

Table of Contents

Trisomic Phase Inference	1
<i>A.G. Clark, E.T. Dermitzakis, S.E. Antonarakis</i>	
An Overview of Combinatorial Methods for Haplotype Inference	9
<i>D. Gusfield</i>	
A Survey of Computational Methods for Determining Haplotypes	26
<i>B.V. Halldórsson, V. Bafna, N. Edwards, R. Lippert, S. Yooseph, S. Istrail</i>	
Haplotype Inference and Its Application in Linkage Disequilibrium Mapping	48
<i>T. Niu, X. Lu, H. Kang, Z.S. Qin, J.S. Liu</i>	
Inferring Piecewise Ancestral History from Haploid Sequences	62
<i>R. Schwartz, A.G. Clark, S. Istrail</i>	
Haplotype Blocks in Small Populations	74
<i>E.A. Thompson, N.H. Chapman</i>	
Simulating a Coalescent Process with Recombination and Ascertainment	84
<i>Y. Wang, B. Rannala</i>	
Dynamic Programming Algorithms for Haplotype Block Partitioning and Tag SNP Selection Using Haplotype Data or Genotype Data	96
<i>K. Zhang, T. Chen, M.S. Waterman, Z.S. Qin, J.S. Liu, F. Sun</i>	
Parametric Bootstrap for Assessment of Goodness of Fit of Models for Block Haplotype Structure	113
<i>M. Zheng, M.S. McPeck</i>	
A Coalescent-Based Approach for Complex Disease Mapping	124
<i>S. Zöllner, J.K. Pritchard</i>	
Abstracts	
Haplotyping as Perfect Phylogeny	131
<i>V. Bafna, D. Gusfield, G. Lancia, S. Yooseph</i>	
Exhaustive Enumeration and Bayesian Phase Inference	132
<i>A. Clark</i>	
How Does Choice of Polymorphism Influence Estimation of LD and Mapping?	133
<i>N. Cox</i>	

VIII Table of Contents

Haplotype Inference in Random Population Samples	134
<i>D. Cutler</i>	
Bayesian Methods for Statistical Reconstruction of Haplotypes	135
<i>P. Donnelly</i>	
Combinatorial Approaches to Haplotype Inference	136
<i>D. Gusfield</i>	
Large Scale Recovery of Haplotypes from Genotype Data Using Imperfect Phylogeny	137
<i>E. Halperin</i>	
Haplotype Inference and Haplotype Information	138
<i>J. Liu</i>	
Multi-locus Linkage Disequilibrium and Haplotype-Based Tests of Association	139
<i>D. Nielsen</i>	
The Pattern of Polymorphism on Human Chromosome 21	140
<i>M. Nordborg</i>	
Use of a Local Approximation to the Ancestral Recombination Graph for Fine Mapping Disease Genes	141
<i>J. Pritchard, S. Zöllner</i>	
Insights into Recombination from Patterns of Linkage Disequilibrium	142
<i>M. Przeworski</i>	
Joint Bayesian Estimation of Mutation Location and Age Using Linkage Disequilibrium	143
<i>B. Rannala</i>	
Evolutionary-Based Association Analysis Using Haplotype Data	144
<i>K. Roeder</i>	
Inferring Piecewise Ancestral History from Haploid Sequences	145
<i>R. Schwartz</i>	
Testing for Differences in Haplotype Frequencies in Case-Control Studies .	146
<i>M. Slatkin</i>	
Haplotypes, Hotspots, and a Multilocus Model for Linkage Disequilibrium	147
<i>M. Stephens</i>	
Dynamic Programming Algorithms for Haplotype Block Partition and Applications to Association Studies	148
<i>F. Sun</i>	

Genome Sharing in Small Populations 149
E. Thompson

Patterns of Linkage Disequilibrium across Human Chromosomes 6, 21,
 AND 22 150
F. de la Vega

A Software System for Automated and Visual Analysis of Functionally
 Annotated Haplotypes 151
J. Zhang

Assessment of Goodness of Fit of Models for Block Haplotype Structure . 152
M. Zheng, M.S. McPeck

Author Index 153



<http://www.springer.com/978-3-540-21249-2>

Computational Methods for SNPs and Haplotype
Inference

DIMACS/RECOMB Satellite Workshop, Piscataway, NJ,
USA, November 21-22, 2002, Revised Papers

Istrail, S.; Waterman, M.; Clark, A. (Eds.)

2004, X, 158 p., Softcover

ISBN: 978-3-540-21249-2