

University of Groningen

Genetical genomics with Affymetrix gene expression arrays

Alberts, Rudi

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version

Publisher's PDF, also known as Version of record

Publication date:

2007

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Alberts, R. (2007). *Genetical genomics with Affymetrix gene expression arrays*. s.n.

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Bibliography

- Albers, C. J., Jansen, R. C., Kok, J., Kuipers, O. P. and Van Hijum, S. A. F. T.: 2006, Sim-
age: simulation of dna-microarray gene expression data, *BMC Bioinformatics* **7**, 205.
- Alberts, R., Terpstra, P., Bystrykh, L. V., de Haan, G. and Jansen, R. C.: 2005, A statistical
multiprobe model for analyzing cis and trans genes in genetical genomics experiments
with short-oligonucleotide arrays, *Genetics* **171**, 1437–1439.
- Bolstad, B. M., Irizarry, R. A., Astrand, M. and Speed, T. P.: 2003, A comparison of
normalization methods for high density oligonucleotide array data based on variance
and bias, *Bioinformatics*. **19**, 185–193.
- Breitling, R., Armengaud, P., Amtmann, A. and Herzyk, P.: 2004, Rank products: a
simple, yet powerful, new method to detect differentially regulated genes in replicated
microarray experiments, *FEBS Lett.* **573**, 83–92.
- Brem, R. B., Yvert, G., Clinton, R. and Kruglyak, L.: 2002, Genetic dissection of transcrip-
tional regulation in budding yeast, *Science* **296**, 752–755.
- Bystrykh, L., Weersing, E., Dontje, B., Sutton, S., Pletcher, M. T., Wiltshire, T., Su, A. I.,
Vellenga, E., Wang, J., Manly, K. F., Lu, L., Chesler, E. J., Alberts, R., Jansen, R. C.,
Williams, R. W., Cooke, M. P. and de Haan, G.: 2005, Uncovering regulatory pathways
that affect hematopoietic stem cell function using 'genetical genomics', *Nat.Genet.*
37, 225–232.
- Carninci, P., Kasukawa, T., Katayama, S., Gough, J. and Frith, M. C. e. a.: 2005, The
transcriptional landscape of the mammalian genome, *Science* **309**, 1559–1563.
- Chesler, E. J., Lu, L., Wang, J., Williams, R. W. and Manly, K. F.: 2004, Webqtl: rapid
exploratory analysis of gene expression and genetic networks for brain and behavior,
Nat.Neurosci. **7**, 485–486.
- Cheung, V. G., Spielman, R., Ewens, K., Weber, T., Morley, M. and Burdick, J.: 2005, Map-
ping determinants of human gene expression by regional and genome-wide association,
Nature **437**, 1365–9.
- Consortium, I. H.: 2005, A haplotype map of the human genome, *Nature* **437**, 1299–1320.
- Doss, S., Schadt, E. E., Drake, T. A. and Lusis, A. J.: 2005, Cis-acting expression quanti-
tative trait loci in mice, *Genome Res.* **15**, 681–691.

- Elo, L. L., Lahti, L., Skottman, H., Kylaniemi, M., Lahesmaa, R. and Aittokallio, T.: 2005, Integrating probe-level expression changes across generations of affymetrix arrays, *Nucleic Acids Res.* **33**, e193.
- Fu, J. and Jansen, R. C.: 2005, Optimal design and analysis of genetic studies on gene expression, *submitted*.
- Gautier, L., Cope, L., Bolstad, B. M. and Irizarry, R. A.: 2004, affy-analysis of affymetrix genechip data at the probe level, *Bioinformatics.* **20**, 307–315.
- Gresham, D., Ruderfer, D. M., Pratt, S. C., Schacherer, J., Dunham, M. J., Botstein, D. and Kruglyak, L.: 2006, Genome-wide detection of polymorphisms at nucleotide resolution with a single dna microarray, *Science* **311**, 1932–1936.
- Hughes, T. R., Mao, M., Jones, A. R., Burchard, J., Marton, M. J., Shannon, K. W., Lefkowitz, S. M., Ziman, M., Schelter, J. M., Meyer, M. R., Kobayashi, S., Davis, C., Dai, H., He, Y. D., Stephanians, S. B., Cavet, G., Walker, W. L., West, A., Coffey, E., Shoemaker, D. D., Stoughton, R., Blanchard, A. P., Friend, S. H. and Linsley, P. S.: 2001, Expression profiling using microarrays fabricated by an ink-jet oligonucleotide synthesizer, *Nat.Biotechnol.* **19**, 342–347.
- Irizarry, R. A., Bolstad, B. M., Collin, F., Cope, L. M., Hobbs, B. and Speed, T. P.: 2003, Summaries of affymetrix genechip probe level data, *Nucleic Acids Res.* **31**, e15.
- Irizarry, R. A., Hobbs, B., Collin, F., Beazer-Barclay, Y. D., Antonellis, K. J., Scherf, U. and Speed, T. P.: 2003, Exploration, normalization, and summaries of high density oligonucleotide array probe level data, *Biostatistics.* **4**, 249–264.
- Jansen, R. C.: 2003, Studying complex biological systems using multifactorial perturbation, *Nat.Rev.Genet.* **4**, 145–151.
- Jansen, R. C. and Nap, J. P.: 2001, Genetical genomics: the added value from segregation, *Trends Genet.* **17**, 388–391.
- Jansen, R. C. and Nap, J. P.: 2004, Regulating gene expression: surprises still in store, *Trends Genet.* **20**, 223–225.
- Klose, J., Nock, C., Herrmann, M., Stuhler, K., Marcus, K., Bluggel, M., Krause, E., Schalkwyk, L. C., Rastan, S., Brown, S. D., Bussow, K., Himmelbauer, H. and Lehrach, H.: 2002, Genetic analysis of the mouse brain proteome, *Nat.Genet.* **30**, 385–393.
- Li, Y., Alvarez, O. A., Gutteling, E. W., Tijsterman, M., Fu, J., Riksen, J. A. G., Hazendonk, E., Prins, P., Plasterk, R. H. A., Jansen, R. C., Breitling, R. and Kammenga, J. E.: 2006, Mapping determinants of gene expression plasticity by genetical genomics in *c. elegans*, *Plos Genetics* **2**, e222.
- Liu, G., Loraine, A. E., Shigeta, R., Cline, M., Cheng, J., Valmeekam, V., Sun, S., Kulp, D. and Siani-Rose, M. A.: 2003, Netaffx: Affymetrix probesets and annotations, *Nucleic Acids Res.* **31**, 82–86.
- Lockhart, D. J., Dong, H., Byrne, M. C., Follettie, M. T., Gallo, M. V., Chee, M. S., Mittmann, M., Wang, C., Kobayashi, M., Horton, H. and Brown, E. L.: 1996, Expression monitoring by hybridization to high-density oligonucleotide arrays, *Nat.Biotechnol.* **14**, 1675–1680.

- Manly, K. F., Wang, J. and Williams, R. W.: 2005, Weighting by heritability for detection of quantitative trait loci with microarray estimates of gene expression, *Genome Biol.* **6**, R27.
- Mecham, B. H., Wetmore, D. Z., Szallasi, Z., Sadovsky, Y., Kohane, I. and Mariani, T. J.: 2004, Increased measurement accuracy for sequence-verified microarray probes, *Physiol Genomics* **18**, 308–315.
- Morley, M., Molony, C. M., Weber, T. M., Devlin, J. L., Ewens, K. G., Spielman, R. S. and Cheung, V. G.: 2004, Genetic analysis of genome-wide variation in human gene expression, *Nature* **430**, 743–747.
- Naef, F. and Magnasco, M. O.: 2003, Solving the riddle of the bright mismatches: labeling and effective binding in oligonucleotide arrays, *Phys.Rev.E.Stat.Nonlin.Soft.Matter Phys.* **68**, 011906.
- Peirce, J., Li, H., Wang, J., Manly, K., Hitzemann, R., Belknap, J., Rosen, G., Goodwin, S., Sutter, T., Williams, R. and Lu, L.: 2006, How replicable are mrna expression qtl?, *Mamm.Genome* **17**.
- Petretto, E., Mangion, J., Dickens, N. J., Cook, S. A., Kumaran, M. K., Lu, H., Fischer, J., Maatz, H., Kren, V., Pravenec, M., Hubner, N. and Aitman, T. J.: 2006, Heritability and tissue specificity of expression quantitative trait loci, *PLoS.Genet.* **2**.
- Pontius, J. U., Wagner, L. and Schuler, G. D.: 2002, National Library of Medicine, Bethesda (MD), chapter UniGene: A Unified View of the Transcriptome, pp. 21–1–21–12.
- Pruitt, K., Tatusova, T. and Ostell, J.: 2002, National Library of Medicine, Bethesda (MD), chapter The Reference Sequence (RefSeq) Project, pp. 18–1–18–20.
- Rockman, M. V. and Kruglyak, L.: 2006, Genetics of global gene expression, *Nat.Rev.Genet.* **7**, 862–872.
- Rostoks, N., Borevitz, J. O., Hedley, P. E., Russell, J., Mudie, S., Morris, J., Cardle, L., Marshall, D. F. and Waugh, R.: 2005, Single-feature polymorphism discovery in the barley transcriptome, *Genome Biol.* **6**.
- SantaLucia, J., J.: 1998, A unified view of polymer, dumbbell, and oligonucleotide dna nearest-neighbor thermodynamics, *Proc.Natl.Acad.Sci.* **95**, 1460–5.
- Schadt, E. E., Monks, S. A., Drake, T. A., Lusk, A. J., Che, N., Colinayo, V., Ruff, T. G., Milligan, S. B., Lamb, J. R., Cavet, G., Linsley, P. S., Mao, M., Stoughton, R. B. and Friend, S. H.: 2003, Genetics of gene expression surveyed in maize, mouse and man, *Nature* **422**, 297–302.
- Sharov, A. A., Dudekula, D. B. and Ko, M. S.: 2005, Genome-wide assembly and analysis of alternative transcripts in mouse, *Genome Res.* **15**, 748–754.
- Swertz, M. A., De Brock, E. O., Van Hijum, S. A., De, J. A., Buist, G., Baerends, R. J., Kok, J., Kuipers, O. P. and Jansen, R. C.: 2004, Molecular genetics information system (molgenis): alternatives in developing local experimental genomics databases, *Bioinformatics.* **20**, 2075–2083.

- Wang, J., Williams, R. W. and Manly, K. F.: 2003, Webqtl: web-based complex trait analysis, *Neuroinformatics*. **1**, 299–308.
- Wolfinger, R. D., Gibson, G., Wolfinger, E. D., Bennett, L., Hamadeh, H., Bushel, P., Afshari, C. and Paules, R. S.: 2001, Assessing gene significance from cDNA microarray expression data via mixed models, *J.Comput.Biol.* **8**, 625–637.
- Wu, C. C., Huang, H. C., Juan, H. F. and Chen, S. T.: 2004, Genenetwork: an interactive tool for reconstruction of genetic networks using microarray data, *Bioinformatics*. **20**, 3691–3693.
- Yang, Y. H., Dudoit, S., Luu, P. and Speed, T. P.: 2001, chapter Normalization for cDNA microarray data, pp. 141–152.
- Yvert, G., Brem, R. B., Whittle, J., Akey, J. M., Foss, E., Smith, E. N., Mackelprang, R. and Kruglyak, L.: 2003, Trans-acting regulatory variation in *saccharomyces cerevisiae* and the role of transcription factors, *Nat.Genet.* **35**, 57–64.
- Zhang, J., Finney, R. P., Clifford, R. J., Derr, L. K. and Buetow, K. H.: 2005, Detecting false expression signals in high-density oligonucleotide arrays by an in silico approach, *Genomics* **85**, 297–308.
- Zhang, L., Miles, M. F. and Aldape, K. D.: 2003, A model of molecular interactions on short oligonucleotide microarrays, *Nat.Biotechnol.* **21**, 818–821.
- Zhang, Z., Schwartz, S., Wagner, L. and Miller, W.: 2000, A greedy algorithm for aligning dna sequences, *J.Comput.Biol.* **7**, 203–214.