Analysis of metabolomics data from twin families
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Bibliography


42. Kriegel, H, Kröger, P, and Zimek, A. Clustering high-dimensional data: a survey on subspace clustering, pattern-based clustering, and correlation clustering. *ACM Transactions on knowledge discovery from data* 2009:3(1, article 1 (58 pages)).


Bibliography

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tir, U, Gretarsdottir, S, Magnusson, K, Stefansson, H, Fossdal, R, Krist-
jansson, K, Gislason, H, Stefansson, T, Leifsson, B, Thorsteinsdottir, U,
452(7186), 423–428.
57. Manolio, T, Collins, F, Cox, N, Goldstein, D, Hindorff, L, Hunter, D,
McCarthy, M, Ramos, E, Cardon, L, Chakravarti, A, Cho, J, Guttmacher,
A, Kong, A, Kruglyak, L, Mardis, E, Rotimi, C, Slatkin, M, Valle, D,
Whittemore, A, Boehnke, M, Clark, A, Eichler, E, Gibson, G, Haines, J,
Mackay, T, McCarthy, S, and Visscher, P. Finding the missing heritability
58. Maher, B. Personal genomes: The case of the missing heritability. *Nature*
2008:456(7218), 18–21.
59. Manolio, T. Genomewide association studies and assessment of the risk
60. Donnelly, P. Progress and challenges in genome-wide association studies
61. Visscher, PM, Yang, J, and Goddard, ME. A commentary on ‘common
SNPs explain a large proportion of the heritability for human height’ by
62. Yang, J, Benyamin, B, McCarthy, M, Gordon, S, Henders, AK, Nyholt,
DR, Madden, PA, Heath, AC, Martin, NG, Montgomery, GW, Goddard,
ME, and Visscher, PM. Common SNPs explain a large proportion of the
63. Manolio, T, Brooks, L, and Collins, F. A HapMap harvest of insights into
64. Sebastiani, P, Timofeev, N, Dworkis, D, Perls, T, and Steinberg, M.
Genome-wide association studies and the genetic dissection of complex
66. Hardy, J and Singleton, A. Genomewide association studies and human
67. Bourgain, C, Genin, E, Cox, N, and Clerget-Darpoux, F. Are genomewide
association studies all that we need to dissect the genetic component of
68. Thomas, D. Gene-environment-wide association studies: emerging
69. Martin, N, Boomsma, D, and Machin, G. A twin-pronged attack on
70. Fischer, K, Bot, A, Zwaan, B, and Brakefield, P. Genetic and environ-
mental sources of egg size variation in the butterfly *Bicyclus anynana.*
71. van der Greef, J, Davidov, E, Verheij, E, Vogels, J, van der Heijden, R,
Adourian, A, Oresic, M, Marple, E, and Naylor, S. The role of metabolom-


95. Sokal, R. Distance as a measure of taxonomic similarity. *Systematic zoology* 1961:10, 70–79.


115. Steinmetz, V, Sévilla, F, and Bellon-Maurel, V. A methodology for sensor


142. Angoff, W. Scales, norms, and equivalent scores. In Thorndike, R, editor,


156. Draisma, H, Reijmers, T, van der Kloet, F, Bobeldijk-Pastorova, I, Spies-Faber, E, Vogels, J, Meulman, J, Boomsma, D, Van der Greef, J, and Han-
kemeier, T. Equating, or correction for between-block effects with application to body fluid LC-MS and NMR metabolomics data sets. Anal. Chem. 2010:82(3), 1039–1046.


