

## Book reviews, discussion contributions, letters and abstracts

Elizabeth Thompson

### Book reviews

- B1. (1976) The Genetic Structure of Populations, by A. Jacquard. *Bull. Math.* **38**, 323-324
- B2. (1978) A First Course in Population Genetics, by C.C. Li. *Ann. Hum. Genet.*
- B3. (1982) Taxonomy and Behavioral Science, by J.E. Mezzich and H. Solomon. *Ann. Hum. Biol.* **9**, 185-6.
- B4. (1983). Essays in Statistical Science. J. Gani and E.J. Hannan eds. *Biometrics*, **39**, 300.
- B5. (1985). Family Studies in Genetic Disorders. Krush and Evans. *Heredity*,
- B6. (1986). Analysis of Human Genetic Linkage, by J. Ott. *Ann. Hum. Biol.*
- B7. (199??). DNA markers. B. S. Weir (ed.)
- B8. (1998). Mathematical and Statistical Methods for Genetic Analysis  
by K. Lange (Springer-Verlag, 1997)  
For Bulletin of Mathematical Biology, Harcourt Brace and Co.

### Discussion Contributions.

- C1. (1976). To: Plausibility Inference, by O. Barndorff-Nielsen. *J.R.S.S.(B)*, **38**, 127.
- C2. (1977). To: The settlement of Iceland, by L.P. Saugstad. *N.A.R.* **10**, 74-76.
- C3. (1977). To: Maximum likelihood from incomplete data via the E.M. algorithm, by A.P. Dempster et al. *J.R.S.S.(B)*, **39**, 33-34.
- C4. (1977). To: The settlement of Iceland, by L.P. Saugstad. *N.A.R.* **11**, 57-58.
- C5. (1979). Letters; The Icelandic admixture problem. *Review of Ethnology*.
- C6. (1980). Vote of thanks to: Genetic algebras, by P. Holgate. *J.R.S.S.(B)*, **43**, 14-15.
- C7. (1983) To: Inferring Phylogenies; J. Felsenstein, *JRSS(A)*, **146**, 265-6.
- C8. Raftery A. and Thompson E.A. (1988). How many nuclear reactor accidents? Letters, *J. Statist. Comp. and Sim.*; **29**, 347-350.
- C9. Raftery, A.E. and Thompson, E.A. (1990). What is the probability of a serious nuclear reactor accident? Letters, *J. Statist. Comp. and Sim.*; **36**, 31-34.
- C.10 (1993). Lin, S and Thompson E.A.  
Discussion contribution to RSS papers on Markov chain Monte Carlo.  
*JRSS (B)* 55; 82-83.
- C.11 (2000). Discussion contribution to Stephens, M. and Donnelly, P., Inference in molecular population genetics. *JRSS(B)* 62: 649

### Abstracts.

- A1. (1977). Human evolutionary trees. *Biometrics*, **33**, 276.
- A2. (1977). Pedigree structure and linkage. *Amer. J. Hum Genet.* **29**, 64A.
- A3. (1978). Probabilities on pedigrees and genotypes of ancestors. *Heredity*, **41**, 125.
- A4. (1978). Probability functions on complex pedigrees. *Biometrics*, (WNA).
- A5. (1978). Some genetic models for the analysis of human pedigrees. *Biometrics*, (WNA).
- A6. (1978). Probabilities on pedigrees and the ancestral origins of traits. *J.A.S.A.*
- A7. (1981). Impossible combinations of gene correlations. *Adv. Appl. Prob.* **13**, 8-9.
- A8. (1981). Thompson and Suter. Regional migration in the Faroe Islands; inferences from genetic data. *S.S.H.B 50 th. General Meeting*, 6-7.

- A9. (1981). Marshall and Thompson. Inferring the existence of a Hodgkin's disease gene in north west Newfoundland. *6 th. Int. Congr. Hum, Genet; Jerusalem. (Progress in Clin. & Biomed. Res., 103, B, 141-142.*
- A10. (1983); Evolutionary Trees; Biometric Society. Dec.'82.
- A11. (1983). Joint linkage analysis. Int. Conf. on medical statistics; Basel.
- A12. (1983). Gene identity. London Mathematical Society one day meeting; invited paper.
- A13. (1984). Genealogical relationships. British Mathematical Colloquium; invited paper; Bristol, April.
- A14. (1984). Likelihood and parsimony. Hennig IV conference; invited paper; London, July.
- A15. (1984). The genes of the founders of Tristan da Cunha. British Association for the Advancement of Science; invited paper; UEA, Sept.
- A16. (1984). Sensitivity LOD scores to a single recombinant observation: linkage of a breast cancer gene to the ABO locus. *Am.J.Hum.Genet. 36 (supplement), 181S.*

**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)
- Thompson E.A. A scoring algorithm for ordering multiple loci. A170.
- Bishop D.T. and Thompson E.A. Information and bias in the presence of interference. A148.
- Goldgar D.E. and Thompson E.A. An interval estimation approach to paternity testing. A235.

**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.  
Am J Hum Genet 51:A14.

**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

Invited paper: CRM Montreal: Workshop on Complex Traits. May 1998.

Stochastic models and statistical analysis of descent of DNA in pedigrees.

Invited paper: Purdue Symposium on Statistical Genetics. June 1998.

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

Linkage Analysis: Past, Present and Future.

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 200: 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,

IGES, New Orleans, Nov 2002. Genetic Epidemiology 23: 267.

Detecting disease genes via a new Markov chain Monte Carlo approach for multipoint linkage analysis.

George AW, Wijsman EM, Thompson EA

IGES, New Orleans, Nov 2002. Genetic Epidemiology 23: 283.

Estimation of the inbreeding coefficient from multipoint marker data.

Leutenegger A-L, Prum B, Clerget-Darpoux F, Thompson EA

IGES, New Orleans, Nov 2002. Genetic Epidemiology 23: 292.