

Pre-1985:

See list; total 113 seminars etc.

1985:

- March 15; Trinity Hall College, Cambridge, (6 th. formers)
Statistical questions on a Newfoundland genetic isolate.
- March 29; Annual Mathematical Genetics Meeting, Cambridge.
Sufficiency and joint likelihood for genealogical inference.
- April 1; Department of Statistics, University of Washington.
The E-M algorithm in statistical genetics.
- April 2; Population genetics seminar, Univ. Washington.
Pedigree analysis in a Newfoundland genetic isolate.
- April 10; Biology Department Seminar; UCSD.
Pedigree analysis in a Newfoundland genetic isolate.
- April 16; Population Biology Group, UCSD.
The how and why of computations on pedigrees.
- April 24; Quantitative Sciences Seminar, UCSD.
Patterns of gene identity by descent for multiple genes.
- May 20; Social anthropology group seminar, Cambridge.
The historical migrations of the Faroese.
- Sept 26; Population Genet. Seminar, University of Alberta; Pedigree computation
The how and why of computations on pedigrees.
- Oct 2 ; Medical Genetics; Dept. Biophysics; Univ. Utah.
The EM algorithm and linkage information.
- Oct 7 ; Genetics Analysis IV Workshop; Snowbird, Utah
Ordering loci by haplotype scoring.
- Nov 9 ; Mathematics Junior Master Class; Trinity Hall, Cambridge.
Ideas in probability and statistics.
- Nov. 29; Joint Bath/Bristol Probability and Statistics Seminar,
University of Bristol.
The E-M algorithm in statistical genetics.
- Dec. 19; Statistics Dept., Rothamstead.
Likelihood analysis of a model of DNA evolution.

1986;

- Feb. 25; Population Genetics seminar; Univ. Wa.
Gene extinction on defined pedigrees.
- March 19; Genetics Department seminar; Univ. Wa.
Genealogical reconstruction; problems and methods.
- April 19; Hereditary Disease Foundation Workshop; Stanford.
Invited participant; Huntingdon's Disease Seminar.
- May 6; Population Genetics seminar; Univ. Wa.
Effects of assortative mating in a finite population.
- May 23; Medical Genetics seminar; Univ. Wa.
Strategies for sampling large pedigrees in genetic epidemiology.
- June 21; AAZPA workshop and software seminar, Creighton University, Omaha.
Invited paper; Variability of descent and loss of alleles.
- July 31; International Biometric Conference.
Contributed paper; genealogy reconstruction and inference.
- Aug. 28; ASA; invited paper
Partial and conditional likelihoods in pedigree analysis.

1987;

- Jan-Mar; Nine seminars on pedigree analysis (Class 592b)
Introduction to pedigree analysis
Gene identity and the specification of relationships
Estimation of relationships and the reconstruction of genealogies
Computation of probabilities on complex pedigrees
Ancestral inferences and the genes of the Tristan da Cunjans
Gene extinction and the Przewalski horse pedigree
Genetic models and the aims of genetic epidemiology
Introduction to linkage analysis
Sampling considerations in pedigree analysis.

- Feb. 24; Population genetics seminar; Univ. Wa.
Making a linkage map with multipoint linkage data.
- April 3; Mathematical Genetics Meeting (Sussex, UK)
Likelihood and crossover counts in multipoint linkage analysis.
- May 26; Population genetics seminar; Univ. Wa.
EM algorithm for pedigree analysis of quantitative traits
- June 22; American Society of Naturalists; Bozeman, Montana
Extinction of genes and survival of genomes in genetic isolates.
- June 24; Society for Conservation Biology; Bozeman, Montana
Survival of genes in prolonged bottleneck; example of the
equus przewalskii pedigree.
- Aug 11; NSF Maths Study Workshop, University of Utah.
Group theory and gene identity.
- Aug 19; NATO-AMS Study Institute, University of Montreal.
Gene identity and genome extinction; two practical applications
of group theory.
- Sept 17; AAZPA Przewalski Horse SSP meeting, Portland.
Gene survival in the Przewalski Horse.
- Sept 22; Dept. Epidemiology and Biostatistics, University of Montreal.
Ancestral paths of genes; inference and prediction.
- Sept 25; SOREP Intl Symp. on Genetic Epidemiology of Isolates.
Ancestral paths of genes; inference and prediction.
- Nov 10; Population genetics and Evolution seminar, University of Washington.
Estimating genealogical relationships.
- Nov 16,18; Two classes in S516; Applied Stochastic Processes
1) The branching process for an X-linked lethal recessive.
2) The Ewens analysis of the Wright-Fisher model, with mutation.
- 1988:
- Feb 20; Department of Human Genetics, University of Utah.
Multilocus kinship: implications for linkage analysis
for recessive diseases.
- Feb 27; Genetic Epidemiology, Dept. Medical Informatics, University of Utah
Gene identity at two and three loci; implications for linkage
analysis.
- April 5; Population Genetics Seminar, Univ. Wa.,
Patterns of multilocus kinship in pedigrees.
- May 24; History seminar; Dept Stat; Univ. Wa.,
Sewall Wright DID invent the analysis of variance.
- June 8; Jackson Laboratories, Bar Harbor; Linkage conference;
Crossover counts, and ordering of loci.
- June 17; WNAR, Biometric Society; Honolulu, Hawaii;
Multilocus kinship in pedigrees.
- Sept 12; Genetics Laboratory, Oxford University, England.
Linkage analysis workshop.
- Oct 6; Convergent questions in demography and genetics, University of Michigan.
From history to genes; from genes to history.
- Oct 12; American Society of Human genetics;
Summary of GAW6 papers on ascertainment and segregation analysis
- Oct 13; American Society of Human genetics;
Ancestry of rare recessive lethals in a genetic isolate.

- Nov 4; PNWSM, UBC, Vancouver.
From history to genes; from genes to history;
via likelihood inference.
- Dec 6; Population Genetics Seminar, Univ. Wa.,
Ancestry of recessive lethals in the Hutterites.
- Dec 20; CALPEG, Asilomar, CA.
Pedigree identifiability and gene identity.
- 1989;
- Mar 2: Stat/Biostat joint departments seminar.
From history to genes; from genes to history;
via likelihood inference.
- Mar 29; Informal Stat Foundations seminar.
Fisher and Fiducial Probability.
- Apr 6; AAPA annual meetings, San Diego.
Invited workshop paper (Morgan & Thompson)
Ancestry of recessive lethals in the Hutterites.
- Apr 26; Informal Stat. Foundations seminar.
More on fiducial probability; Barnard's papers.
- May 22; Department of Statistics, University of Chicago
Estimation of relationship; New data types; New models.
- June 6; Population Genetics Seminar, Univ. Wa.,
Fisher's theory of Junctions.
- June 27; Davis; WNAR
Fisher's theory of Junctions, and molecular biology.
- Aug 18; Genetical Statistics Series, Univ. Wa.,
Genealogical analysis in conservation biology.
- Nov ??; Genetical Statistics Series, Univ. Wa.
Renwick and the Bayesian approach to linkage analysis.
- Nov 23; Species conservation workshop, Front Royal
Gene survival and genome survival in complex pedigrees
- Dec 5; Population Genetics Seminar, Univ. Wa.,
Rare variants in Amerindian tribes.
- 1990;
- Jan 31; Local ASA Chapter meeting.
R. A. Fisher's contributions to Population Genetics.
- Feb 20; Population Genetics Seminar, Univ. Wa.,
Computation of likelihoods of complex models for quantitative traits.
- May 9; Dept. Biological Sciences & CTAG, Rutgers University,
Survival of genomes and relationship estimation from DNA fingerprint
data; two novel issues in Conservation Biology.
- May 11; Dept. Psychiatry, Washington Univ., St. Louis,
Large pedigrees, complex models, and the computation of likelihoods.
- May 21; Dept. Statistics, UC Berkeley,
Monte Carlo approaches to the evaluation of complex likelihoods.
- May 29; Population Genetics Seminar, Univ. Wa.,
Gibbs' sampler on pedigrees, and the evaluation of likelihoods on
complex pedigrees for complex genetic models.
- July 2; International Biometric Conference, invited talk, plenary session,
Budapest, Hungary.
R. A. Fisher's contributions to Statistical Genetics.
- October 10; Genetical Statistics Seminar, Univ. Wa.,
Sex and sibship-size; questions of ascertainment bias of Galton (1904)
- October 18; Graph seminar, Dept Statistics, Univ. Washington,
Relationships between image analysis, expert systems and pedigree
analysis; the pedigree analysis version.
- November 23; Dept Mathematics and Statistics, Simon Fraser University
Monte Carlo methods for linkage and segregation analysis.
- 1991:
- Jan 17; "Fisher Seminar", Dept Statistics, UW
R.A. Fisher's contributions to Statistical Genetics.

- Feb 17; Bayesian Computation Workshop; Columbus, Ohio.
Stochastic simulation for complex genetic analyses.
- March 8; "Fisher seminar", Dept Statistics, UW.
R.A.Fisher and significance testing.
- March 25; Invited talk; ENAR Spring Meeting; Houston, Texas.
Monte Carlo methods for segregation and linkage analysis.
- March 25; Population Genetics Center, Houston, Texas.
Panel on lineage and segregation analysis.
- March 27; Statistical Genetics seminar; UW.
Segregation analysis; past, present and future.
- April 11; Women in Science seminar series, University of Michigan.
Monte Carlo methods for segregation and linkage analysis.
- April 17; Statistical Genetics seminar; UW.
Sequential sampling and ascertainment in pedigree analysis.
- April 22; Molecular Computation Workshop, Seattle; invited speaker.
Monte Carlo methods for likelihood estimation for complex models
- April 24; Interface Conference, Seattle; invited speaker
Probabilities on complex pedigrees; a Gibbs sampler approach.
- June 3; Department of Statistics, UW
Monte Carlo methods for probabilities on complex pedigrees.
- June 25; IMA summer research workshop in Mathematical Biology; invited speaker.
Models and inference for complex genetic traits.
- July 1; IMS Special Invited Paper; Western Regional Meetings, Santa Barbara.
Resolving complex genetic traits via the Gibbs sampler and the EM algorithm
- August 19; Joint Statistical Meetings, Atlanta Georgia.
Statistical Genetics session organizer and discussant.
- September 27; Research Day, Dept. Statistics, Univ. Washington
New opportunities or the application of statistics in genetic epidemiology.
- October 30; Statistical genetics group seminar, U. Washington.
Discussion of use of DNA data in forensic work; some statistical issues
- November 6; Department of Genetics, University of Georgia, Athens, GA
Relationships from multilocus DNA fingerprints: a problem of binary dependent data.
- November 6; Population genetics evening seminar, University Georgia,
Genetics importance and conservation of genomes in managed populations
- November 7; Research Triangle area joint evening population genetics meeting.
Estimation of relationship from DNA fingerprints; a problem of genetic management in the California Condor.
- November 8; Department of Statistics, North Carolina State University.
Resolving complex genetic traits via the Gibbs sampler and the EM algorithm.
- November 18; Invited participant; Banbury Conference; Cold Spring Harbor.
Complex segregation analysis for psychiatric disorders.
- December 11; Royal Statistical Society Discussion Paper, London. (with C. Geyer)
Constrained Monte Carlo maximum likelihood for dependent data.
- 1992:
- January 11; Keynote speaker, Mathematical and Molecular Biology symposium.
CTAG, Rutgers University.
Estimating relationships: From behaviour, to genes, to DNA.
- January 27; NHLBI expert panel one day meeting
Methodology and resources; sampling and design;
- February 4; Department of Statistics, Yale University
Constrained Monte Carlo Likelihood Analysis;
Application to analysis of the California DNA fingerprint data
- February 11; Dept. Biostatistics, University of Rochester
Monte Carlo approach to the analysis of complex genetic traits
- February 28; Guest Lecture in class on Evolution and Ecology, Rutgers
Gene identity, complex relationships, and Canadian Hutterites
- March 3; Women's Science Program, Douglass College, Rutgers University.
Pedigrees, California condors and Canadian Hutterites
- March 4; Department of Statistics, Rutgers University,
Monte Carlo Likelihood Analysis and California Condors

March 18-19; Dept of Psychiatry, Washington University, St. Louis.
Short course on Monte Carlo Methods in Genetic Analysis.

March 19-20; NHLBI expert panel; St Louis;
Methodology and resources subcommittee.

March 30; MSRI workshop in Molecular Biology, Berkeley, CA
Monte Carlo methods in statistical genetics.

April 30; Genetic Epidemiology workshop; NIH; Bethesda;
Monte Carlo methods in statistical genetics.

May 14 ; Statistical Genetics group, University of Washington
Monte Carlo EM and likelihood ratio evaluation for genetic models

July 14; NHLBI expert panel one day meeting
Final report review.

July 16; Statistical Genetics group, University of Washington
Monte Carlo EM for the GAW8 data.

Sept 6-10; Book workshop, Boulder Colorado.

Sept 14; Pedigree Analysis Session organizer; EMS, Bath England.

Sept 28; Department of Statistics, UW; Research Day.
Markov chain Monte Carlo in the reconstruction of genealogies.

Oct 15 ; Statistical Genetics Seminar, University of Washington;
Fisher, Haldane and the early days of linkage analysis.

Dec 8; Human and Plant Genetics session organizer; IBC, Hamilton, New Zealand

1993:

Jan 14; Statistical Genetics Seminar (part), University of Washington;
Linkage analysis of Quantitative traits; Tanksley's tomatoes.

Feb 11; Statistical Genetics Seminar (part)
Introduction to linkage disequilibrium.

March 4; USC Statistics Seminar
Monte Carlo Likelihood Analysis for Two Genetic Problems.

March 24; Math Day, UW;
Genes in pedigrees and reestablishing the Przewalski Horse in Asia.

May 13; Biostat/Stat 111 lecture.
Who's who? Are why it is important to an endangered species.

May 17; UW Statistics Seminar
Monte Carlo Likelihood in Missing-Data Problems.

May 28; NCHGR Workshop on Statistical Methods in Gene Mapping
Monte Carlo methods for the estimation of LOD score curve.

August 8; IMS Workshop, Stanford University.
Monte Carlo Likelihood in Genetic Analysis.

August 17; International Congress of Genetics, Birmingham, England.
Monte Carlo methods for the estimation of genetic parameters.

September 22; QERM Research Day, UW.
Statistical aspects of conservation genetics.

September 23; STAT Research Day, UW.
Fitting genetic models, and estimating pedigrees.

September 30; Statistical genetics seminar, UW.
What is the mixed model? A confusion of terminology.

November 1; Statistics Dept seminar
A history of Monte Carlo in Pedigree Analysis; 1925-1989.

November 18; Department of Biostatistics, University of Michigan
Monte Carlo Likelihood in genetic analysis.

December 8; Royal Society Meeting, London,
Monte Carlo Likelihood in the genetic analysis of complex traits.

1994:

January 6; Statistical genetics seminar, UW.
Markov chain Monte Carlo methods for the mixed model.

January 20; Department of Statistics, University of Minnesota.
Monte Carlo likelihood in the genetic analysis of complex traits.

January 21; Department of Ecology and Evolutionary Biology, Univ. Minnesota.
Relationships from genetic data; Birds, Plants and Mammals.

March 10; NIAAA meeting, Bethesda, MD.

- Monte Carlo estimation of LOD scores.
April 28; Statistical genetics seminar, UW.
Multilocus homozygosity mapping and autozygosity probabilities.
May 9; Statistical Society of Canada, Banff, Alberta.
Monte Carlo Likelihood in the Genetic Epidemiology of Complex Traits.
May 16-20; Wageningen Agricultural University, Netherlands.
A one week course in Monte Carlo Methods in Genetics Analysis.
June 18; Interface Meeting, North Carolina
Monte Carlo Estimation of autozygosity patterns.
June 24; IMS/Bernoulli Society meeting Chapel Hill, NC
Monte Carlo likelihood in genetic analysis.
August 18; Annual Statistics Joint Meetings, Toronto.
The R.A.Fisher Lecture:
Likelihood and linkage, from Fisher to the future.
Oct 27; Biostatistics Department, University of Michigan.
Monte Carlo linkage likelihoods using multilocus gene identity probabilities.
Nov 22; Statistics Department, Northwestern University.
Monte Carlo estimation of probabilities on complex pedigrees.
Dec 9; Statistics Department, University of Michigan.
Monte Carlo estimation of probabilities on complex pedigrees.
Dec 20; Statistical Genetics Group, University of Michigan.
How many private polymorphisms in the Amerindian population?
- 1995:
Jan 11; Rockefeller University, NY.
Monte Carlo likelihood in the genetic analysis of complex traits.
Jan 14; PMMB, Napa, CA.
A general model for dependent binary data.
Jan 27; NCHGR, Washington DC.
Monte Carlo likelihood in the genetic analysis of complex traits.
Feb 6; DIMACS meeting, Princeton University.
An autologistic model for ordering loci.
Feb 15; Gordon Conference, Ventura CA.
Monte Carlo likelihood in the genetic analysis of complex traits.
Feb 22; Evolution class, Rutgers University.
Human evolution; genetic diversity within Amerindian populations.
Feb 24; Department of Mathematics, U. Delaware.
Monte Carlo on complex pedigrees.
March 1; Biodiversity seminar, Rutgers University.
Variation in the Amerindian population; implications for biodiversity.
March 15; Clinical Genetics Society Annual Meeting, Renwick Symposium, London.
Linkage detection via multilocus gene identity in sets of affected relatives.
March 16; Linkage symposium, Galton Laboratory, London.
Locus ordering; the missing data problem.
March 17; Linkage and Phylogenies meeting, Hinxton Hall, Cambridge.
Conditional independence structure in binary data;
locus ordering and gene phylogenies.
March 22; Biostatistics, Fox Chase Cancer Center, Philadelphia.
Monte Carlo methods for genetic analysis.
May 11; Statistical Genetics Group, McGill University.
Genome sharing in individuals related as half-sibs.
May 27-June 3; Cancer Research Center, Copenhagen.
8 sessions in a course on Genetic Epidemiology.
May 30; Statistics Department, University of Copenhagen.
Monte Carlo on very large and complex pedigrees.
June 6; Biostatistics Department, McGill University
Monte Carlo likelihood in genetic analysis. (half-day workshop)
August 17; Environmental Sciences, Griffith University, Brisbane, Australia.
Monte Carlo estimation of probabilities on large pedigrees.
August 21; Animal Genetics Department, University of New England, Armidale.
Monte Carlo methods in genetic analysis.

- August 29; Department of Statistics, University of Adelaide, Australia.
Monte Carlo likelihood in genetic analysis. (half-day workshop)
- August 30; Australian Statistical Society, South Australia section.
Monte Carlo estimation of probabilities on large pedigrees.
- September 7; Statistics Department, Australian National University, Canberra.
Monte Carlo estimation on large and complex pedigrees.
- September 11; Statistics Department, University of Auckland, New Zealand.
Monte Carlo likelihood in genetic linkage analysis.
- December 16; EU Conference on "Genetic Mapping of Disease Genes." Oxford, UK
Conditional gene identity in affected individuals.

1996:

- April 15; Statistics Department, University of Washington.
Inferences from the distribution of variant alleles in human populations
- April 22,24; Mathematical Biology Training Program, UW (2 lectures)
Genes from History, or History from Genes?
- April 26; Washington Defender Conference, Winthrop, WA
Statistical issues in forensic DNA evidence.
- May 25; Program in Mathematics and Molecular Biology, Yountville, CA.
Segregation patterns and genome sharing.
- Aug 5; Joint Statistical Meetings, Chicago.
Neyman Lecture.
Inferring gene descent and ancestry; complicated but not uninteresting.
- Aug 28; Bernoulli Society World Congress, Vienna, Austria
Special Invited lecture.
Estimation of gene identity and inference of gene ancestry.
- Sept 24; UW Dept Statistics Research Day
Is she my half-sister or my aunt?
- Oct 8; UW Statistical Genetics seminar
Monte Carlo in Genetic Analysis
- Oct 26; Department of Mathematics, University of Portland.
Estimation of gene identity and inference of gene ancestry.

1997:

- Feb 25; UW Statistical Genetics seminar
RAPDs and their use as genetic markers.
- Mar 5; UW COMBI seminar
Probabilities of multilocus gene descent patterns on complex pedigrees.
- April 15, ASA, Puget Sound Chapter Meeting
Quantifying the weight of DNA evidence.
- April 30; UW Statistics Dept, Math Genetics group
Monte Carlo likelihood computations on pedigrees.
- May 10; PMMB Coolfont retreat (joint with Simon Heath)
Sampling based approaches to multipoint linkage analysis
- May 13; Statistical Genetics Seminar, UW (joint with Warwick Daw)
Selective sampling for genetic analysis of discrete traits.
- June 23; Invited talk; SIAM Statistical Genetics Workshop; Seattle.
Gene identity in individuals affected for complex traits.
- Aug 27 ; Invited talk; International Statistical Institute, Istanbul.
Gene identity in the analysis of complex traits.
- Oct 28; Statistical Genetics Seminar, UW
When is linkage analysis "non-parametric"
- Dec 10; Invited speaker, NIGMS Workshop, Washington DC.
Theoretical perspectives: sampling designs, genetic scale,
and locus specificity.

1998:

- Jan 9; Mathematical Genetics Discussion Group, Statistics, UW.
Monte Carlo pedigree samplers, and problems of irreducibility.
- Mar 28; PNWWMB Meeting, Friday Harbor
Realizing the ancestry of a rare allele, and why we want to.
- Apr 2; Biostatistics Department, Harvard School of Public Health.
Computational paradigms for pedigree analysis

- Apr 7; Statistical Genetics Seminar
Realizing the history of an allele: implications for disequilibrium mapping.
- Apr 10; Mathematical Genetics Discussion Group, Statistics, UW.
Monte Carlo estimation of conditional probabilities of genome sharing.
- May 3-5; SWI Madison Wisconsin (1 plenary lecture; 1 other)
Monte Carlo estimation of conditional probabilities of genome sharing on large complex pedigrees.
Realizing the ancestry of a rare allele, and why we want to.
- May 6-7; Department of Biostatistics, University of Michigan.
Computation of likelihoods for linkage detection on complex pedigrees.
- May 10-16; CRM workshop, Universite' d'Montre'al (6 hours)
Computational approaches to likelihoods on pedigrees
- June 22; Purdue Symposium
What is missing in modern linkage likelihood computations?
- June 25; BWF Workshop, Berkeley California
Stochastic models for meiosis.
- June 30; WVAR Contributed paper; San Diego California (w/ Jinko Graham)
Fine scale disequilibrium mapping from realized allelic ancestries.
- July 1; PMMB Short Course; 3 hour session
Stochastic models and statistical analysis of descent of DNA in pedigrees.
- Sept 18; The Galton Institute, London, UK
Human Pedigrees and Human Genetics
- 1999:
- March 15-19; SEMSTAT, Eindhoven, Netherlands. 3 lectures
MCMC for the analysis of genetic data on pedigrees.
- March 23; Royal Statistical Society. London, UK
MCMC estimation of multilocus genome sharing and multipoint gene location scores
- March 25; HSSS Workshop, Lammi, Finland.
MCMC estimation of multilocus genome sharing, including estimation in the presence of interference
- April 23; PNWSM, Pullman, Washington
MCMC estimation of multilocus genome sharing and linkage likelihoods
- May 3; Statistics Department, NCSU
MCMC estimation of multilocus genome sharing and linkage likelihoods, including estimation under interference
- May 10; Genetic Epidemiology, Johns Hopkins, Baltimore
MCMC estimation of multilocus genome sharing and linkage likelihoods, including estimation under interference
- May 21; ACMS colloquium, University of Washington.
Genes, relationships, and endangered species:
from California condors to Pacific Northwest salmon.
- July 19-23; NSF, CBMS Summer Short Course,
Michigan Technical University, Houghton, MI
Inferences from Genetic Data on Pedigrees. (15 hours)
- Aug 9; IMS invited lecture at JSM, Baltimore MD.
The latent structures of genetic analysis.
- Aug 16; International Statistical Institute, Helsinki, Finland.
MCMC Likelihoods for Population Genetics.
- Sep 8; Morton Symposium, St. Louis, MO.
Linkage Disequilibrium Mapping:
the role of population history, size and structure.
- Sep 27; Research Day, Statistics, UW
Statistical Genetics at the University of Washington.
- Oct 15; Invited lecture; International Society of Psychiatric Genetics,
Monterey, CA
Identity by descent in linkage detection for complex traits
- Dec 12; CMS Winter meeting, Montreal, Quebec.
Identity by descent in the mapping of complex traits

2000;

- Feb 21; AAAS, Washington DC
Human population structure and evolution
- March 1; Genetics Department Seminar, Univ Washington
Linkage analysis and genome sharing and among relatives.
- March 22; ENAR Theme session lecture.
A century of genetic linkage analysis.
- June 12-15; NCSU Summer Institute; Module 12; Joint with Shili Lin
Monte Carlo Analysis of Genetic Data on Pedigrees (11 hours)
- June 23; PMMB Berkeley Summer Short Course (2 lectures)
Monte Carlo Likelihood for genetic analyses.
Coalescents, phylogenies, and disequilibrium mapping.
- June 25; MSRI Workshop in Mathematics and Molecular Biology
Linkage analysis; past, present and future.
- Sept 11-15; European Summer Short Course (Pavia Italy); 20 hours
Statistical Analysis of Genetic Data on Pedigrees.
- Oct 14-17; Jackson Labs Shortcourse; Bar Harbor, Maine
Genetic mapping from data on pedigrees.
- Nov 30; Reed College, Portland, Oregon.
Probabilities on Pedigrees: What, How and Why?

2001;

- April 23: Statistics Department, UW
Probabilities on Pedigrees: What, How and Why?
- May 14-18: European Short Course: Rotterdam
Statistical Analysis of Genetic Data on Pedigrees
- June 6: NCSU Summer Institute; one section of module 7
Basics of Probabilities on Pedigrees.
- June 10; SSC/WNAR Short Course: Vancouver BC
Statistical Analysis of Genetic Data on Pedigrees
- Oct 3: COMBI Seminar, UW
Statistical Genetics meets Computational Molecular Biology
(or vice versa)
- Dec 16: Workshop in Computational Molecular Biology and Statistical Genetics
Inferring gene locations from genetic data on related individuals

2002:

- Jan 5-10: PMMB meeting Santa Fe
Statistical Genetics at UW and elsewhere. Workshop report.
- April 6-8: EMGM-30, Sheffield, UK. Special invited speaker.
Estimating Multipoint LOD scores using Monte Carlo on pedigrees
- April 26; Univ. Idaho; IBEST seminar
Estimating Multipoint LOD scores using Monte Carlo on pedigrees
- May 23; David Andrews Symposium, Fields Institute, Toronto
Estimating Multipoint LOD scores using Monte Carlo on pedigrees
- June 12-14: NCSU Summer Institute; module 13 (joint with Shili Lin)
Inferences from Genetic Data on Pedigrees.
- July 24: IBC Freiburg, Germany; contributed paper
Allele-sharing methods on large pedigrees.
- Oct 11: Cockerham Symposium, NCSU
Gene IBD and the mapping of complex traits
- Oct 21: Weldon Lecture, Oxford University, UK
Mapping complex traits in the post-genome era
- Nov 5: Cold Spring Harbor Symposium
Gene descent in pedigrees of inbred lines
- Nov 22: DIMACS meeting, Rutgers University
Genome sharing in small populations

2003:

- Feb 5: Genetic Epidemiology Meeting, Oberwolfach, Germany
Detection of linkage via genomic ibd imputation
- Feb 19: Population Genetics Group, NCSU
Gene ibd in structured populations

- Feb 26: Biostatistics Department, University of North Carolina, Chapel Hill, NC
Detecting linkage for complex traits using pedigree data:
a new approach to assessing significance
- March 6: Statistical genetics group, Glaxo Smith Kline, Research Triangle, NC
Detecting linkage for complex traits using pedigree data:
a new approach to assessing significance
- March 21: ISDS, Duke University, Durham, NC
Monte Carlo Estimation of Likelihood Functions:
the example of multipoint linkage lod scores.
- April 21-22: University of Iowa: Allen T. Craig Lectures
General talk: Linkage detection for complex traits.
Specialist talk:
Monte Carlo Estimation of Likelihood Functions:
the example of multipoint linkage lod scores.
- May 2: UW Science forum
Mapping complex traits in the post-genome era
- May 16: UW Mathgen group:
Gene ibd in structured populations
- July 16-18: Southern Summer Statistical Genetics Institute, Melbourne, Australia
Pedigree analysis module (15 hours lectures)
- Aug 13-20: Invited presentation, ISI, Berlin Germany
Linkage detection for complex traits
- Sept 23: UW Workshop on Statistical Genetics and Computational Molecular Biology.br
Linkage detection for complex traits.
- Nov 3: Invited plenary talk; IGES, Redondo Beach, CA.
Inference of population structure from genetic data.
- Dec 15: Invited Talk: Science of Modelling Meeting; Yokohama, Japan.
Information from data on pedigree structures.
- 2004:
- Jan 21: Invited seminar: UW COMBI seminar
Inference of population structure from genetic data.
- Feb 9: Invited seminar, Department of Human Genetics, UCLA
Gene descent in pedigrees and the detection of linkage.
- Feb 12: Invited talk; MSRI Workshop on Genetics of complex disease.
Information from imputed IBD on pedigree structures.
- Feb 27: UW ACMS seminar
Estimation of relationships from genetic data.
- Mar 22-25: MCMC Workshop, IMS, National University of Singapore
MCMC for the analysis of genetic data on pedigrees: Tutorial Session 1
MCMC for the analysis of genetic data on pedigrees: Tutorial Session 2
Pseudo-Bayes MCMC for the estimation of multipoint linkage likelihoods
- Apr 2: UW Medical Genetics Markey Seminar
Gene descent in Pedigrees and the detection of linkage
- Apr 19-23: Buehler-Martin Lectures, Univ Minnesota: 3 lectures
Estimation of relationships from genetic data
Gene descent in pedigrees and the detection of linkage
Pseudo-Bayes MCMC for the estimation of multipoint linkage likelihoods
- May 4,6: UW Mathematical Biology research seminar (two lectures).
Estimation of relationships from genomic data.
- June 9-11: NCSU Summer Statistical Genetics Institute: 8 hours lectures.
Module on MCMC on pedigrees (joint w/Shili Lin)
- 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 1: UW Genome Center: Olson Research Group:

- Fuzzy P-values: testing hypotheses when variables are latent.
 Apr 14,16: UW Mathematical Biology research seminar (two lectures).
 Fuzzy P-values: What, Why, and How.
 Apr 19: Sobel Lecture, Dept Statistics, Univ. California Santa Barbara
 Fuzzy p-values in the detection of genetic linkage
 May 17-20: NIHES course: Erasmus University, Rotterdam
 Advanced Pedigree Analysis: 18 hrs lectures; 6 hrs computing labs
 May 25 : Biostat 111 Class. HSB, UW
 Estimating relationships: What, Why and How?
 Sept 26 : UW Department of Statistics: Research Day.
 Fuzzy p-values and finding genes
 Nov 21 : Third Biostatistics Symposium, Seattle: Keynote lecture.
 Uncertainty in inheritance: assessing evidence for linkage
 Dec 8 : Department of Biostatistics, University of Michigan
 Uncertainty in inheritance and the detection of genetic linkage

2006:

- March 31: First Canadian Genetic Epidemiology Workshop, Toronto
 Fuzzy p-values in trait-model-free linkage detection
 April 3,4: Fields Institute Distinguished Lecturer in Statistical Science
 Lecture 1: Latent Variables, Uncertainty and Evidence.
 Lecture 2: Uncertainty in inheritance and the inference of
 genetic linkage
 April 21: UW Genome Center: Olson Research Group
 The impact of population structure on genetic inferences
 May 1: UW Statistics Department Seminar
 Uncertainty and evidence in latent variable problems
 May 5: UW Statistics: Mathematical Genetics Group
 Uncertainty in inheritance and the estimation of genetic linkage.
 May 8-12: Bahadur Lectures, University of Chicago
 May 8: Monte Carlo likelihood inference in latent variable problems
 May 11: Uncertainty and evidence in the face of unseen data
 June 21-23: UW, Summer Institute in Statistical Genetics
 Advanced Pedigree Analysis: 2.5 day module with Shili Lin.
 June 28: WNAR Meeting, Flagstaff, Arizona.
 Linkage disequilibrium in family-based genetic mapping.
 (Work with Audrey Fu.)
 July 19: XXIII IBC Meetings, Montreal, Quebec.
 Fuzzy p-values and permutation tests for genetic linkage.
 (Work with Yanming Di and Saonli Basu.)
 Aug 1: Invited speaker, Workshop on Genetic Epidemiology, Sheffield UK.
 Advances and challenges in the statistical analysis of data
 on pedigrees.
 Sept 19, and Sept 25: Genome Sciences Retreat and Statistics Research Day
 Fuzzy p-values and permutation tests for genetic linkage.
 Nov 15: Weir evening research discussion group
 Fisher Lectures and the Isaac Newton Institute: a brief history of
 linkage detection and linkage estimation, up to 1953 and beyond.
 Dec 4: Fisher XXVII Memorial Lecture, Cambridge, UK.
 1953: an unrecognized summit in human genetic linkage analysis.
 Dec 11: Rothschild Lecture, Isaac Newton Institute, Cambridge, UK.
 Uncertainty and evidence in likelihoods for genetic linkage

2007:

- Mar 2: UW Department of Statistics, Student Recruiting Day
 Inferences from unobservable variables:
 An example from genetic data on pedigrees.
 Mar 23: Invited speaker, AISTATS Meeting, Puerto Rico.
 Uncertainty and significance in testing for genetic linkage.
 May 8: Invited speaker, ICMS workshop on Genetic Epidemiology, Edinburgh, UK.
 Assessing the significance of linkage findings.
 June 23: Invited speaker, Seattle Showcase Statistical Genetics Symposium
 Measuring uncertainty in inheritance

seminars

Thu Jun 12 13:21:43 2008

12

- July 3: Keynote lecture, BIRS workshop, Banff, Canada
Relationships among and within populations
(work with Arindam RoyChoudhury)
(Also given as UW PopGen seminar, June 12)
- Aug 2: Joint Statistical Meetings, Salt Lake City, UT
Uncertainty in inheritance: P-values and confidence levels
- Oct 2: UW Population Genetics research seminar
Inferring relationships between 2 and among 4 genomes,
from dense SNP marker data with linkage disequilibrium.
- Dec 6: Invited speaker, Microsoft Research Meeting, Kirkland, WA.
Probabilities on Pedigrees.

- 2008:
- May 9: UW Population Genetics research seminar
Coancestry of individuals in populations:
Inferences from dense genomic data
- July 3: Invited Keynote Speaker, Australian Statistical Meetings, Melbourne
Probabilities on the gene identity graph:
Combining Pedigrees and Populations in the Genomic Data Era
- July 14: Inaugural Tukey Lecturer, IMS and Bernoulli Society World Congress, Singapore
Genome sharing among related individuals:
an approximate answer to the right question.
- Sept 12: Invited Speaker, Workshop for Chris Cannings on
Advances in Statistical Genetics and Mathematical Biology, Sheffield, UK.
Computing on the gene identity graph:
Combining Pedigrees and Populations in the Genomic Data Era