Book reviews, discussion contributions, letters and abstracts
Elizabeth Thompson

Book reviews
B7. (199?). DNA markers. B. S. Weir (ed.)

Discussion Contributions.
C12 (1994) Letter to the NRC Committee on DNA Forensic Science: An Update.

Abstracts.
A10. (1983); Evolutionary Trees; Biometric Society. Dec.’82.

1986:
Int. Biometrics Conference; Seattle WA; July; abstract C-20.2;
Likelihood inference of genealogical relationships.
ASA Annual meetings ; Chicago USA; August; invited paper;
Partial and conditional likelihoods in pedigree analysis.
ASHG Annual meeting (Philadelphia; Nov), AJHG 39 (Supplement). abstracts; (all three accepted for presentation)

1987
Annual Mathematical Genetics Meeting (Sussex, England; March)
Likelihood and crossover counts in multipoint linkage analysis.
Information for Interference (With Tim Bishop)

1988:
WNAR, Hawaii, June.
Gene identity at two and three loci.
International Congress of Genetics, Toronto, August.
Multilocus kinship in pedigrees.
ASHG; New Orleans, October; (Thompson and Morgan)
Recursive descent probabilities for the ancestry of recessive lethals.

1989
AAPA, San Diego, April; (Morgan and Thompson)
Analysis of complex genealogies of the Hutterite Brethren.
ASHG, November; (Sheehan, Possolo and Thompson)
Image processing methods applied to the inference of genotypes on pedigrees.
Abstract #0975, A248, AJHG.

1990
ASA local chapter meeting, Seattle; February.
R.A. Fisher's contributions to statistical genetics.
International Biometric Conference, Budapest, Hungary; July.
R.A. Fisher's contributions to statistical genetics.

1991

1992
S Lin, EA Thompson, and EM Wijsman
Multiple alleles and Markov chain Monte Carlo methods in genetic analysis.

1993.

1994.
H Li and EA Thompson,
Modeling age of onset: Cox model with latent major gene effects.
Am J Hum Genet
EA Thompson and EM Wijsman,
Multilocus homozygosity mapping and autozygosity probabilities.
Am J Hum Genet

1995:
Charles J. GEYER and Elizabeth A. THOMPSON
Annealing Markov Chain Monte Carlo with Applications to Ancestral Inference
Joint Statistical Meetings; Orlando, Florida; IMS invited paper.

1996:
Inferring gene descent and ancestry; complicated but not uninteresting
Neyman Lecture, IMS; Joint Statistical Meetings, Chicago.
Estimation of gene identity and inference of gene ancestry.
Invited talk (IMS); Bernoulli Society World Congress.

1997:
Gene identity in individuals affected for complex traits
Invited paper: Joint AMS-IMS-SIAM Summer Conference on Statistics in Molecular Biology
MCMC samplers for multilocus analyses on complex pedigrees.
S.C.Heath and E.A.Thompson
Am J Hum Genet, 61, A278.
Disequilibrium Mapping via Coalescent Models of Gene Ancestry
J. Graham and E. A. Thompson
Am J Hum Genet, 61, A
Theoretical perspectives:
sampling designs, genetic scale, and locus specificity.
Invited paper, NIGMS workshop, December 1997
1998:
Realizing the history of a disease allele, and why it’s useful to do so.
PNWWMB, Friday Harbor, WA: March 1998
Computational approaches to likelihoods on pedigrees
Stochastic models and statistical analysis of descent of DNA in pedigrees.
Fine scale disequilibrium mapping from realized allelic ancestries
E. A. Thompson and J. Graham, WNAR annual meeting, June 1998
Stochastic models and statistical analysis of descent of DNA in pedigrees
PMMB SHort Course abstract; Berkeley, CA. June 1998.

1999:
The role of population size and structure.
N. H. Chapman and E. A. Thompson
Invited paper: N.E.Morton Symposium, St. Louis, MO; Sept 1999
Validation of pedigree data in the presence of genotyping error.
Kumm, J., Browning, S., and Thompson, E. A.
Am J. Hum Genet: 65: Suppl; A208 (1147)
Interference in the analysis of genetic marker data.
Browning, S. and Thompson, E. A.,
Am J. Hum Genet: 65: Suppl; A244 (1356)
A score for MCMC genome screening
Daw, E.W., Thompson, E. A., and Wijsman, E. M.
Am J. Hum Genet: 65: Suppl; A247 (1371)
Multipoint linkage analysis of complex traits with Markov chain Monte Carlo linkage analysis
Snow, G., Wijsman, E., Thompson, E., and Heath, S.
Am J. Hum Genet: 65: Suppl; A446 (2532)
Conditional genome sharing from dense marker maps
Invited Paper: Mathematical Genetics and Genomics Symposium, CMS Winter Meeting, Montreal, December 1999
Identity by descent in linkage detection for complex traits.
International Congress on Psychiatric Genetics, Monterey CA, October 1999.

2000:
A century of genetic linkage analysis.
Thompson EA
ENAR: special invited talk, March 2000
Population history affects the expected number of ancestral chromosome segments.
Chapman NC, Crumley J, Fujiwara TM, Morgan K, and Thompson EA.
Am J. Hum Genet: 67: Suppl;
Monte Carlo Likelihood for genetic analyses, and
Coalescents, phylogenies, and disequilibrium mapping
PMMB Summer School, Berkeley, CA, June 2000
PMMB/MSRI Workshop, June 24-26, 2000
2001

The importance of undetected relationships in linkage studies
Leutenegger A-L, Genin E, Thompson EA, Clerget-Darpoux F.
IGES, Garmisch, Germany, September 2001. Genetic Epidemiology 21:164

Estimation of small map distances using chromosome data from an isolated population.
Chapman NC, Crumley J, Fujiwara TM, Morgan K, and Thompson EA.
ASHG, San Diego, October 2001

Monte Carlo methods for the calculation of likelihoods in genetic linkage studies.
George AW, Bogdan M, Wijsman EM, Thompson EA
ASHG, San Diego, October 2001

Relationship inference from trios of individuals in the presence of typing error.
Sieberts SK, Wijsman EM and Thompson EA,
ASHG, San Diego, Oct 2001

2002

Relationship inference from trios of individuals in the presence of typing error.
Sieberts SK, Wijsman EM and Thompson EA
PMMB, Santa Fe, January 2002.

Markov chain Monte Carlo methods for lod score estimation
Stewart W, George AW and Thompson EA
PMMB, Santa Fe, January 2002

Caution in applying the Maximum Lod Score affected sib-pair method in inbred populations
Leutenegger A-L, Genin E, Thompson EA, Clerget-Darpoux F.
EMGM-30, Sheffield UK, April 2002

A new Monte Carlo approach to Multipoint LOD scores
George, A. W. and Thompson E. A.
WNAR. Los Angeles, CA. June 2002

Estimating Multipoint LOD scores using Monte Carlo on pedigrees
Thompson E. A. and George, A. W.
IBC. Freiburg, Germany, July 2002

Allele-sharing methods on large pedigrees.
S. Basu, E. M. Wijsman, and E. A. Thompson,

Detecting disease genes via a new Markov chain Monte Carlo approach for multipoint linkage analysis.
George AW, Wijsman EM, Thompson EA

Estimation of the inbreeding coefficient from multipoint marker data.
Leutenegger A-L, Prum B, Clerget-Darpoux F, Thompson EA

Gene IBD and the mapping of complex traits.
NCSU Cockerham Symposium: Oct 2002

Weldon Lecture: Oct 2002

Cold Spring Harbor Symposium on Sequence Diversity in Plants Banbury Center, Cold Spring Harbor: November 2002

Genome sharing in small populations
DIMACS workshop on Computational Methods for SNPs and Haplotype Inference.  
DIMACS Center, Rutgers University. November 2002

2003: Detection of linkage via genomic ibd imputation  
Workshop on Genetic Architecture of Complex Traits  
Oberwolfach, Germany, February 2002

UNC: Feb 2003

Glaxo March 2003

Monte Carlo Estimation of Likelihood Functions:  
the example of multipoint linkage lod scores.  
Duke University, ISDS, March 2003

1) Linkage detection for complex traits.  
2) Monte Carlo Estimation of Likelihood Functions:  
the example of multipoint linkage lod scores.  
Allen T. Craig Lectures, University of Iowa, April 2003

Statistical Genetics in the Post-Genome Era  
University of Washington Science Forum Lectures: May 2003

Melbourne, July 2003

ISI: August 2003

UW StatGen Workshop 2003

Dec AIC2003: Japan

2004:

Jan: COMBI

Feb: UCLA

Feb: MSRI

March?: UW Medical Genetics

March: Singapore

April: Minnesota

June NCSU Summer Inst.

July 11-16: IBC, Cairns Australia  
   Session on Genetic Association Studies (Invited Discussant)  
   Aug 7-12: Banff Center workshop on Stochastic Processes in Evolution and Disease  
   Genealogy and genome sharing in diploid populations. 2005 Jan 24: Dept seminar,  
   Statistics UW  
   Fuzzy P-values and the detection of genetic linkage Feb 25: Mary Cartwright Lecture, London Mathematical Society (London, UK)
Relatedness, genome sharing, and the detection of genes. Apr 19: Sobel Lecture, Dept Statistics, Univ. California Santa Barbara
Fuzzy p-values in the detection of genetic linkage