

Publications are numbered in chronological order. They are listed in reverse chronological order, by category.

Books

160. Thompson, E. A. (2000) *Statistical Inferences from Genetic Data on Pedigrees* NSF-CBMS Regional Conference Series in Probability and Statistics. Volume 6. IMS, Beachwood, OH. (169 pages)
70. Thompson, E.A. (1986). *Pedigree Analysis in Human Genetics*. Johns Hopkins University Press, Baltimore (210 pages).
47. Cannings, C. and Thompson, E.A. (1981). *Genealogical and Genetic Structure*. Cambridge University Press (160 pages).
8. Thompson E.A. (1975). *Human Evolutionary Trees*. Cambridge University Press, Cambridge (158 pages).

Papers in Refereed Journals

206. RoyChoudhury, A., Felsenstein, J., and Thompson, E. A. (2008) A two-stage pruning algorithm for likelihood computation for a population tree. *Genetics*: in press.
204. Basu, S, Di, Y., and Thompson, E. A. (2008) Exact trait-model-free tests for linkage detection in pedigrees. *Annals of Human Genetics*:
Published online: DOI: 10.1111/j.1469-1809.2008.00451.x
203. Bink, M.C.A.M., Anderson, A.D., van de Weg, W.E., and Thompson, E. A. (2008) Comparison of marker-based pairwise relatedness estimators on a pedigreed plant population. *Theoretical and Applied Genetics*: Published online: DOI: 10.1007/s00122-008-0824-1.
201. Thompson, E. A. (2008) The IBD process along four chromosomes. *Theoretical Population Biology* **73**: 369--373.
Published online: <http://dx.doi.org/10.1016/j.tpb.2007.11.011>
200. Tong L. and Thompson, E. A. (2008) Multilocus lod scores in large pedigrees: Combination of exact and approximate calculations. *Human Heredity* **65**: 142--153.
197. Thompson, E. A. (2007) 1953: An unrecognized summit in human genetic linkage analysis. *Statistical Surveys* **1**: 1--15.
195. Thompson, E. A. and Geyer, C. J. (2007) Fuzzy p-values in latent variable problems. *Biometrika* **90**: 49--60.
(Early draft available as Technical report No. 481, Department of Statistics, University of Washington: <http://www.stat.washington.edu/www/research/reports/2005/tr481.pdf>)
194. Sung, Y. J., Thompson, E. A., and Wijsman, E. M. (2006) MCMC-based linkage analysis for complex traits on general pedigrees: multipoint analysis with a two-locus model and a polygenic component. *Genetic Epidemiology* **31**: 103--114.
193. Wijsman, E. M., Rothstein, J. H., and Thompson, E. A. (2006) Multipoint linkage analysis with many multiallelic or dense diallelic markers: Markov chain Monte Carlo provides practical approaches for genome scans on general pedigrees. *American Journal of Human Genetics* **79**: 846--858.
<http://www.journals.uchicago.edu/AJHG/journal/issues/v79n5/43843/43843.html>
191. Stewart, W. C. L. and Thompson, E. A. (2006) Improving estimates of genetic maps: A maximum likelihood approach. *Biometrics* **62**: 728--734.
<http://www.blackwell-synergy.com/doi/pdf/10.1111/j.1541-0420.2006.00532.x>
187. George, A. W., Wijsman, E. M. and Thompson, E. A. (2005) MCMC Multilocus Lod Scores: Application of a New Approach. *Human Heredity*: **59**: 98--108.

184. George, A. W. and Thompson, E. A. (2003) Discovering disease genes: Multipoint linkage analysis via a new Markov Chain Monte Carlo approach. *Statistical Science*: **18**: 515--531.
180. Thompson, E. A. and Basu, S. (2003) Genome sharing in large pedigrees: multiple imputation of *ibd* for linkage detection. *Human Heredity* **56**: 119--125.
177. Leutenegger, A.-L., Prum, B., Genin, E., Verny, C., Lemainque, A., Clerget-Darpoux, F., and Thompson, E. A. (2003) Estimation of the inbreeding coefficient through use of genomic data. *American Journal of Human Genetics* **73**: 516--523.
176. Chapman, N.H. and Thompson E.A. (2003) A model for the length of tracts of identity by descent in finite random mating populations. *Theoretical Population Biology* **64**: 141--150.
175. Daw, E.W., Thompson, E.A., and Wijsman, E. M (2003) A Score for Bayesian genome screening. *Genetic Epidemiology* **24**: 181--190.
174. Leutenegger, A-L., Genin, E., Thompson, E.A., and Clerget-Darpoux, F. (2002) Impact of parental relationships in maximum lod score affected sib-pair method. *Genetic Epidemiology* **23**: 413--425.
173. Chapman, N.H. and Thompson E.A. (2002) The effect of population history on the lengths of ancestral chromosome segments. *Genetics* **162**: 449--458.
168. Anderson, E.C. and Thompson E.A. (2002) A model-based method for identifying species hybrids using multilocus genetic data. *Genetics* **160**: 1217-1229.
167. Sieberts, S., Wijsman, E.M., and Thompson, E. A. (2002) Relationship inference from trios of individuals in the presence of typing error. *American Journal of Human Genetics* **70**: 170--180.
165. Silverman E. D., Kot, M., and Thompson, E.A. (2001). Testing a simple stochastic model for the dynamics of waterfowl aggregations. *Oecologia* **128**: 608--617 (<http://link.springer.com/link/service/journals/00442/contents/01/00684/>)
163. Anderson, E.C., Williamson, E.G., and Thompson, E.A. (2000). Monte Carlo evaluation of the likelihood for N_e from temporally spaced samples *Genetics* **156**, 2109--2118.
162. Daw, E.W., Thompson, E. A., and Wijsman, E. M. (2000). Bias in multipoint linkage analysis arising from map misspecification. *Genetic Epidemiology* **19**, 366--380.
158. Graham, J. and Thompson, E. A. (2000). A coalescent model of ancestry for a rare allele. *Genetics* **156**, 375--384.
156. Thompson, E. A. (2000). MCMC estimation of multi-locus genome sharing and multipoint gene location scores. *International Statistical Review* **68**, 53--73.
152. Thompson, E. A. and Meagher T. R. (1998). Genetic linkage in the estimation of pairwise relationship. *Theoretical and Applied Genetics* **97**, 857--864.
150. Graham, J. and Thompson, E.A. (1998) Disequilibrium likelihoods for fine-scale mapping of a rare allele. *American Journal of Human Genetics* **63**, 1517--1530.
(Also, Technical report No. 331, Department of Statistics, University of Washington)
148. Li, H., Thompson, E. A., and Wijsman, E.M. (1998). Semiparametric estimation of major gene effects for age of onset. *Genetic Epidemiology* **15**, 279--298.
147. Prohdohl, P.A., Loughry, W.J., McDonough, C.M., Nelson, W.S., Thompson, E.A., and Avise, J.C. (1998) Genetic maternity and paternity in a local population of armadillos assessed by microsatellite DNA markers and field data. *American Naturalist* **151**, 7--19.
146. Thompson, E. A. (1998). Inferring gene ancestry: estimating gene descent. *International Statistical Review* **66**, 29--40.
141. Li, H. and Thompson, E. A. (1997). Semiparametric estimation of major gene and family-specific random effects for age of onset. *Biometrics* **53**, 282--293
139. Thompson, E. A. and Neel, J. V. (1997). Allelic association and allele frequency distribution as a function of social and demographic history. *American Journal of Human Genetics* **60**, 197--204

138. Bickeboller, H. and Thompson, E. A. (1996). Distribution of genome shared IBD by half sibs: approximation via the Poisson clumping heuristic. *Theoretical Population Biology* **50**, 66--90
137. Thompson, E. A. (1996). Likelihood and linkage: from Fisher to the future. (1994 JSM Fisher Lecture.) *Ann. Statist.* **24**, 449--465
135. Bickeboller, H. and Thompson, E. A. (1996) The probability distribution of the amount of an individual's genome surviving to the following generation *Genetics* **143**, 1043-1049
134. Thompson, E. A. and Neel, J. V. (1996). Private Polymorphisms. How many? How old? How useful for genetic taxonomies? *Molecular Phylogenetics and Evolution*: **5**, 220-231
131. Geyer, C. J. and Thompson, E. A. (1995) Annealing Markov chain Monte Carlo with applications to ancestral inference. *Journal of the American Statistical Association* **90**, 909-920.
126. Thompson, E. A. (1994) Monte Carlo likelihood in genetic mapping. *Statistical Science*, **9**, 355-366.
125. Lin, S., Thompson, E. A., and Wijsman, E. M. (1994) An algorithm for Monte Carlo estimation of genotype probabilities on complex pedigrees. *Ann. Hum. Genet.* **58**, 343-357.
124. Thompson, E. A. (1994). Monte Carlo likelihood in the genetic mapping of complex traits. *Phil. Trans. Roy. Soc. (Lond.) Series B* **344**, 345-351.
122. Guo S.W. and Thompson, E. A. (1994). Monte Carlo estimation of mixed models for large complex pedigrees. *Biometrics* **50**, 417-432.
120. Lin, S., Thompson, E. A., and Wijsman, E. M. (1994) Finding non-communicating sets for Markov chain Monte Carlo estimations on pedigrees. *Amer. J. Hum. Genet.*: **54**,695-704.
117. Laikre, L., Ryman, N., and Thompson, E. A. (1993). Hereditary blindness in a captive wolf (*Canis lupus*) population: frequency reduction of a deleterious allele in relation to gene conservation. *Conservation Biology*, **7**, 592-601.
116. Lin, S., Thompson, E. A., and Wijsman, E. M. (1993). Achieving irreducibility of the Markov chain Monte Carlo method applied to pedigree data. *I.M.A. J. Math. Appl. Med. & Biol.*, **10**, 1-17.
114. Geyer, C. J., Ryder, O. A., Chemnick, L. G. and Thompson, E. A. (1993) Analysis of relatedness in the California condors from DNA fingerprints. *Mol. Biol. Evol.*: **10**, 571-589.
112. Guo S.W. and Thompson, E. A. (1992) A Monte Carlo method for combined segregation and linkage analysis. *Amer. J. Hum. Genet.* **51**, 1111-1126.
111. Thompson, E. A., Neel, J. V., Smouse, P. E. and Barrantes, R. (1992). Microevolution of the Chibcha-speaking peoples of lower Central America: rare genes in an Amerindian Complex. *Amer. J. Hum. Genet.* **51**, 609-626.
110. Thompson, E.A. and Shaw, R.G. (1992). Estimating polygenic models for multivariate data on large pedigrees. *Genetics*, **131**, 971-978.
109. Geyer, C.J. and Thompson, E.A. (1992). Constrained Monte Carlo maximum likelihood for dependent data (with Discussion). *J. Roy. Statist. Soc. (B)*, **54**, 657-699.
108. Guo, S-W. and Thompson, E. A. (1992). Performing the exact test of Hardy-Weinberg proportion for multiple alleles. *Biometrics*, **48**, 361-372.
105. Guo, S-W. and Thompson, E. A. (1991). Monte Carlo EM for the estimation of multiple random effects models on large pedigrees. *I.M.A. J. Math. Appl. Med. & Biol.*, **8**, 171-189.
104. Thompson, E. A. and Guo, S-W. (1991). Evaluation of likelihood ratios for complex genetic models. *I.M.A. J. Math. Appl. Med. & Biol.*, **8**, 149-169.
98. Zhao, L P., Thompson, E. A. and Prentice, R. (1990). Joint estimation of recombination fractions and interference coefficients in multilocus linkage analysis. *Amer. J. Hum. Genet.*, **47**, 255-265.

97. Thompson, E. A. (1990). Inference of a gene and its paths of descent: the Newfoundland example. *Amer. J. Hum. Biol.*, **2**, 291-301.
96. Thompson E.A. and Shaw R.G. (1990). Pedigree analysis for quantitative traits; variance components without matrix inversion. *Biometrics*, **46**, 399-414.
94. Geyer C. J., Thompson E. A. and Ryder O. A. (1989). Gene survival in the Asian Wild Horse (*Equus Przewalskii*): II. Gene survival in the whole population, in subgroups, and through history. *Zoo Biology*, **8**, 313-329.
92. Thompson E. A. and Morgan K. (1989). Recursive descent probabilities for rare recessive lethals. *Ann. Hum. Genet.*, **53**, 357-374.
91. Prokosch, H.U., Seuchter, S.A., Thompson, E.A. and Skolnick, M.H. (1989). Applying expert system techniques to human genetics. *Computers and Biomedical Research*, **22**, 234-247.
90. Thompson E.A. (1988). Two-locus and three-locus gene identity by descent in pedigrees. *I.M.A. J. Math. Appl. in Med and Biol.* **5**, 261-280.
88. Geyer C.J. and Thompson E.A. (1988). Gene survival in the Asian Wild Horse (*Equus Przewalskii*): I. Dependence in gene survival in the Calgary Breeding Group pedigree. *Zoo Biology* **7**, 313-327.
87. Bishop D.T. and Thompson, E.A. (1988). Linkage information and bias in the presence of interference. *Genetic Epidemiology*, **5**, 107-120.
84. Goldgar D.E. and Thompson E.A. (1988). Bayesian interval estimation of genetic relationships: application to paternity testing. *Amer. J. Hum. Genet.* **42**, 135-142.
83. Thompson E.A., Deeb S., Walker D., and Motulsky A.G. (1988). The detection of linkage disequilibrium between closely linked markers: RFLPs at the AI-CIII apolipoprotein genes. *Amer. J. Hum. Genet.* **42**, 113-124
82. Thompson E.A. (1987). Likelihoods in pedigree analysis under sequential sampling. *American Journal of Human Genetics*: **41**, 687-689.
81. Thompson E.A. and Meagher T.R. (1987). Parental and sib likelihoods in genealogy reconstruction. *Biometrics*, **43**, 585-600.
80. Meagher T.R. and Thompson E.A. (1987). Analysis of parentage for naturally established seedlings within a population of *Chamaelirium luteum* (Liliaceae). *Ecology*: **68**, 803-812.
78. Thompson E.A. (1987). Crossover counts and likelihood in multipoint linkage analysis. *I.M.A J. of Math. Appl. in Med. and Biol.* **4**, 93-108.
77. Thompson, E.A. (1986). A scoring method for multipoint linkage analysis: application to the Utah-11p data. *Genetic Epidemiology*, **3**, (supplement); 171-176.
76. Thompson, E.A. (1986). Likelihood inference of paternity. *Am. J. Hum. Genet.* **39**, 285-287.
75. Thompson, E.A. (1986). Genetic epidemiology: a review of the statistical basis. *Statistics in Medicine* **5**, 291-302
74. Bishop, M.J. and Thompson, E.A. (1986). Maximum likelihood alignment of DNA sequences. *J. Molec. Biol.* **190**, 159-165.
69. Thompson, E.A. (1986). Ancestry of alleles and extinction of genes in populations with defined pedigrees. *Proceedings of Workshop on Genetic Management of Captive Populations* (August 1984); *Zoo Biology* **5**, 161-170.
68. Thompson, E.A. (1986). Likelihood and parsimony; comparison of criteria and solutions. *Cladistics* **2**, 43-52.
67. Meagher, T.R. and Thompson, E.A. (1986). The relationship between single parent and parent pair genetic likelihoods in genealogy reconstruction. *Theor. Pop. Biol.* **29**, 87-106.
66. Thompson, E.A. (1985). The history of a lethal X-linked mutation. *I.M.A J. of Math. Appl. in Med. and Biol.* **2**, 75-92.

65. Thompson, E.A. and Bishop, D.T. (1985). Alternative explanations of normal variability in Antithrombin-III levels. *Ann. Hum. Biol.* **12**, 339-344.
64. Skolnick, M.H., Thompson, E.A., Bishop, D.T. and Cannon, L. (1984). Possible linkage of a breast-cancer-susceptibility locus to the ABO locus; sensitivity of LOD scores to a single new recombinant observation. *Genetic Epidemiology* **1**, 363-373.
63. Thompson, E.A. (1984). Interpretation of LOD scores with a set of marker loci. *Genetic Epidemiology* **1**, 357-362.
62. Bishop, M.J. and Thompson, E.A. (1984). Fast computer search for similar DNA sequences. *Nucleic Acids Res.* **12**, 5471-5474.
61. Thompson, E.A. (1984). Information gain in joint linkage analysis. *I.M.A J. of Math. Appl. in Med. and Biol.* **1**, 31-50.
60. Thomas, A. and Thompson, E.A. (1984). Gene survival in an isolated population; the number of distinct genes on Tristan da Cunha. *Ann. Hum. Biol.* **11**, 101-111.
59. Thompson, E.A. and Edwards, A.W.F. (1984). The nonequivalence of conditional and unconditional likelihood in multinomial sampling. *Amer. J. Hum. Genet.* **36**, 229-232.
57. Thompson, E.A. (1983). Gene extinction and allelic origins in complex genealogies. *Proc. Roy. Soc. (Lond.) B* **219**, 241-251.
56. Thompson, E.A. (1983). Optimal sampling for pedigree analysis: parameter estimation and genotype uncertainty. *Theor. Pop. Biol.* **24**, 39-58.
55. Thompson, E.A. (1983). A recursive algorithm for inferring gene origins. *Ann. Hum. Genet.* **47**, 143-152.
54. Solomon, P.J., Thompson, E.A. and Rissanen, A. (1983). The inheritance of height in a Finnish population. *Ann. Hum. Biology* **10**, 247-256.
51. Thompson, E.A. (1982). Optimal sampling for pedigree analysis: tracing a rare gene. *Adv. Appl. Prob.* **14**, 752-762.
49. Thompson, E.A. (1981). Optimal sampling for pedigree analysis: relatives of affected probands. *Am. J. Hum. Genet.* **33**, 968-977.
46. Thompson, E.A. (1981). Pedigree analysis of Hodgkin's disease in a Newfoundland genealogy. *Ann. Hum. Genet.* **45**, 279-292.
45. Thompson, E.A. (1981). Optimal sampling for pedigree analysis: sequential schemes for sibships. *Biometrics* **37**, 313-325.
44. Thompson, E.A. (1980). Genetic etiology and clusters in a pedigree. *Heredity* **45**, 323-334.
43. Thompson, E.A. (1980). The gene identity states of a descendant. *Theor. Pop. Biol.* **18**, 76-93.
42. Parker, G.A. and Thompson E.A. (1980). Dung fly struggles: a test of the war of attrition. *Behavioral Ecology and Sociobiology*, **7**, 37-44.
38. Thompson, E.A. and Roberts, D.F. (1980). Kinship structure and heterozygosity on Tristan da Cunha. *American Journal of Human Genetics* **32**, 445-452.
37. Thompson, E.A. (1979). Ancestral inference III: The ancestral structure of the population of Tristan da Cunha. *Ann. Hum. Genet.* **43**, 167-176.
36. Anderson, M.W., Bonne-Tamir, B., Carmelli, D. and Thompson, E.A. (1979). Linkage analysis and the inheritance of arches in a Habbanite Isolate. *Amer. J. Hum. Genet.* **31**, 620-629.
32. Thompson, E.A. (1979). Fission models of population variability. *Genetics* **93**, 479-495.
31. Thompson, E.A. (1979). Genealogical structure and correlations in gene extinction. *Theor. Pop. Biol.* **16**, 191-222.
30. Thompson, E.A. (1978). Ancestral inference II: The founders of Tristan da Cunha. *Ann. Hum. Genet.* **42**, 239-253.

29. Thompson, E.A., Cannings, C. and Skolnick, M.H. (1978). Ancestral inference I: The problem and method. *Ann. Hum. Genet.* **42**, 95–108.
28. Neel, J.V. and Thompson, E.A. (1978). Founder effect and the number of private polymorphisms in a tribal population. *Proc. Nat. Acad. Sci. (USA)*: **75**, 1904–1908.
27. Thompson, E.A. and Neel, J.V. (1978). The probability of founder effect in a tribal population. *Proc. Nat. Acad. Sci. (USA)*: **75**, 1442–1445.
26. Thompson, E.A. (1978). The number of ancestral haplotypes contributing to a sample of B8 alleles. *Nature* **272**, 288.
24. Cannings, C., Thompson, E.A. and Skolnick, M.H. (1978). Probability functions on complex pedigrees. *Adv. Appl. Prob.* **10**, 26–61.
22. Cannings, C. and Thompson, E.A. (1977). Ascertainment in the sequential sampling of pedigrees. *Clin. Genet.* **12**, 208–212.
15. Thompson, E.A. (1976). A restriction of the space of genetic relationships. *Ann. Hum. Genet.* **40**, 201–204.
14. Thompson, E.A. (1976). Estimation of the age and rate of increase of rare variants. *Amer. J. Hum. Genet.* **28**, 442–452.
13. Thompson, E.A. (1976). Population correlation and population kinship. *Theor. Pop. Biol.* **10**, 105–226.
12. Thompson, E.A. (1976). Inference of genealogical structure. III. The reconstruction of genealogies. *Soc. Sci. Inform.* **15**, 507–526.
11. Thompson, E.A. (1976). Inference of genealogical structure. II. Quantifying genetic information. *Soc. Sci. Inform.* **15**, 491–506.
10. Thompson, E.A. (1976). Inference of genealogical structure. I. The theoretical basis. *Soc. Sci. Inform.* **15**, 477–490.
9. Thompson, E.A. (1975). The estimation of pairwise relationship. *Ann. Hum. Genet.* **39**, 173–188.
6. Thompson, E.A. (1974). Gene identities and multiple relationships. *Biometrics* **30**, 667–680.
4. Thompson, E.A. (1973). The Icelandic admixture problem. *Ann. Hum. Genet.* **37**, 69–80.
3. Thompson, E.A. (1973). The method of minimum evolution. *Ann. Hum. Genet.* **36**, 333–341.
2. Thompson, E.A. (1972). The likelihood for multinomial proportions under stereographic projection. *Biometrics* **28**, 618–620.
1. Thompson, E.A. (1972). Rates of change of world ABO blood-group frequencies. *Ann. Hum. Genet.* **35**, 357–361.

Computing Technical Reports, Theses, etc

205. Thompson, E. A. (2008) Analysis of data on related individuals through inference of identity by descent. Technical report No. 539, Department of Statistics, University of Washington.
198. Fu, A. Q. and Thompson, E. A. (2007) Inference of identity by descent in sib pairs: Analysis with and without linkage disequilibrium. Technical report No. 519, Department of Statistics, University of Washington.
172. Basu, S. and Thompson, E. A. (2002) A study of an allele sharing statistics on extended pedigrees. Technical report No. 413, Department of Statistics, University of Washington.
171. Stewart, W. C. L., George, A. W. and Thompson, E. A. (2002) Using Markov chain Monte Carlo for multipoint linkage analysis: Improved estimates of lod scores. Technical report No. 412, Department of Statistics, University of Washington.
133. Thompson, E. A. (1995) Inference of the conditional independence structure of dependent binary data. In: *Proceedings of Phylogeny Workshop* S. Tavare ed. DIMACS Technical

- Report 95-48. Pp 58--61.
132. Thompson, E. A. (1995). Monte Carlo in Genetic Analysis. Technical report No. 294, Department of Statistics, University of Washington.
 121. Wilson, C. C. and Thompson, E.A. (1994). Inference of the Askania Nova Przewalski's horse pedigree. Technical report No. 271, Department of Statistics, University of Washington.
 119. Thompson, E.A. (1994). Monte Carlo programs for Pedigree Analysis. Technical report No. 267, Department of Statistics, University of Washington.
 115. Geyer, C. J. and Thompson, E. A. (1993). Annealing Markov chain Monte Carlo, with applications to pedigree analysis. Technical Report No. 589, School of Statistics, University of Minnesota.
 113. Thompson, E. A. (1993). Sampling and ascertainment in genetic epidemiology; a tutorial review. Technical report No. 243, Department of Statistics, University of Washington.
 107. Guo, Sun Wei and Thompson, E. A. (1992). Two papers on the Monte Carlo estimation of models for complex genetic traits. Technical report No. 229, Department of Statistics, University of Washington.
 101. Thompson, E. A. and Wijsman E. M. (1990). The Gibbs sampler on extended pedigrees: Monte Carlo methods for the genetic analysis of complex traits. Technical report No. 193, Department of Statistics, University of Washington.
 93. Guo, S-W and Thompson, E. A. (1989). Analysis of sparse contingency tables: Monte Carlo estimation of exact P-values. Technical report No. 187, Department of Statistics, University of Washington.
 89. Thompson, E.A. and Shaw, R.G. (1988). Pedigree analysis of quantitative traits; variance components without matrix inversion. Technical report No. 154, Department of Statistics, University of Washington.
 86. Raftery, A., Smith, P.J. and Thompson, E.A. (1988). "How many ----?" Technical report No. 119, Department of Statistics, University of Washington.
 85. Thompson, E.A. (1988). GENEX -- an expert system for genetic analysis. A technical reports of DMS Systems Inc., Salt Lake City, Utah.
 71. Thompson, E.A. (1986). Genetic analyses of complex genealogies: outline of programs. Technical Report No. 21, Genetic Epidemiology, Department of Medical Informatics, University of Utah.
 41. Thompson, E.A. (1980). Recursive routines for computations on pedigrees. Technical Report No. 17, Department of Medical Biophysics and Computing, University of Utah.
 21. Thompson, E.A. (1977). Peeling programs for pedigrees of arbitrary complexity. March, 1977. Technical Report No. 6, Department of Medical Biophysics & Computing, University of Utah.
 18. Thompson, E.A. (1976). Peeling programs for zero-loop pedigrees. December, 1976. Technical Report No. 5, Department of Medical Biophysics & Computing, University of Utah.
 5. Thompson, E.A. (1974). *Mathematical Analysis of Human Evolution and Population Structure*. Ph.D. Thesis; University of Cambridge.
 0. Thompson, E. A. (1972). *The Reconstruction of Human History; Likelihood Inference in a Genetic Evolutionary Tree Problem*. Smith's Prize Essay; University of Cambridge (1973).

Invited book chapters and conference papers

202. Thompson, E. A. (2008) Uncertainty in inheritance: assessing linkage evidence. JSM Proceedings, Salt Lake City 2007. Pp. 3751-3758.

199. Sung, Y.J., Di, Y., Fu, A.Q., Rothstein, J.H., Sieh, W., Tong, L., Thompson, E.A. and Wijsman, E.M. (2007) Comparison of multipoint linkage analyses for quantitative traits: parametric lod scores, variance components lod scores and Bayes factors in the CEPH data. *BMC Proceedings*, **1**:S1 P. S93.
Online: <http://www.biomedcentral.com/content/pdf/1753-6561-1-S1-S93.pdf>
196. Thompson, E. A. (2007) Chapter 33: Linkage Analysis. (Extensively revised and updated.) In *Handbook of Statistical Genetics 3rd ed.* D.J.Balding, M.J.Bishop and C.Cannings (eds). Wiley: Chichester, UK. Pp 1141--1167.
192. Thompson, E. A. (2006) Uncertainty in Inheritance: Assessing evidence for linkage. Paper presented at the *Third University of Washington Biostatistics Symposium: Nov 2005*. Technical report No. 498, Department of Statistics, University of Washington.
(<http://www.stat.washington.edu/www/research/reports/2006/tr498.pdf>)
188. Thompson, E. A. (2005) Comment: Fuzzy and Randomized Confidence Intervals and P-Values. (Discussion contributions to Geyer and Meeden). *Statistical Science*, **20**: 382-383.
190. Thompson, E. A. (2005) MCMC in the Analysis of Genetic Data on Pedigrees. In *Markov Chain Monte Carlo: Innovations and Applications*. Pp. 183--216. F. Liang, J-S Wang, and W. Kendall (eds). Lecture Note Series of the IMS, National University of Singapore. World Scientific Co Pte Ltd, Singapore.
189. Sieh W, Basu S, Fu AQ, Rothstein JH, Scheet PA, Stewart WCL, Sung YJ, Thompson EA, Wijsman EM (2005) Comparison of marker types and map assumptions using Markov chain Monte Carlo-based linkage analysis of COGA data. *BMC Genetics*, **6** (Suppl 1):S11
186. Thompson, E. A. and N. H. Chapman (2004) Haplotype blocks in small populations. In *Computational methods for SNPs and Haplotype Inference: DIMACS/RECOMB Satellite Workshop, Piscataway, NJ, Nov.2002*. S. Istrail, M. Waterman and A. Clark (eds.). Springer-Verlag Lecture Notes in Computer Science, Vol. 2983, Pp. 74--83.
185. Thompson, E. A. (2004) The importance of Why?. Discussion contribution to Hamada and Sitter: Statistical Research; Some advice for beginners. *American Statistician* **58**: 198.
183. George, A. W., Basu, S., Li, N., Rothstein, J.H., Sieberts, S. K., Stewart W., Wijsman, E.M., and Thompson E. A. (2003) Approaches to mapping genetically correlated complex traits. Genetic Analysis Workshop 13 paper; *BMC Genetics* **4**: S71 <http://www.biomedcentral.com/1471-2156/4/s1/S71>.
182. Thompson, E. A. (2003) Lod Score. In *Nature Encyclopedia of the Human Genome*. Nature Publishing Group: MacMillan.
181. Thompson, E. A. (2003) Information from data on pedigree structures. In: *Science of Modeling: Proceedings of AIC 2003*. T. Higuchi, Y. Iba, and M. Ishiguro (eds) Pp. 307--316. Research Memorandum of the Institute of Statistical Mathematics, Tokyo, Japan.
179. Thompson, E. A. (2003) Linkage detection for complex traits. In *Invited Proceedings of the 54th Session of the International Statistical Institute*.
178. Thompson, E. A. (2003) Chapter 30: Linkage Analysis. (Revised and expanded) In *Handbook of Statistical Genetics 2nd ed.* D.J.Balding, M. Bishop and C.Cannings (eds). Pp. 893-918. Wiley: Chichester, UK.
170. Thompson, E. A. (2002) Human Genetics: Overview. In *Biostatistical Genetics and Genetic Epidemiology* Pp. 386-390. R. C, Elston, Olson J., and Palmer (eds.). Wiley; New York.
169. Thompson, E. A. (2001) Detection of Human genetic linkage: Foundations. *Theoretical Population Biology* **60**: 203-213.
166. Chapman NH, Leutenegger A-L, Badzioch MD, Bogdan M, Conlon EM, Daw EW, Gagnon F, Li N, Maia JM, Wijsman EM, Thompson EA (2001) The Importance of Connections: Joining components of the Hutterite pedigree. In *Genetic Analysis Workshop 12. Genetic Epidemiology*, **21**(Suppl 1): S230-S235

164. Thompson, E. A. (2001). Linkage Analysis. In *Handbook of Statistical Genetics* D.J.Balding, M. Bishop and C.Cannings (eds). Pp. 541--563. Wiley: Chichester, UK.
161. Chapman, N.H. and Thompson E. A. (2000). Linkage disequilibrium mapping: The role of population history, size, and structure. In *Advances in Genetics, Vol 42: Genetic Dissection of Complex Traits* D.C.Rao and M.A.Province (eds). Pp. 413--437. Academic Press: San Diego, CA.
159. Thompson, E. A. (2000). Monte Carlo methods on genetic structures. In *Complex Stochastic Systems* O.E. Bandorff-Nielsen, D.R. Cox and C. Kluppelberg (eds.) (Chapter 4, Pp.176--218) Proceedings of the fourth European Seminar in Statistics, Eindhoven, Netherlands, March 1999. CRC Press, Boca Raton.
157. Elston, R. C. and Thompson, E. A. (2000). A century of biometrical genetics. *Biometrics* **56**, 659--666.
155. Daw, E.W., Kumm, J., Snow, G.L., Thompson, E. A., and Wijsman, E. M. (1999) Monte Carlo Markov chain methods for genome screening. In *Genetic Analysis Workshop 11. Genetic Epidemiology*, **17**, Supplement 1, S133-138.
154. Anderson, E. C. and Thompson, E. A. (1999) MCMC likelihoods for population genetics. *Proceedings of the 52nd Session of the International Statistical Institute*, Vol. 3, Pp 347-348.
153. Thompson, E. A. (1999). Human pedigrees and human genetics. In: *Human Pedigree Studies* (Proceedings of a Galton Institute Conference, 1998.) Robert A. Peel (Ed.) Pp. 45-61. The Galton Institute, London.
151. Thompson, E. A. and Heath, S. C. (1999) Estimation of conditional multilocus gene identity among relatives. In: *Statistics in Molecular Biology and Genetics: Selected Proceedings of a 1997 Joint AMS-IMS-SIAM Summer Conference on Statistics in Molecular Biology*. F. Seillier-Moiseiwitsch (Ed), IMS Lecture Note--Monograph Series Volume 33, Pp.95--113. Institute of Mathematical Statistics (Hayward, CA) and the American Mathematical Society (Providence, RI).
(Also: Tech report No. 334, Dept Statistics, University of Washington).
149. Thompson, E. A. (1998). Human Genetics: Review and History. In *Encyclopedia of Biostatistical Sciences*. P. Armitage and T. Colton (eds.). Vol. 3, Pp. ???. Wiley; New York.
145. Heath, S.C., Snow, G.L., Thompson, E.A., Tseng, C., and Wijsman, E.M. (1997). Segregation and linkage analysis using MCMC. In *Genetic Analysis Workshop 10. Genetic Epidemiology*, **14**, 1011--1016.
144. Thompson, E.A. (1997). Gene identity in the analysis of complex traits. *Proceedings of the 51st Session of the International Statistical Institute*, Vol. 1, Pp 243-246.
143. Thompson, E. A. (1997) Chapter 10: Conditional gene identity in affected individuals. In *Genetic Mapping of Disease Genes*, editors I. Pawlowitzki, J.H.Edwards, and E.A.Thompson. Proceedings of EU Conference at St. Catherine's College, Oxford, December 1995. Pp. 137-146. Academic Press; London.
142. Thompson, E. A. (1997) Chapter 21: Final Comments. In *Genetic Mapping of Disease Genes*, editors I. Pawlowitzki, J.H.Edwards, and E.A.Thompson. Proceedings of EU Conference at St. Catherine's College, Oxford, December 1995. Pp. 275-277. Academic Press; London.
140. Thompson, E. A. (1997). Linkage, Genetic. In *Encyclopedia of Statistical Sciences; Updates Volume 1*. S. Kotz, C. B. Read, and D. L. Banks (eds.). Pp. 366-370. Wiley: New York.
136. Thompson, E. A. (1996). Statistical Genetics. Chapter 14 in: *Advances in Biometry: The last 50 years* P. Armitage and H. David (eds.) Wiley: New York. Pp. 263-285.
130. Geyer, C.J., and Thompson, E.A. (1995). A new approach to the joint estimation of relationship from DNA fingerprint data. In: *Population Management for Survival & Recovery*. J.D.Ballou, M. Gilpin, and T.J.Foose (eds.) Proceedings of the 1989 Front Royal Workshop on *Analytical Methods for Population Viability Analyses*, Pp. 245-260. Columbia University

Press, New York.

129. Thompson, E. A. (1995). Genetic importance and genomic descent. In: *Population Management for Survival & Recovery*. J.D.Ballou, M. Gilpin, and T.J.Foose (eds.) Proceedings of the 1989 Front Royal Workshop on *Analytical Methods for Population Viability Analyses*, Pp. 112-123. Columbia University Press, New York.
128. Lacy, R. C., Ballou, J. D., Princee, F., Starfield, A., and Thompson, E.A. (1995). Pedigree analysis for population management. In: *Population Management for Survival & Recovery*. J.D.Ballou, M. Gilpin, and T.J.Foose (eds.) Proceedings of the 1989 Front Royal Workshop on *Analytical Methods for Population Viability Analyses*, Pp. 57-75. Columbia University Press, New York.
127. Thompson, E.A. (1994). Monte Carlo estimation of multilocus autozygosity probabilities. *Proceedings of the 1994 Interface conference* J. Sall and A. Lehman (eds.) Pp. 498-506. Interface Foundation of North America: Fairfax Station, VA.
123. Thompson, E. A. (1994). Monte Carlo likelihood in genetic analysis. In *Probability, Statistics, Optimization: a tribute to Peter Whittle*. F.P. Kelly (ed.). Wiley; New York. Chapter 21, Pp. 281-293.
118. Thompson, E. A., Lin, S., Olshen, A. B. and Wijsman, E.M. (1993). Monte Carlo analysis on a large pedigree. In *Genetic Analysis Workshop 8. Genetic Epidemiology: 10: 677-682*.
106. Blossey, H., Guo, S-W., McKnight, B., Thompson, E.A., Tierney C. and Wijsman, E.M. (1992). Linkage analysis of malignant melanoma with the chromosome 1 markers D1S47 and PND. In *Genetic Analysis Workshop 7; Issues in Gene Mapping and Detection of Major Genes*. MacCluer JW, Chakravarti A, Cox D, Bishop DT, Bale SJ, and Skolnick MH (eds.) Cytogenetics and Cell Genetics (Suppl.). Basel; S. Karger. Pp. 182-184.
103. Thompson E. A. (1991) Probabilities on complex pedigrees; the Gibbs sampler approach. *Computer Science and Statistics: Proceedings of the 23rd Symposium on the Interface*, (E.M. Keramidas and S. M. Kaufman, eds.) Pp 321-328. Interface Foundation of North America, Fairfax Station, VA.
102. Thompson, E. A. (1991). Estimation of relationships from genetic data. In *Handbook of Statistics, Volume 8, Statistical Methods in Biological and Medical Sciences*. C.R. Rao and R. Chakraborty, eds., North Holland, New York, pp. 255-270.
100. Thompson, E. A. (1990). R. A. Fisher's contributions to statistical genetics. *Biometrics*, **46**, 905-914. (Earlier version; Pp. 7-13; Proceedings of the XV th IBC; Budapest, Hungary)
99. Thompson, E. A. (1990). From history to genes: from genes to history. In *Convergent Questions in Genetics and Demography*. J. Adams, A. Hermalin, D. Lam and P. Smouse, eds. Pp. 27-43. Oxford University Press; New York.
95. Walters, E. and Thompson, E.A. (1989). Mapping rare recessives from data on affected individuals: a comparative analysis. In *Multipoint Mapping and Linkage based on Affected Pedigree Members: Genetic Analysis Workshop 6*. Elston, R.C., Spence, M.A., Hodge, S.E., and MacCluer, J.W. (eds.) Pp. 213-218. Alan R. Liss Inc.; New York.
79. Bishop, M.J., Friday A.E. and Thompson, E.A. (1987). Inference of evolutionary relationships. In *Nucleic Acid and Protein Sequence Analysis*. (M.J.Bishop and C. J. Rawlings eds.) Pp. 359-396. IRL Press; Oxford, England.
73. Thompson E.A. (1988). Partial and conditional likelihood in pedigree analysis. Technical Report #141, Department of Statistics, University of Washington. Invited paper to *American Statistical Association Annual Meetings, Chicago, August 1986*.
72. Thompson E.A. (1986). Variability of descent and loss of alleles in a genetic isolate: The example of the Przewalski Horse. *Report to the AAZPA workshop; Omaha, June 1986*.
58. Thompson, E.A. (1983). Conditional likelihoods in pedigree analysis. *44th Session of the International Statistical Institute*, contributed papers, 846-849.

53. Thompson, E.A. (1984). Estimation of migration history from current genetic data: application to the Faroe Islands. In *Migration and Mobility* SSHB Symposium Volume (Cambridge, 1982). **23** (A.J. Boyce, ed.). Taylor and Francis, London (pp. 123-142).
52. Thompson, E.A. (1982). Sampling theory for pedigree analysis. Invited paper, *Proceedings of the 11th International Biometrics Conference*, Toulouse (pp. 199-205).
50. Thompson, E.A. (1982). Gene competition without selection. In *Current Problems in Sociobiology* (King's College Sociobiology Group, eds.). Cambridge University Press (pp. 113-131).
48. Thompson, E.A. (1981). Population structure and gene extinction. In *The Mathematical Theory of the Dynamics of Biological Populations II* (R.W. Hiorns and D. Cooke, eds.). Academic Press, New York (pp. 249-261).
40. Thompson, E.A. (1980). Sequential sampling schemes for sibships. *Adv. Appl. Prob.* **12**, 10-11.
39. Cannings, C., Thompson, E.A. and Skolnick, M.H. (1980). Pedigree analysis of complex models. In *Current Developments in Anthropological Genetics* (J. Mielke and M. Crawford, eds.). Plenum Press, New York (pp. 251-298).
35. Thompson, E.A. and Cannings, C. (1979). Sampling schemes and ascertainment. In *Genetic Analysis of Common Diseases* (C.F. Sing and M. Skolnick, eds.). Alan R. Liss Inc., New York (pp. 363-382).
34. Cannings, C., Thompson, E.A. and Skolnick, M.H. (1979). Extension of pedigree analysis to include assortative mating and linear models. In *Genetic Analysis of Common Diseases* (C.F. Sing and M. Skolnick, eds.). Alan R. Liss Inc., New York (pp. 407-416).
33. Thompson, E.A. (1979). Extinction probabilities and pedigree structure. *Adv. Appl. Prob.* **11**, 12-13.
25. Thompson, E.A., Kravitz, K., Hill, J. and Skolnick, M.H. (1978). Linkage and the power of a pedigree structure. In *Genetic Epidemiology*. N.E. Morton (ed.), pp. 247-253. Academic Press, New York.
23. Thompson, E.A. (1978). Impossible gene identity states. *Adv. Appl. Prob.* **10**, 19-22.
20. Thompson, E.A. and Skolnick, M.H. (1977). Likelihoods on complex pedigrees for quantitative traits. *Proc. Int. Conf. on Quantitative Genetics, Ames, 1976*. Pp. 815-818. The Iowa State University Press, Ames, Iowa.
19. Thompson, E.A. (1977). Estimation of the characteristics of rare variants. *Proceedings of the Ove Frydenberg Memorial Symposium, Aarhus, 1976*. 531-543. Springer-Verlag; Berlin.
17. Thompson, E.A. (1976). A paradox of genealogical inference. *Adv. Appl. Prob.* **8**, 648-650.
16. Cannings, C., Thompson, E.A. and Skolnick, M.H. (1976). The recursive derivation of likelihoods on complex pedigrees. *Adv. Appl. Prob.* **8**, 622-625.
7. Thompson, E.A. (1975). Multiple gene identities. *Adv. Appl. Prob.* **7**, 35-36.

Book reviews, discussion contributions or letters, abstracts, etc.

Not listed here.