Book reviews, discussion contributions, letters and abstracts

Elizabeth Thompson

Book reviews

B1. (1976) The Genetic Structure of Populationsi, by A. Jacquard. Biol.*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.

C10 (1992) Expert Report to Superior State Court of State of Washington.
Kelly-Frye hearing on Hollis case.

C.11 (1993). Lin, S and Thompson E.A.
Discussion contribution to RSS papers on Markov chain Monte Carlo.
JRSS (B) 55; 82-83.

C12 (1994) Letter to the NRC Committee on DNA Foresic Science: An Update.
Letter send to Professor J.F.Crow (Chair) after the NRC meeting.

C.13 (2000). Discussion contribution to Stephens, M. and Donnelly, P., Inference in molecular population genetics. JRSS(B) 62: 649

Abstracts.

A0. (1975) Multiple gene identities *Adv. Appl. Prob.* **7,** 26-27.

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. OR,*Biometrics,(WNAR,*Eugene, A5. (1978). Some genetic models for the analysis of human pedigrees. *Biometrics,(WNAR).*

A6. (1978). Probabilities on pedigrees and the ancestral origins of traits. *J.A.S.A.*

A7a. (1979) Extinction Probabilities and Pedigree Structure. *Adv. Appl. Prob.* **11,** 12-13.

A7b. (1980) Sequential sampling schemes for sibships. *Adv. Appl. Prob.* **12,** 10-11.

A7c. (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; Jerumsalem. (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:

E. A. Thompson
Inference of the conditional independence structure of dependent binary data
For DIMACS meeting, Princeton University, February 1995. (3-page summary).

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 Habor, 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 om Statistical Genetics. June 1998.

Fine scale disequilibrium mapping from realized allelic ancestries
E. A. Thompson and J. Graham, WNAR annual meeting, UCSD, June 1998

Stochastic models and statistical analysis of descent of DNA in pedigrees
PMMB SHort Course abstract; Berkeley, CA. June 1998.

1999:

Importance sampling for Monte Carlo Evaluation of the likelihood for effective population size
 E. C. Anderson, E. A. Thompson and E.G. Williamson; WNAR annual meeting, Seattle, June 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; Program Nr 1271

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: Nr 1336

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: Nr 1337

Relationship inference from trios of individuals in the presence of typing error.
Sieberts SK, Wijsman EM and Thompson EA,
ASHG, San Diego, Oct 2001: Nr 1357

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.

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

2011: Posters at ICHG and ASHG, Montreal Canada

Browning S. R. and E. A. Thompson
Statistical power of population-based linkage analysis

Cheung, C.Y.K., E.A. Thompson, and E. M. Wijsman
Detection of genotyping errors in dense markers on large pedigrees

Thompson, E. A., M. D. Brown, C.G. Glazner and C. Zheng
Inferring coanncestry in the presence of linkage disequilibrium

Thompson, E. A., M. D. Brown, C.G. Glazner and C. Zheng
Inferring coanncestry in population samples in the presence of linkage disequilibrium (Final/draft??)

C. Zheng and E. A. Thompson
Bayesian inference of genealogy from population genomic data by the spatial Markov coalescent with recombination.

Note:

Copies of many of the abstracts from 200 onwards can be found in the files in /Castor_saved_2019/Papers/Abstracts