Meta-analysis and Combining Information in Genetics

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1 Introduction

1.1 A Primer of Meta-analysis and Combining Information

Authors: David Allison (Alabama), Rudy Guerra (Rice)

1.2 Statistical Genetics

Authors: Rudy Guerra (Rice)

1.3 Bioinformatics and Proteomics

Authors: Hongyu Zhao (Yale)

2 Microarrays

2.1 Meta-analysis or combining data?

Authors: Darlene Goldstein (Ecole Polytechnique Federale de Lausanne)

2.2 Using partial probe-sets to pool information across microarray studies using using different Affymetrix chip types

Authors: J.S. Morris, L. Zhang, C. Wei, K.A. Baggerly, K.R. Coombes (MD Anderson Cancer Center)

2.3 Statistical analysis of Affymetric cross-generation microarray chips

Authors: R. Guerra and J. Noyola-Martinez (Rice)

2.4 Local pooled error for differential gene expression

Authors: Jae K. Lee (University of Virginia School of Medicine)

2.5 Significance testing for small microarray experiments

Authors: C.L. Kooperberg, A. Aragaki, A.D. Strand, J.M. Olson (Fred Hutchinson Cancer Research Center)

2.6 Composite hypothesis testing from multiple experiments: An approach built on intersection-union tests and Bayesian posterior probabilities

Authors: Kim, K. and Allison, D.B. (Alabama)

3 Gene Mapping

3.1 Utilizing information from multiple genome scans in an empirical Bayes framework for strengthening inferences and narrowing QTL location estimates

Authors: Zhang, K. (Alabama), Beasley, T.M. (Alabama), Weiner, H. (Alabama), Amos, C.I. (MD Anderson) Allison, D.B. (Alabama)

3.2 Meta-analysis methods for genomewide linkage studies

Authors: Cathryn Lewis (Kings College, UK)

3.3 Combining information about population structure and demography with linkage disequilibrium to map a complex genetic disease

Authors: B. Peng (Statistics, Rice), W. Amos (Cambridge), F. Balloux (Cambridge), M. Kimmel (Rice)

3.4 Comparative analysis of meta-analytic methods for genome scans: A case study in blood pressure and obesity

Authors: R. Cooper et al. (Loyola University Medical Center) (maybe with Hirschhorn et al, Harvard)

3.5 Strategies for pooling evidence for linkage from GenomEUtwin scans

Authors: J.C. van Houwelingen and J. Lebrec (Leiden University Medical Centre)

3.6 Combining information across genome screens

Authors: Carol Etzel (MD Anderson Cancer Center)

4 Combining Different Data Types

4.1 Pathway estimation by combining gene expression and protein-interaction data

Authors: H. Zhao et al. (Yale School of Medicine)

4.2 Expression Trait Loci: SNPs and Gene Expression

Authors: Christina Kendziorski (Wisconsin)

4.3 Combining genomic data in human studies

Authors: Debashis Ghosh, Hyungwon Choi, Ronglai Shen (Biostatistics,U Michigan), Dan Rhodes (Pathology/Bioinformatics, UM) and Arul Chinnaiyan (Pathology, UM)

4.4 The genetic basis of time-course gene expression

Authors: B. Christian and R. Guerra (Rice)

5   Proteomics

5.1   Gene-ontology for cross-species/cross-platform list comparisons

Authors: C. Shaw (Baylor College of Medicine)

5.2   Integrated approaches for protein function prediction

Authors: Tim Ting Chen and Fengzhu Sun (University of Southern California)

5.3   Phylogenetic networks from combining gene trees

Authors: Luay Nikhaleh (Rice) and Hideki Innan (University of Texas, Houston)

5.4   From DNA to organisms: integrating comparative and functional genomic data

Author: C.I. Castillo-Davis (Harvard)