Noe pathways construction by tabu search. *Bioinformatics*, 21(10):2356–2361, 2005.
- [65] Xiaochen Bo and Shengqi Wang. Targetfinder: A software for anti-sense oligonucleotide target site selection based on mast and secondary structures of target mrna. *Bioinformatics*, 21(8):1401–1402, 2005.
- [66] T. Boby, A.-M. Patch, and S.J. Aves. Trbase: A database relating tandem repeats to disease genes for the human genome. *Bioinformatics*, 21(6):811–816, 2005.
- [67] Christoph Bock, Sabine Reither, Thomas Mikeska, Martina Paulsen, Jörn Walter, and Thomas Lengauer. Biq analyzer: Visualization and

- quality control for dna methylation data from bisulfite sequencing. *Bioinformatics*, 21(21):4067–4068, 2005.
- [68] Mikael Bodén and John Hawkins. Prediction of subcellular localization using sequence-biased recurrent networks. *Bioinformatics*, 21(10):2279–2286, 2005.
- [69] Shahid H. Bokhari and Jon R. Sauer. A parallel graph decomposition algorithm for dna sequencing with nanopores. *Bioinformatics*, 21(7):889–896, 2005.
- [70] Nadia Bolshakova, Francisco Azuaje, and Pádraig Cunningham. An integrated tool for microarray data clustering and cluster validity assessment. *Bioinformatics*, 21(4):451–455, 2005.
- [71] Nadia Bolshakova, Francisco Azuaje, and Pádraig Cunningham. A knowledge-driven approach to cluster validity assessment. *Bioinformatics*, 21(10):2546–2547, 2005.
- [72] Ezgi O. Booth, Nancy Van Driessche, Olga Zhuchenko, Adam Kuspa, and Gad Shaulsky. Microarray phenotyping in dictyostelium reveals a regulon of chemotaxis genes. *Bioinformatics*, 21(24):4371–4377, 2005.
- [73] Andrew J. Bordner and Ruben Abagyan. Revcom: A robust bayesian method for evolutionary rate estimation. *Bioinformatics*, 21(10):2315–2321, 2005.
- [74] Karsten M. Borgwardt, Cheng Soon Ong, Stefan Schönauer, S.V.N. Vishwanathan, Alex J. Smola, and Hans-Peter Kriegel. Protein function prediction via graph kernels. *Bioinformatics*, 21(S1):47–56, 2005.
- [75] Frédéric Boyer, Anne Morgat, Laurent Labarre, Joël Pothier, and Alain Viari. Syntons, metabolons and interactons: An exact graph-theoretical approach for exploring neighbourhood between genomic and functional data. *Bioinformatics*, 21(23):4209–4215, 2005.
- [76] John Boyle. Gene-expression omnibus integration and clustering tools in seqexpress. *Bioinformatics*, 21(10):2550–2551, 2005.

- [77] Ian Bradford, Robin Winter, Carl Evans, and Jonathan Bard. Human-mouse gene searcher: A tool to assist discovery of malformation-associated genes by using phenotype databases. *Bioinformatics*, 21(3):408–409, 2005.
- [78] James R. Bradford and David R. Westhead. Improved prediction of protein-protein binding sites using a support vector machines approach. *Bioinformatics*, 21(8):1487–1494, 2005.
- [79] Brona Brejová, Daniel G. Brown, Ming Li, and Tomás Vinar. Exon-hunter: A comprehensive approach to gene finding. *Bioinformatics*, 21(S1):57–65, 2005.
- [80] J. Michael Brockman, Priyam Singh, Donglin Liu, Sean Quinlan, Jesse Salisbury, and Joel H. Graber. Pacdb: PolyA cleavage site and 3'-utr database. *Bioinformatics*, 21(18):3691–3693, 2005.
- [81] Kevin R. Brown and Igor Jurisica. Online predicted human interaction database. *Bioinformatics*, 21(9):2076–2082, 2005.
- [82] T.J. Brunette and Oliver Brock. Improving protein structure prediction with model-based search. *Bioinformatics*, 21(S1):66–74, 2005.
- [83] Svetlana Bulashevskaya and Roland Eils. Inferring genetic regulatory logic from expression data. *Bioinformatics*, 21(11):2706–2713, 2005.
- [84] Andreas Buness, Wolfgang Huber, Klaus Steiner, Holger Sültmann, and Annemarie Poustka. arraymagic: Two-colour cDNA microarray quality control and preprocessing. *Bioinformatics*, 21(4):554–556, 2005.
- [85] S. Burden, Y.-X. Lin, and R. Zhang. Improving promoter prediction for the nnpp2.2 algorithm: A case study using escherichia coli DNA sequences. *Bioinformatics*, 21(5):601–607, 2005.
- [86] Anke Busch, Sebastian Will, and Rolf Backofen. Secisdesign: A server to design secis-elements within the coding sequence. *Bioinformatics*, 21(15):3312–3313, 2005.
- [87] Christian H. Busold, Stefan Winter, Nicole Hauser, Andrea Bauer, Jürgen Dippon, Jörg D. Hoheisel, and Kurt Fellenberg. Integration of GO annotations in correspondence analysis: Facilitating the interpretation of microarray data. *Bioinformatics*, 21(10):2424–2429, 2005.

- [88] Lawrence Cabusora, Electra Sutton, Andy Fulmer, and Christian V. Forst. Differential network expression during drug and stress response. *Bioinformatics*, 21(12):2898–2905, 2005.
- [89] Jun Cai, Jing Zhang, Ying Huang, and Yanda Li. Atid: A web-oriented database for collection of publicly available alternative translational initiation events. *Bioinformatics*, 21(23):4312–4314, 2005.
- [90] Isabelle Callebaut and Jean-Paul Mornon. Ocre: A novel domain made of imperfect, aromatic-rich octamer repeats. *Bioinformatics*, 21(6):699–702, 2005.
- [91] Carlos J. Camacho and Chao Zhang. Fastcontact: Rapid estimate of contact and binding free energies. *Bioinformatics*, 21(10):2534–2536, 2005.
- [92] J.M. Cameron, T. Hurd, and B.H. Robinson. Computational identification of human mitochondrial proteins based on homology to yeast mitochondrially targeted proteins. *Bioinformatics*, 21(9):1825–1830, 2005.
- [93] Davide Campagna, Chiara Romualdi, Nicola Vitulo, Micky Del Favero, Matej Lexa, Nicola Cannata, and Giorgio Valle. Rap: A new computer program for de novo identification of repeated sequences in whole genomes. *Bioinformatics*, 21(5):582–588, 2005.
- [94] Adrian A. Canutescu and Jr. Dunbrack, Roland L. Molid: A homology modeling framework you can click with. *Bioinformatics*, 21(12):2914–2916, 2005.
- [95] Emidio Capriotti, Piero Fariselli, Remo Calabrese, and Rita Casadio. Predicting protein stability changes from sequences using support vector machines. *Bioinformatics*, 21(S2):54–58, 2005.
- [96] Gilles Caraux and Sylvie Pinloche. Permutmatrix: A graphical environment to arrange gene expression profiles in optimal linear order. *Bioinformatics*, 21(7):1280–1281, 2005.
- [97] Vincent J. Carey, Jeff Gentry, Elizabeth Whalen, and Robert Gentleman. Network structures and algorithms in bioconductor. *Bioinformatics*, 21(1):135–136, 2005.

- [98] Ö. Carlborg, D.J. de Koning, K.F. Manly, E. Chesler, R.W. Williams, and C.S. Haley. Methodological aspects of the genetic dissection of gene expression. *Bioinformatics*, 21(10):2383–2393, 2005.
- [99] Christopher S. Carlson, Mark J. Reider, Deborah A. Nickerson, Michael A. Eberle, and Leonid Kruglyak. Comment on "discrepancies in dbsnp confirmations rates and allele frequency distributions from varying genotyping error rates and patterns". *Bioinformatics*, 21(2):141–143, 2005.
- [100] K. Cartharius, K. Frech, K. Grote, B. Klocke, M. Haltmeier, A. Klingenhoff, M. Frisch, M. Bayerlein, and T. Werner. MatInspector and beyond: Promoter analysis based on transcription factor binding sites. *Bioinformatics*, 21(13):2933–2942, 2005.
- [101] Reed A. Cartwright. Dna assembly with gaps (dawg): Simulating sequence evolution. *Bioinformatics*, 21(S3):31–38, 2005.
- [102] Tim J. Carver, Kim M. Rutherford, Matthew Berriman, Marie-Adele Rajandream, Barclay G. Barrell, and Julian Parkhill. Act: The artemis comparison tool. *Bioinformatics*, 21(16):3422–3423, 2005.
- [103] Sònia Casillas, Natalia Petit, and Antonio Barbadilla. Dpdb: A database for the storage, representation and analysis of polymorphism in the drosophila genus. *Bioinformatics*, 21(S2):26–30, 2005.
- [104] A. Cavallo and A.C.R. Martin. Mapping snps to protein sequence and structure data. *Bioinformatics*, 21(8):1443–1450, 2005.
- [105] Julie Chabalier, Cécile Capponi, Yves Quentin, and Gwennaele Fichant. Isymod: A knowledge warehouse for the identification, assembly and analysis of bacterial integrated systems. *Bioinformatics*, 21(7):1246–1256, 2005.
- [106] F. Chalmel, A. Lardenois, J.D. Thompson, J. Muller, J.-A. Sahel, T. Léveillard, and O. Poch. Goanno: Go annotation based on multiple alignment. *Bioinformatics*, 21(9):2095–2096, 2005.
- [107] Chi Yu Chan, Charles E. Lawrence, and Ye Ding. Structure clustering features on the sfold web server. *Bioinformatics*, 21(20):3926–3928, 2005.

- [108] H.L. Chan, T.W. Lam, W.K. Sung, Prudence W.H. Wong, S.M. Yiu, and X. Fan. The mutated subsequence problem and locating conserved genes. *Bioinformatics*, 21(10):2271–2278, 2005.
- [109] Kai M.A. Chan and Brian R. Moore. Symmetree: Whole-tree analysis of differential diversification rates. *Bioinformatics*, 21(8):1709–1710, 2005.
- [110] Aaron N. Chang, Jason McDermott, and Ram Samudrala. An enhanced java graph applet interface for visualizing interactomes. *Bioinformatics*, 21(8):1741–1742, 2005.
- [111] Chih-Yu (Carol) Chang and Joshua LaBaer. Dna polymorphism detector: An automated tool that searches for allelic matches in public databases for discrepancies found in clone or cdna sequences. *Bioinformatics*, 21(9):2133–2135, 2005.
- [112] D. Charif, J. Thioulouse, J.R. Lobry, and G. Perrière. Online synonymous codon usage analyses with the ade4 and seqinr packages. *Bioinformatics*, 21(4):545–547, 2005.
- [113] Abhijit Chatterjee, Kapil Mayawala, Jeremy S. Edwards, and Dionisios G. Vlachos. Time accelerated monte carlo simulations of biological networks using the binomial τ -leap method. *Bioinformatics*, 21(9):2136–2137, 2005.
- [114] Sreenivas Chavali, Anubha Mahajan, Rubina Tabassum, Souvik Maiti, and Dwaipayan Bharadwaj. Oligonucleotide properties determination and primer designing: A critical examination of predictions. *Bioinformatics*, 21(20):3918–3925, 2005. see Erratum in *Bioinformatics*, Vol. 21, 2005, No. 22, 4198-4198.
- [115] Sreenivas Chavali, Anubha Mahajan, Rubina Tabssum, Souvik Maiti, and Dwaipayan Bharadwaj. Erratum to "oligonucleotide properties determination and primer designing: A critical examination of predictions". *Bioinformatics*, 21(22):4198–4198, 2005. Originally in *Bioinformatics*, Vol. 21, 2005, No. 20, 3918-3925.
- [116] Dongsheng Che, Shane Jensen, Liming Cai, and Jun S. Liu. Best: Binding-site estimation suite of tools. *Bioinformatics*, 21(12):2909–2911, 2005.

- [117] Bor-Sen Chen, Yu-Chao Wang, Wei-Sheng Wu, and Wen-Hsiung Li. A new measure of the robustness of biochemical networks. *Bioinformatics*, 21(11):2698–2705, 2005.
- [118] Dung-Tsa Chen, James J. Chen, and Seng-jaw Soong. Probe rank approaches for gene selection in oligonucleotide arrays with a small number of replicates. *Bioinformatics*, 21(12):2861–2866, 2005.
- [119] Feng-Chi Chen and Trees-Juen Chuang. Estviewer: A web interface for visualizing mouse, rat, cattle, pig and chicken conserved ests in human genes and human alternatively spliced variants. *Bioinformatics*, 21(10):2510–2513, 2005.
- [120] Jonathan Chen, S. Joshua Swamidass, Yimeng Dou, Jocelyne Bruand, and Pierre Baldi. Chemdb: A public database of small molecules and related chemoinformatics resources. *Bioinformatics*, 21(22):4133–4139, 2005.
- [121] Kuang-Chi Chen, Tse-Yi Wang, Huei-Hun Tseng, Chi-Ying F. Huang, and Cheng-Yan Kao. A stochastic differential equation model for quantifying transcriptional regulatory network in *saccharomyces cerevisiae*. *Bioinformatics*, 21(12):2883–2890, 2005.
- [122] Liang Chen and Hongyu Zhao. Negative correlation between compositional symmetries and local recombination rates. *Bioinformatics*, 21(21):3951–3958, 2005.
- [123] Lifeng Chen, Hongfang Liu, and Carol Friedman. Gene name ambiguity of eukaryotic nomenclatures. *Bioinformatics*, 21(2):248–256, 2005.
- [124] Luonan Chen, Ruiqi Wang, Tianshou Zhou, and Kazuyuki Aihara. Noise-induced cooperative behavior in a multicell system. *Bioinformatics*, 21(11):2722–2729, 2005.
- [125] Luonan Chen, Tianshou Zhou, and Yun Tang. Protein structure alignment by deterministic annealing. *Bioinformatics*, 21(1):51–62, 2005.
- [126] Te-Ming Chen, Chung-Chin Lu, and Wen-Hsiung Li. Prediction of splice sites with dependency graphs and their expanded bayesian networks. *Bioinformatics*, 21(4):471–482, 2005.

- [127] Xue-Wen Chen and Mei Liu. Prediction of protein-protein interactions using random decision forest framework. *Bioinformatics*, 21(24):4394–4400, 2005.
- [128] Yu Chen and Dong Xu. Understanding protein dispensability through machine-learning analysis of high-throughput data. *Bioinformatics*, 21(5):575–581, 2005.
- [129] Jianlin Cheng and Pierre Baldi. Three-stage prediction of protein β -sheets by neural networks, alignments and graph algorithms. *Bioinformatics*, 21(S1):75–84, 2005.
- [130] Kei-Hoi Cheung, Kevin Y. Yip, Andrew Smith, Remko deKnikker, Andy Masiar, and Mark Gerstein. Yeasthub: A semantic web use case for integrating data in the life sciences domain. *Bioinformatics*, 21(S1):85–96, 2005.
- [131] Vijay Chickarmane, Sri R. Paladugu, Frank Bergmann, and Herbert M. Sauro. Bifurcation discovery tool. *Bioinformatics*, 21(18):3688–3690, 2005.
- [132] Jung Kyoon Choi, Ungsik Yu, Ook Joon Yoo, and Sangsoo Kim. Differential coexpression analysis using microarray data and its application to human cancer. *Bioinformatics*, 21(24):4348–4355, 2005.
- [133] Kwangmin Choi, Yu Ma, Jeong-Heyon Choi, and Sun Kim. Platcom: A platform for computational comparative genomics. *Bioinformatics*, 21(10):2514–2516, 2005.
- [134] Benny Chor and Tamir Tuller. Maximum likelihood of evolutionary trees: Hardness and approximation. *Bioinformatics*, 21(S1):97–106, 2005.
- [135] Kuo-Chen Chou. Using amphiphilic pseudo amino acid composition to predict enzyme subfamily classes. *Bioinformatics*, 21(1):10–19, 2005.
- [136] Kuo-Chen Chou and Yu-Dong Cai. Predicting protein localization in budding yeast. *Bioinformatics*, 21(7):944–950, 2005.
- [137] Rajesh Chowdhary, R. Ayesha Ali, Werner Albig, Detlef Doenecke, and Vladimir B. Bajic. Promoter modeling: The case study of mammalian histone promoters. *Bioinformatics*, 21(11):2623–2628, 2005.

- [138] Wei Chu, Zoubin Ghahramani, Francesco Falciani, and David L. Wild. Biomarker discovery in microarray gene expression data with gaussian processes. *Bioinformatics*, 21(16):3385–3393, 2005.
- [139] Won-Hyong Chung, Sung-Keun Rhee, Xiu-Feng Wan, Jin-Woo Bae, Zhe-Xue Quan, and Yong-Ha Park. Design of long oligonucleotide probes for functional gene detection in a microbial community. *Bioinformatics*, 21(22):4092–4100, 2005.
- [140] Francesca D. Ciccarelli and Peer Bork. The why domain mediates the response to desiccation in plants and bacteria. *Bioinformatics*, 21(8):1304–1307, 2005.
- [141] Marcus J. Claesson and Douwe van Sinderen. Blastxtract — a new way of exploring translated searches. *Bioinformatics*, 21(18):3667–3668, 2005.
- [142] Melissa S. Cline, John Blume, Simon Cawley, Tyson A. Clark, Jing-Shan Hu, Gang Lu, Nathan Salomonis, Hui Wang, and Alan Williams. Anosva: A statistical method for detecting splice variation from expression data. *Bioinformatics*, 21(S1):107–115, 2005.
- [143] P. Clote, J. Waldispühl, B. Behzadi, and J.-M. Steyaert. Energy landscape of k -point mutants of an rna molecule. *Bioinformatics*, 21(22):4140–4147, 2005.
- [144] D.R. Clutterbuck, A. Leroy, M.A. O’Connell, and C.A.M. Semple. A bioinformatic screen for novel a-i rna editing sites reveals recoding editing in bc10. *Bioinformatics*, 21(11):2590–2595, 2005.
- [145] Karen Coeytaux and Anne Poupon. Prediction of unfolded segments in a protein sequence based on amino acid composition. *Bioinformatics*, 21(9):1891–1900, 2005.
- [146] Steve W. Cole, Weihong Yan, Zoran Galic, Jesusa Arevalo, and Jerome A. Zack. Expression-based monitoring of transcription factor activity: The telis database. *Bioinformatics*, 21(6):803–810, 2005.
- [147] Ana Conesa, Stefan Götz, Juan Miguel García-Gómez, Javier Terol, Manuel Talón, and Montserrat Robles. Blast2go: A universal tool for

- annotation, visualization and analysis in functional genomics research. *Bioinformatics*, 21(18):3674–3676, 2005.
- [148] Darrell Conklin, Betty Haldeman, and Zeren Gao. Gene finding for the helical cytokines. *Bioinformatics*, 21(9):1776–1781, 2005.
- [149] J. Cortés, T. Siméon, V. Ruiz de Angulo, D. Guieysse, M. Remaud-Siméon, and V. Tran. A path planning approach for computing large-amplitude motions of flexible molecules. *Bioinformatics*, 21(S1):116–125, 2005.
- [150] Ivan G. Costa, Alexander Schönhuth, and Alexander Schliep. The graphical query language: A tool for analysis of gene expression time-courses. *Bioinformatics*, 21(10):2544–2545, 2005.
- [151] Charles F. Crane and Yan M. Crane. A nearest-neighboring-end algorithm for genetic mapping. *Bioinformatics*, 21(8):1579–1591, 2005.
- [152] C.J. Creevey and J.O. McInerney. Clann: Investigating phylogenetic information through supertree analyses. *Bioinformatics*, 21(3):390–392, 2005.
- [153] Gavin E. Crooks and Steven E. Brenner. An alternative model of amino acid replacement. *Bioinformatics*, 21(7):975–980, 2005.
- [154] Gavin E. Crooks, Richard E. Green, and Steven E. Brenner. Pairwise alignment incorporating dipeptide covariation. *Bioinformatics*, 21(19):3704–3710, 2005.
- [155] Qinghua Cui, Bing Liu, Tianzi Jiang, and Songde Ma. Characterizing the dynamic connectivity between genes by variable parameter regression and kalman filtering based on temporal gene expression data. *Bioinformatics*, 21(8):1538–1541, 2005.
- [156] Xinping Cui, Jin Xu, Rehana Asghar, Pascal Condamine, Jan T. Svensson, Steve Wanamaker, Nils Stein, Mikeal Roose, and Timothy J. Close. Detecting single-feature polymorphisms using oligonucleotide arrays and robustified projection pursuit. *Bioinformatics*, 21(20):3852–3858, 2005.

- [157] Yuehua Cui and Rongling Wu. Mapping genome-genome epistasis: A high-dimensional model. *Bioinformatics*, 21(10):2447–2455, 2005.
- [158] Aedín C. Culhane, Jean Thioulouse, Guy Perrière, and Desmond G. Higgins. Made4: An r package for multivariate analysis of gene expression data. *Bioinformatics*, 21(11):2789–2790, 2005.
- [159] Tomaz Curk, Janez Demsar, Qikai Xu, Gregor Leban, Uros Petrovic, Ivan Bratko, Gad Shaulsky, and Blaz Zupan. Microarray data mining with visual programming. *Bioinformatics*, 21(3):396–398, 2005.
- [160] Iwona A. Cymerman, Gregor Meiss, and Janusz M. Bujnicki. Dnase ii is a member of the phospholipase d superfamily. *Bioinformatics*, 21(21):3959–3962, 2005.
- [161] Alan R. Dabney. Classification of microarrays to nearest centroids. *Bioinformatics*, 21(22):4148–4154, 2005.
- [162] Davide D’Alimonte, David Lowe, Ian T. Nabney, Vassilis Mersinias, and Colin P. Smith. Milva: An interactive tool for the exploration of multidimensional microarray data. *Bioinformatics*, 21(22):4192–4193, 2005.
- [163] Cyril Dalmasso, Philippe Broët, and Thierry Moreau. A simple procedure for estimating the false discovery rate. *Bioinformatics*, 21(5):660–668, 2005.
- [164] B. DasGupta, K.M. Konwar, I.I. Măndoiu, and A.A. Shvartsman. Dna-bar: Distinguisher selection for dna barcoding. *Bioinformatics*, 21(16):3424–3426, 2005.
- [165] Shailesh V. Date and Edward M. Marcotte. Protein function prediction using the protein link explorer (plex). *Bioinformatics*, 21(10):2558–2559, 2005.
- [166] Susmita Datta and Somnath Datta. Empirical bayes screening of many p -values with applications to microarray studies. *Bioinformatics*, 21(9):1987–1994, 2005.

- [167] G. D’Avenio, M. Grigioni, G. Orefici, and R. Creti. Swift (sequence-wide investigation with fourier transform): A software tool for identifying proteins of a given class from the unannotated genome sequence. *Bioinformatics*, 21(13):2943–2949, 2005.
- [168] Alberto M.R. Dávila, Daniel M. Lorenzini, Pablo N. Mendes, Thiago S. Satake, Gabriel R. Sousa, Linair M. Campos, Camila J. Mazzoni, Glauber Wagner, Paulo F. Pires, Edmundo C. Grisard, Maria C.R. Cavalcanti, and Maria Luiza M. Campos. Garsa: Genomic analysis resources for sequence annotation. *Bioinformatics*, 21(23):4302–4303, 2005.
- [169] Fred P. Davis and Andrej Sali. Pibase: A comprehensive database of structurally defined protein interfaces. *Bioinformatics*, 21(9):1901–1907, 2005.
- [170] Sven Degroeve, Yvan Saeys, Bernard de Baets, Pierre Rouzé, and Yves van de Peer. Splicemachine: Predicting splice sites from high-dimensional local context representations. *Bioinformatics*, 21(8):1332–1338, 2005.
- [171] Paul Delmar, Stéphane Robin, and Jean Jacques Daudin. Varmixt: Efficient variance modelling for the differential analysis of replicated gene expression data. *Bioinformatics*, 21(4):502–508, 2005.
- [172] Mark DeLong, Guang Yao, Quanli Wang, Adrian Dobra, Esther P. Black, Jeffrey T. Chang, Andrea Bild, Mike West, Joseph R. Nevins, and Holly Dressman. Dig — a system for gene annotation and functional discovery. *Bioinformatics*, 21(13):2957–2959, 2005.
- [173] Cigdem Demir, S. Humayun Gultekin, and Bülent Yener. Augmented cell-graphs for automated cancer diagnosis. *Bioinformatics*, 21(S2):7–12, 2005.
- [174] Omer Demirkaya, Musa H. Asyali, and Mohamed M. Shoukri. Segmentation of cdna microarray spots using markov random field modeling. *Bioinformatics*, 21(13):2994–3000, 2005.
- [175] Pawan K. Dhar, Tan Chee Meng, Sandeep Somani, Li Ye, Kishore Sakharkar, Arun Krishnan, Azmi B.M. Ridwan, Sebastian Ho Kok

- Wah, Mandar Chitre, and Zhu Hao. Grid cellware: The first grid-enabled tool for modelling and simulating cellular processes. *Bioinformatics*, 21(7):1284–1287, 2005.
- [176] Xiaojun Di, Hajime Matsuzaki, Teresa A. Webster, Earl Hubbell, Guoying Liu, Shoulian Dong, Dan Bartell, Jing Huang, Richard Chiles, Geoffrey Yang, Mei-mei Shen, David Kulp, Giulia C. Kennedy, Rui Mei, Keith W. Jones, and Simon Cawley. Dynamic model based algorithms for screening and genotyping over 100k snps on oligonucleotide microarrays. *Bioinformatics*, 21(9):1958–1963, 2005.
- [177] L. Diambra and L. da F. Costa. Complex networks approach to gene expression driven phenotype imaging. *Bioinformatics*, 21(20):3846–3851, 2005.
- [178] Guido Dieterich, Uwe Kärst, Jürgen Wehland, and Lothar Jänsch. Mineblast: A literature presentation service supporting protein annotation by data mining of blast results. *Bioinformatics*, 21(16):3450–3451, 2005.
- [179] Matthew W. Dimmic, Melissa J. Hubisz, Carlos D. Bustamante, and Rasmus Nielsen. Detecting coevolving amino acid sites using bayesian mutational mapping. *Bioinformatics*, 21(S1):126–135, 2005.
- [180] J. Ding, K. Viswanathan, D. Berleant, L. Hughes, E.S. Wurtele, D. Ashlock, J.A. Dickerson, A. Fulmer, and P.S. Schnable. Using the biological taxonomy to access biological literature with pathbinderh. *Bioinformatics*, 21(10):2560–2562, 2005.
- [181] Jing Ding and Daniel Berleant. Medkit: A helper toolkit for automatic mining of medline/pubmed citations. *Bioinformatics*, 21(5):694–695, 2005.
- [182] Anna Divoli and Teresa K. Attwood. Bioie: Extracting informative sentences from the biomedical literature. *Bioinformatics*, 21(9):2138–2139, 2005.
- [183] Amira Djebbari, Svetlana Karamycheva, Eleanor Howe, and John Quackenbush. Mesher: Identifying biological concepts in microarray assays based on pubmed references and mesh terms. *Bioinformatics*, 21(15):3324–3326, 2005.

- [184] Kevin K. Dobbin, Joanna H. Shih, and Richard M. Simon. Comment on "evaluation of the gene-specific dye bias in cdna microarray experiments". *Bioinformatics*, 21(12):2803–2804, 2005.
- [185] K.K. Dobbin, E.S. Kawasaki, D.W. Petersen, and R.M. Simon. Characterizing dye bias in microarray experiments. *Bioinformatics*, 21(10):2430–2437, 2005.
- [186] Mary E. Dolan, Li Ni, Evelyn Camon, and Judith A. Blake. A procedure for assessing go annotation consistency. *Bioinformatics*, 21(S1):136–143, 2005.
- [187] Núria Domedel-Puig and Lorenz Wernisch. Applying gift, a gene interactions finder in text, to fly literature. *Bioinformatics*, 21(17):3582–3583, 2005.
- [188] Jason E. Donald, Isaac A. Hubner, Veronica M. Rotemberg, Eugene I. Shakhnovich, and Leonid A. Mirny. Coc: A database of universally conserved residues in protein folds. *Bioinformatics*, 21(10):2539–2540, 2005.
- [189] Jason E. Donald and Eugene I. Shakhnovich. Determining functional specificity from protein sequences. *Bioinformatics*, 21(11):2629–2635, 2005. see Erratum in *Bioinformatics*, Vol. 21, 2005, No. 17, 3586–3586.
- [190] Jason E. Donald and Eugene I. Shakhovich. Erratum to "determining functional specificity from protein sequences". *Bioinformatics*, 21(17):3586–3586, 2005. Originally in *Bioinformatics*, Vol. 21, 2005, No. 11, 2629–2635.
- [191] Ian John Donaldson, Michael Chapman, and Berthold Göttgens. Tfb-cluster: A resource for the characterization of transcriptional regulatory networks. *Bioinformatics*, 21(13):3058–3059, 2005.
- [192] Adi Doron-Faigenboim, Adi Stern, Itay Mayrose, Eran Bacharach, and Tal Pupko. Selecton: A server for detecting evolutionary forces at a single amino-acid site. *Bioinformatics*, 21(9):2101–2103, 2005.
- [193] Zsuzsanna Dosztányi, Veronika Csizmok, Peter Tompa, and István Simon. Iupred: Web server for the prediction of intrinsically unstructured

- regions of proteins based on estimated energy content. *Bioinformatics*, 21(16):3433–3434, 2005.
- [194] Gideon Dror, Rotem Sorek, and Ron Shamir. Accurate identification of alternatively spliced exons using support vector machine. *Bioinformatics*, 21(7):897–901, 2005.
- [195] Oranit Dror, Ruth Nussinov, and Haim Wolfson. Arts: Alignment of rna tertiary structures. *Bioinformatics*, 21(S2):47–53, 2005.
- [196] R.D. Drummond, A. Pinheiro, C.S. Rocha, and M. Menossi. Iser: Selection of differentially expressed genes from dna array data by non-linear data transformations and local fitting. *Bioinformatics*, 21(24):4427–4429, 2005.
- [197] Delbert Dueck, Quaid D. Morris, and Brendan J. Frey. Multi-way clustering of microarray data using probabilistic sparse matrix factorization. *Bioinformatics*, 21(S1):144–151, 2005.
- [198] Jean-François Dufayard, Laurent Duret, Simon Penel, Manolo Gouy, François Rechenmann, and Guy Perrière. Tree pattern matching in phylogenetic trees: Automatic search for orthologs or paralogs in homologous gene sequence databases. *Bioinformatics*, 21(11):2596–2603, 2005.
- [199] Franck Dupuis, Jean-François Sadoc, Rémi Jullien, Borislav Angelov, and Jean-Paul Mornon. Voro3d: 3d voronoi tessellations applied to protein structures. *Bioinformatics*, 21(8):1715–1716, 2005.
- [200] Alan M. Durham, André Y. Kashiwabara, Fernando T.G. Matsunaga, Paulo H. Ahagon, Flávia Rainone, Leonardo Varuzza, and Arthur Gruber. Egene: A configurable pipeline generation system for automated sequence analysis. *Bioinformatics*, 21(12):2812–2813, 2005.
- [201] Steffen Durinck, Yves Moreau, Arek Kasprzyk, Sean Davis, Bart De Moor, Alvis Brazma, and Wolfgang Huber. Biomart and bioconductor: A powerful link between biological databases and microarray data analysis. *Bioinformatics*, 21(16):3439–3440, 2005.
- [202] J.E. Eckel, C. Gennings, T.M. Therneau, L.D. Burgoon, D.R. Boverhof, and T.R. Zacharewski. Normalization of two-channel microarray

- experiments: A semiparametric approach. *Bioinformatics*, 21(7):1078–1083, 2005.
- [203] Robert C. Edgar and Eugene W. Myers. Piler: Identification and classification of genomic repeats. *Bioinformatics*, 21(S1):152–158, 2005.
- [204] Richard J. Edwards and Denis C. Shields. Badasp: Predicting functional specificity in protein families using ancestral sequences. *Bioinformatics*, 21(22):4190–4191, 2005.
- [205] Paul H.C. Eilers and Renée X. de Menezes. Quantile smoothing of array cgh data. *Bioinformatics*, 21(7):1146–1153, 2005.
- [206] Liat Ein-Dor, Itai Kela, Gad Getz, David Givol, and Eytan Domany. Outcome signature genes in breast cancer: Is there a unique set? *Bioinformatics*, 21(2):171–178, 2005.
- [207] Thierry Emonet, Charles M. Macal, Michael J. North, Charles E. Wickersham, and Philippe Cluzel. Agentcell: A digital single-cell assay for bacterial chemotaxis. *Bioinformatics*, 21(11):2714–2721, 2005.
- [208] Jason Ernst, Gerard J. Nau, and Ziv Bar-Joseph. Clustering short time series gene expression data. *Bioinformatics*, 21(S1):159–168, 2005.
- [209] Jordi Espadaler, Oriol Romero-Isart, Richard M. Jackson, and Baldo Oliva. Prediction of protein-protein interactions using distant conservation of sequence patterns and structure relationships. *Bioinformatics*, 21(16):3360–3368, 2005.
- [210] Graham J. Etherington, Jo Dicks, and Ian N. Roberts. Recombination analysis tool (rat): A program for the high-throughput detection of recombination. *Bioinformatics*, 21(3):278–281, 2005.
- [211] Jayson Falkner and Philip Andrews. Fast tandem mass spectra-based protein identification regardless of the number of spectra or potential modifications examined. *Bioinformatics*, 21(10):2177–2184, 2005.
- [212] M. Falque. Irilmap: Linkage map distance correction for intermated recombinant inbred lines/advanced recombinant inbred strains. *Bioinformatics*, 21(16):3441–3442, 2005.

- [213] Niklaus Fankhauser and Pascal Mäser. Identification of gpi anchor attachment signals by a kohonen self-organizing map. *Bioinformatics*, 21(9):1846–1852, 2005.
- [214] Hassan M. Fathallah-Shaykh. Noise and rank-dependent geometrical filter improves sensitivity of highly specific discovery by microarrays. *Bioinformatics*, 21(23):4255–4262, 2005.
- [215] A.V. Favorov, M.S. Gelfand, A.V. Gerasimova, D.A. Ravcheev, A.A. Mironov, and V.J. Makeev. A gibbs sampler for identification of symmetrically structured, spaced dna motifs with improved estimation of the signal length. *Bioinformatics*, 21(10):2240–2245, 2005.
- [216] Marius Felder, Karol Szafranski, Rüdiger Lehmann, Ludwig Eichinger, Angelika A. Noegel, Matthias Platzer, and Gernot Glöckner. Dictymold — a dictyostelium discoideum genome browser database. *Bioinformatics*, 21(5):696–697, 2005.
- [217] Luca Ferrarini, Luca Bertelli, Jacob Feala, Andrew D. McCulloch, and Giovanni Paternostro. A more efficient search strategy for aging genes based on connectivity. *Bioinformatics*, 21(3):338–348, 2005.
- [218] F. Ferrè and P. Clote. Disulfide connectivity prediction using secondary structure information and diresidue frequencies. *Bioinformatics*, 21(10):2336–2346, 2005.
- [219] C. Ferrer-Costa, H.P. Shanahan, S. Jones, and J.M. Thornton. Hthquery: A method for detecting dna-binding proteins with a helix-turn-helix structural motif. *Bioinformatics*, 21(18):3679–3680, 2005.
- [220] Carles Ferrer-Costa, Josep Lluís Gelpí, Leire Zamakola, Ivan Parraga, Xavier de la Cruz, and Modesto Orozco. Pmut: A web-based tool for the annotation of pathological mutations on proteins. *Bioinformatics*, 21(14):3176–3178, 2005.
- [221] G. Finak, N. Godin, M. Hallett, F. Pepin, Z. Rajabi, V. Srivastava, and Z. Tang. Bias: Bioinformatics integrated application software. *Bioinformatics*, 21(8):1745–1746, 2005.

- [222] Robert D. Finn, Mhairi Marshall, and Alex Bateman. Ipfam: Visualization of protein-protein interactions in pdb at domain and amino acid resolutions. *Bioinformatics*, 21(3):410–412, 2005.
- [223] Andrew E. Firth and Chris M. Brown. Detecting overlapping coding sequences with pairwise alignments. *Bioinformatics*, 21(3):282–292, 2005.
- [224] Andrew E. Firth and Wayne M. Patrick. Statistics of protein library construction. *Bioinformatics*, 21(15):3314–3315, 2005.
- [225] Patrick Flaherty, Guri Giaever, Jochen Kumm, Michael I. Jordan, and Adam P. Arkin. A latent variable model for chemogenomic profiling. *Bioinformatics*, 21(15):3286–3293, 2005.
- [226] Imola K. Fodor, David O. Nelson, Michelle Alegria-Hartman, Kristin Robbins, Richard G. Langlois, Kenneth W. Turteltaub, Todd H. Corzett, and Sandra L. McCutchen-Maloney. Statistical challenges in the analysis of two-dimensional difference gel electrophoresis experiments using decydeTM. *Bioinformatics*, 21(19):3733–3740, 2005.
- [227] Rasmus H. Fogh, Wayne Boucher, Wim F. Vranken, Anne Pajon, Tim J. Stevens, T.N. Bhat, John Westbrook, John M.C. Ionides, and Ernest D. Laue. A framework for scientific data modeling and automated software development. *Bioinformatics*, 21(8):1678–1684, 2005.
- [228] Paolo Fontana, Eckart Bindewald, Stefano Toppo, Riccardo Velasco, Giorgio Valle, and Silvio C.E. Tosatto. The ssea server for protein secondary structure alignment. *Bioinformatics*, 21(3):393–395, 2005.
- [229] Gersende Fort and Sophie Lambert-Lacroix. Classification using partial least squares with penalized logistic regression. *Bioinformatics*, 21(7):1104–1111, 2005.
- [230] Milana Frenkel-Morgenstern, Hillary Voet, and Shmuel Pietrokovski. Enhanced statistics for local alignment of multiple alignments improves prediction of protein function and structure. *Bioinformatics*, 21(13):2950–2956, 2005.

- [231] Valerio Freschi and Alessandro Bogliolo. Using sequence compression to speedup probabilistic profile matching. *Bioinformatics*, 21(10):2225–2229, 2005.
- [232] Caroline C. Friedel, Katharina H.V. Jahn, Selina Sommer, Stephen Rudd, Hans W. Mewes, and Igor V. Tetko. Support vector machines for separation of mixed plant-pathogen est collections based on codon usage. *Bioinformatics*, 21(8):1383–1388, 2005.
- [233] Joachim Friedrich, Thomas Dandekar, Matthias Wolf, and Tobias Müller. Profdist: A tool for the construction of large phylogenetic trees based on profile distances. *Bioinformatics*, 21(9):2108–2109, 2005.
- [234] Rongwei Fu, Dipak K. Dey, and Kent E. Holsinger. Bayesian models for the analysis of genetic structure when populations are correlated. *Bioinformatics*, 21(8):1516–1529, 2005.
- [235] Wenjiang J. Fu, Raymond J. Carroll, and Suojin Wang. Estimating misclassification error with small samples via bootstrap cross-validation. *Bioinformatics*, 21(9):1979–1986, 2005.
- [236] Wenjiang J. Fu, Edward R. Dougherty, Bani Mallick, and Raymond J. Carroll. How many samples are needed to build a classifier: A general sequential approach. *Bioinformatics*, 21(1):63–70, 2005.
- [237] Ruta Furmonaviciene, Brian J. Sutton, Fabian Glaser, Charlie A. Laughton, Nick Jones, Herb F. Sewell, and Farouk Shakib. An attempt to define allergen-specific molecular surface features: A bioinformatic approach. *Bioinformatics*, 21(23):4201–4204, 2005.
- [238] Matthias E. Futschik and Toni Crompton. Olin: Optimized normalization, visualization and quality testing of two-channel microarray data. *Bioinformatics*, 21(8):1724–1726, 2005.
- [239] Toni Gabaldón and Martijn A. Huynen. Lineage-specific gene loss following mitochondrial endosymbiosis and its potential for function prediction in eukaryotes. *Bioinformatics*, 21(S2):144–150, 2005.
- [240] Michael D. Gadberry, Simon T. Malcomber, Andrew N. Doust, and Elizabeth A. Kellogg. Primaclade — a flexible tool to find conserved

- per primers across multiple species. *Bioinformatics*, 21(7):1263–1264, 2005.
- [241] Yuan Gao and George Church. Improving molecular cancer class discovery through sparse non-negative matrix factorization. *Bioinformatics*, 21(21):3970–3975, 2005.
- [242] H.M. Garay-Malpartida, J.M. Occhiucci, J. Alves, and J.E. Belizário. Caspredictor: A new computer-based tool for caspase substrate prediction. *Bioinformatics*, 21(S1):169–176, 2005.
- [243] Per Gärdén, Rikard Alm, and Jari Häkkinen. Proteios: An open source proteomics initiative. *Bioinformatics*, 21(9):2085–2087, 2005.
- [244] J.L. Gardy, M.R. Laird, F. Chen, S. Rey, C.J. Walsh, M. Ester, and F.S.L. Brinkman. Psortb v.2.0: Expanded prediction of bacterial protein subcellular localization and insights gained from comparative proteome analysis. *Bioinformatics*, 21(5):617–623, 2005.
- [245] George M. Garrity and Timothy G. Lilburn. Self-organizing and self-correcting classifications of biological data. *Bioinformatics*, 21(10):2309–2314, 2005.
- [246] Zoltán Gáspári, Kristian Vlahovicek, and Sándor Pongor. Efficient recognition of folds in protein 3d structures by the improved pride algorithm. *Bioinformatics*, 21(15):3322–3323, 2005.
- [247] S. Gaudan, H. Kirsch, and D. Rebholz-Schuhmann. Resolving abbreviations to their senses in medline. *Bioinformatics*, 21(18):3658–3664, 2005.
- [248] Elisabeth Georgii, Lothar Richter, Ulrich Rückert, and Stefan Kramer. Analyzing microarray data using quantitative association rules. *Bioinformatics*, 21(S2):123–129, 2005.
- [249] Naum I. Gershenzon and Ilya P. Ioshikhes. Synergy of human pol ii core promoter elements revealed by statistical sequence analysis. *Bioinformatics*, 21(8):1295–1300, 2005.
- [250] Victor E. Gerth and Peter D. Vize. A java tool for dynamic web-based 3d visualization of anatomy and overlapping gene or protein expression patterns. *Bioinformatics*, 21(7):1278–1279, 2005.

- [251] Pierre Geurts, Marianne Fillet, Dominique de Seny, Marie-Alice Meuwis, Michel Malaise, Marie-Paule Merville, and Louis Wehenkel. Proteomic mass spectra classification using decision tree based ensemble methods. *Bioinformatics*, 21(14):3138–3145, 2005.
- [252] Walter R. Gilks, Brian D.M. Tom, and Alvis Brazma. Fusing microarray experiments with multivariate regression. *Bioinformatics*, 21(S2):137–143, 2005.
- [253] Alejandro Giorgetti, Domenico Raimondo, Adriana Erica Miele, and Anna Tramontano. Evaluating the usefulness of protein structure models for molecular replacement. *Bioinformatics*, 21(S2):72–76, 2005.
- [254] Georgios V. Gkoutos, Eain C.J. Green, Simon Greenaway, Andrew Blake, Ann-Marie Mallon, and John M. Hancock. Crave: A database, middleware and visualization system for phenotype ontologies. *Bioinformatics*, 21(7):1257–1262, 2005.
- [255] Galina Glazko, Alexander Gordon, and Arcady Mushegian. The choice of optimal distance measure in genome-wide datasets. *Bioinformatics*, 21(S3):3–11, 2005.
- [256] Andrean Goede, Mathias Dunkel, Nina Mester, Cornelius Frommel, and Robert Preissner. Superdrug: A conformational drug database. *Bioinformatics*, 21(9):1751–1753, 2005.
- [257] Jelle J. Goeman, Jan Oosting, Anne-Marie Cleton-Jansen, Jakob K. Anninga, and Hans C. van Houwelingen. Testing association of a pathway with survival using gene expression data. *Bioinformatics*, 21(9):1950–1957, 2005.
- [258] Leon Goldovsky, Paul Janssen, Dag Ahrén, Benjamin Audit, Ildefonso Cases, Nikos Darzentas, Anton J. Enright, Núria López-Bigas, José M. Peregrin-Alvarez, Mike Smith, Sophia Tsoka, Victor Kunin, and Christos A. Ouzounis. Cogent++: An extensive and extensible data environment for computational genomics. *Bioinformatics*, 21(19):3806–3810, 2005.
- [259] Sungsam Gong, Giseok Yoon, Insoo Jang, Dan Bolser, Panos Dafas, Michael Schroeder, Hansol Choi, Yoobok Cho, Kyungsook Han,

- Sunghoon Lee, Hwanho Choi, Michael Lappe, Liisa Holm, Sangsoo Kim, Donghoon Oh, and Jonghwa Bhak. Psibase: A database of protein structural interactome map (psimap). *Bioinformatics*, 21(10):2541–2543, 2005.
- [260] Juan M. Gonzalez, Johannes Zimmermann, and Cesareo Saiz-Jimenez. Evaluating putative chimeric sequences from pcr-amplified products. *Bioinformatics*, 21(3):333–337, 2005.
- [261] Didier Gonze, Sylvie Pinloche, Olivier Gascuel, and Jacques van Helden. Discrimination of yeast genes involved in methionine and phosphate metabolism on the basis of upstream motifs. *Bioinformatics*, 21(17):3490–3500, 2005.
- [262] Peddinti V. Gopalacharyulu, Erno Lindfors, Catherine Bounsaythip, Teemu Kivioja, Laxman Yetukuri, Jaakko Hollmén, and Matej Oresic. Data integration and visualization system for enabling conceptual biology. *Bioinformatics*, 21(S1):177–185, 2005.
- [263] D. Benjamin Gordon, Lena Nekludova, Scott McCallum, and Ernest Fraenkel. Tamo: A flexible, object-oriented framework for analyzing transcriptional regulation using dna-sequence motifs. *Bioinformatics*, 21(14):3164–3165, 2005.
- [264] Derek Gordon, Chad Haynes, Jon Blumenfeld, and Stephen J. Finch. Pawe-3d: Visualizing power for association with error in case-control genetic studies of complex traits. *Bioinformatics*, 21(20):3935–3937, 2005.
- [265] Swanand P. Gore, David F. Burke, and Tom L. Blundell. Provat: A tool for voronoi tessellation analysis of protein structures and complexes. *Bioinformatics*, 21(15):3316–3317, 2005.
- [266] D.R. Goucher, S.M. Wincovitch, S.H. Garfield, K.M. Carbone, and T.H. Malik. A quantitative determination of multi-protein interactions by the analysis of confocal images using a pixel-by-pixel assessment algorithm. *Bioinformatics*, 21(15):3248–3254, 2005.
- [267] Julian Gough. Convergent evolution of domain architectures (is rare). *Bioinformatics*, 21(8):1464–1471, 2005.

- [268] Niels Grabe and Karsten Neuber. A multicellular systems biology model predicts epidermal morphology, kinetics and ca^{2+} flow. *Bioinformatics*, 21(17):3541–3547, 2005.
- [269] Jinko Graham, Brad McNeney, and Françoise Seillier-Moiseiwitsch. Stepwise detection of recombination breakpoints in sequence alignments. *Bioinformatics*, 21(5):589–595, 2005.
- [270] Gregory R. Grant, Junmin Liu, and Jr. Stoeckert, Christian J. A practical false discovery rate approach to identifying patterns of differential expression in microarray data. *Bioinformatics*, 21(11):2684–2690, 2005.
- [271] Eain C.J. Green, Georgios V. Gkoutos, Heena V. Lad, Andrew Blake, Joseph Weekes, and John M. Hancock. Empress: European mouse phenotyping resource for standardized screens. *Bioinformatics*, 21(12):2930–2931, 2005.
- [272] Sam Griffiths-Jones. Ralee — rna alignment editor in emacs. *Bioinformatics*, 21(2):257–259, 2005.
- [273] M. Michael Gromiha and Makiko Suwa. A simple statistical method for discriminating outer membrane proteins with better accuracy. *Bioinformatics*, 21(7):961–968, 2005.
- [274] Dominik Gront and Andrzej Kolinski. Hcpm — program for hierarchical clustering of protein models. *Bioinformatics*, 21(14):3179–3180, 2005.
- [275] Dominik Gront and Andrzej Kolinski. A new approach to prediction of short-range conformational propensities in proteins. *Bioinformatics*, 21(7):981–987, 2005.
- [276] Sheng Gu, Andrew J. Pakstis, and Kenneth K. Kidd. Haplot: A graphical comparison of haplotype blocks, tagsnp sets and snp variation for multiple populations. *Bioinformatics*, 21(20):3938–3939, 2005.
- [277] Xun Gu, Wei Huang, Dongping Xu, and Hongmei Zhang. Genecontent: Software for whole-genome phylogenetic analysis. *Bioinformatics*, 21(8):1713–1714, 2005.

- [278] Zhong Guan and Hongyu Zhao. A semiparametric approach for marker gene selection based on gene expression data. *Bioinformatics*, 21(4):529–536, 2005.
- [279] Chittibabu Guda and Shankar Subramainian. Erratum to "ptarget: A new method for predicting protein subcellular localization in eukaryotes". *Bioinformatics*, 21(24):4434–4434, 2005. Originally in *Bioinformatics*, Vol. 21, 2005, No. 21, 3963-3969.
- [280] Chittibabu Guda and Shankar Subramaniam. ptarget: A new method for predicting protein subcellular localization in eukaryotes. *Bioinformatics*, 21(21):3963–3969, 2005. see Erratum in *Bioinformatics*, Vol. 21, 2005, No. 24, 4434-4434.
- [281] Laurent Guéguen. Sarment: Python modules for hmm analysis and partitioning of sequences. *Bioinformatics*, 21(16):3427–3428, 2005.
- [282] Jiang Gui and Hongzhe Li. Penalized cox regression analysis in the high-dimensional and low-sample size settings, with applications to microarray gene expression data. *Bioinformatics*, 21(13):3001–3008, 2005.
- [283] Anyuan Guo, Kun He, Di Liu, Shunong Bai, Xiaocheng Gu, Liping Wei, and Jingchu Luo. Datf: A database of arabidopsis transcription factors. *Bioinformatics*, 21(10):2568–2569, 2005.
- [284] Reinhard Guthke, Ulrich Möller, Martin Hoffmann, Frank Thies, and Susanne Töpfer. Dynamic network reconstruction from gene expression data applied to immune response during bacterial infection. *Bioinformatics*, 21(8):1626–1634, 2005.
- [285] Daniel H. Haft, Jeremy D. Selengut, Lauren M. Brinkac, Nikhat Zafar, and Owen White. Genome properties: A system for the investigation of prokaryotic genetic content for microbiology, genome annotation and comparative genomics. *Bioinformatics*, 21(3):293–306, 2005.
- [286] Yoonsoo Hahn and Byungkook Lee. Identification of nine human-specific frameshift mutations by comparative analysis of the human and the chimpanzee genome sequences. *Bioinformatics*, 21(S1):186–194, 2005.

- [287] Eran Halperin, Gad Kimmel, and Ron Shamir. Tag *snp* selection in genotype data for maximizing *snp* prediction accuracy. *Bioinformatics*, 21(S1):195–203, 2005.
- [288] S.E. Hampson, B.S. Gaut, and P. Baldi. Statistical detection of chromosomal homology using shared-gene density alone. *Bioinformatics*, 21(8):1339–1348, 2005.
- [289] Sangjo Han, Byung-chul Lee, Seung Taek Yu, Chan-seok Jeong, Soyoung Lee, and Dongsup Kim. Fold recognition by combining profile-profile alignment and support vector machine. *Bioinformatics*, 21(11):2667–2673, 2005.
- [290] Julia Handl, Joshua Knowles, and Douglas B. Kell. Computational cluster validation in post-genomic data analysis. *Bioinformatics*, 21(15):3201–3212, 2005.
- [291] Sridhar Hannenhalli and Li-San Wang. Enhanced position weight matrices using mixture models. *Bioinformatics*, 21(S1):204–212, 2005.
- [292] Pei Hao, Wei-Zhong He, Yin Huang, Liang-Xiao Ma, Ying Xu, Hong Xi, Chuan Wang, Bo-Shu Liu, Jin-Miao Wang, Yi-Xue Li, and Yang Zhong. Mpss: An integrated database system for surveying a set of proteins. *Bioinformatics*, 21(9):2142–2143, 2005.
- [293] Yu Hao, Xiaoyan Zhu, Minlie Huang, and Ming Li. Discovering patterns to extract protein-protein interactions from the literature: Part ii. *Bioinformatics*, 21(15):3294–3300, 2005.
- [294] Johan Hattne, David Fange, and Johan Elf. Stochastic reaction-diffusion simulation with mesord. *Bioinformatics*, 21(12):2923–2924, 2005.
- [295] Vassily Hatzimanikatis, Chunhui Li, Justin A. Ionita, Christopher S. Henry, Matthew D. Jankowski, and Linda J. Broadbelt. Exploring the diversity of complex metabolic networks. *Bioinformatics*, 21(8):1603–1609, 2005.
- [296] Marc Daniel Haunschild, Bernd Freisleben, Ralf Takors, and Wolfgang Wiechert. Investigating the dynamic behavior of biochemical networks using model families. *Bioinformatics*, 21(8):1617–1625, 2005.

- [297] Sampsa Hautaniemi, Sourabh Kharait, Akihiro Iwabu, Alan Wells, and Douglas A. Lauffenburger. Modeling of signal-response cascades using decision tree analysis. *Bioinformatics*, 21(9):2027–2035, 2005.
- [298] Jakob Hull Havgaard, Rune B. Lyngsø, Gary D. Stormo, and Jan Gorodkin. Pairwise local structural alignment of rna sequences with sequence similarity less than 40%. *Bioinformatics*, 21(9):1815–1824, 2005.
- [299] Celine A. Hayden, Travis J. Wheeler, and Richard A. Jorgensen. Evaluating and improving cdna sequence quality with cqc. *Bioinformatics*, 21(24):4414–4415, 2005.
- [300] Quan-Yuan He, Jing Cao, Xiang-Hua Liu, Miao-Xin Li, Yi-Song Liu, Jin-Yun Xie, and Song-Ping Liang. Depd: A novel database for differentially expressed proteins. *Bioinformatics*, 21(18):3694–3696, 2005.