

Seminars 2003– 2019

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
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
- 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 Society Meetings,
Melbourne
Probabilities on the gene identity graph:
Combining Pedigrees and Populations in the Genomic Data Era
- July 14: Inaugural Tukey Lecturer, Bernoulli and IMS Society 7 th 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
- Oct 8: Invited talk, CSHL Symposium on Kinship, Ancestry and Society
Inferring identity-by-descent from genomic SNP data
in the absence of pedigree structure information

- Oct 10: 2008 Krishnaiah Lecture, Department of Statistics, Penn State
Genetic variation and coancestry
- Oct 24: UW Popgen discussion seminar
Models for identity by descent of chromosome segments in populations
- Nov 12: Plenary session, American Society of Human Genetics, Philadelphia.
Testing Hardy-Weinberg Equilibrium.

2009:

- Feb 6: Cockerham Lecture, Department of Statistics, NCSU.
Identity by descent in pedigrees and populations
- Mar 6: UW Popgen discussion seminar
The IBD process among multiple genomes; genotypic data.
- May 29: Stat 111 Class: Lectures in Applied Statistics
Estimating relationships from genetic data.
- June 4: Invited talk; Jurg Ott Symposium, The Rockefeller University.
The structure of genetic data for linkage analysis:
From LIPED to SNPs
- June 15: Contributed paper; WNAR, Portland State University.
The latent variable structure of genetic data on related individuals.
- June 22-24: Summer Institute in Statistical Genetics, Seattle;
Module 11 (15 hours: joint with Eric Anderson)
Inference of Relationships and Relatedness
- Aug 17: Invited paper for 57 th. ISI, Durban, South Africa
Inferring coancestry of genome segments in populations
- Sept 28: UW Statistics, Research Day.
Three graphical models for genetic data.
- Oct 21: UW Popgen discussion seminar.
The reduced space of IBD equivalence classes is Markov.

2010:

- Jan 28: Meeting of UCI Markers research group (Seattle)
The structure of genetic data for linkage analysis
Introduction to linkage lod scores
- Feb 24: UW Popgen discussion seminar.
IBD graphs and their equivalence classes for genetic
analysis of data on pedigrees
- Apr 1: University at Buffalo Distinguished Scholars Lectures in
Biostatistics
The conditional independence structure of genetic data.
- June 28-30: Summer Institute in Statistical Genetics, Seattle;
Module 17 (15 hours: joint with Eric Anderson)
Inference of Relationships and Relatedness
- July 18: CAIMS Meeting, St. John's, Newfoundland (Plenary speaker)
The estimation of latent coancestry in pedigrees and populations
- Sept 28: Randall Lecture, University of Idaho.
Resolving complex traits through coancestry and the shared
inheritance of genome
- Oct 22: Queensland Workshop Frontiers in Statistical Genetics
and Genomics pdf(QUT and QIMR, Brisbane, Australia)
Resolving complex traits through coancestry and the shared
inheritance of genome
- Dec 10: XXVth International Biometric Conference Floreanopolis, Brazil.
Descent patterns in pedigrees imputed from genomic marker data

2011:

- Feb 9: WEHI, Melbourne, Australia
Resolving complex traits through coancestry and the shared
inheritance of genome
- Feb 14-18: Short course (30 hours);
University of New England, Armidale, Australia

- Identity by descent in pedigrees and populations;
 methods for genome-wide linkage and association.
- March 10: MathAcrossCampus Talk, University of Washington
 Relationships, Relatedness, and the Coancestry of Genome
- April 19: CRM workshop, Montreal, Quebec, Canada
 Conditional independence structures in the analysis of genetic
 data in pedigrees and populations
- June 20: WVAR Annual Meeting, San Luis Obispo, CA.
 Modeling IBD Processes along Chromosomes in Populations
- June 29–July 1: SISG–16 Module 24 (joint with Eric Anderson)
 Inference of Relationships and Relatedness
- July 20: ICFIS, University of Washington
 The Anthrax mailings: replication and resampling in the
 FBIR and RMR–1029.
- July 27: GCC Tower research meeting, University of Washington
 Inferring coancestry in populations in the presence of
 linkage disequilibrium
- Aug 25: ISI, Dublin, Ireland
 Gene coancestry in pedigrees and populations
- Sept 26: UW Stat Research Day
 Genetic data on related individuals.
- 2012:
- Jan 27: UW PopGen:
 Population growth, the survival of rare variants and the
 potential for IBD mapping.
- Feb 6: UCLA, Human Genetics and Biomathematics.
 Coancestry in pedigrees and populations.
- Mar 5: Oregon State University, Statistics.
 Combining coancestry in pedigrees and populations.
- Mar 9: UW School of Aquatic and Fishery Science.
 Variance in coancestry, in relatives and over genomes.
- May 1: Canadian Human and Statistical Genetics Meeting (invited speaker)
 Ancestry and descent in large Canadian pedigrees
 (Special session in honor of Ken Morgan)
- May 7: 57th RBras Annual meeting, Piracicaba, Brazil. (Invited speaker)
 Population-based identity by descent mapping.
- May 8: 57th RBras Annual meeting, Piracicaba, Brazil. (Invited plenary
 speaker)
 Inferring coancestry in populations in the presence of linkage
 disequilibrium.
- June 27–June 29: European Institute in Statistical Genetics (EISG),
 Edinburgh, Scotland, UK. Module 9 (joint with Eric Anderson)
 Inference of Relationships and Relatedness
- July 3–July 6: Training course (4 days). Wageningen University,
 Netherlands.
 Statistical inference on identity by descent in genome association
 studies
- July 18–20: UW SISG–17 Module 14 (joint with Eric Anderson)
 Inference of Relationships and Relatedness
- July 30: Joint Statistical Meetings, San Diego (invited speaker)
 Resolving complex traits via coancestry in pedigrees and
 populations.
- Aug 28: XXVI International Biometric Conference, Kobe, Japan.
 Multiple identity by descent in population-based genetic mapping.
- Oct 19: Woodroffe Lecture, Dept Statistics, University of Michigan.
 Assessing the significance and uncertainty of identity by descent
 in pedigrees and populations.
- Oct 26: UW Genome Sciences, PopGenLunch seminar.

Assessing the significance and uncertainty of identity by descent in pedigrees and populations.
Nov 10: American Society of Human Genetics Annual Meeting, San Francisco (invited paper)
Identity by descent in pedigrees and populations.
Nov 14: UW Statistical Genetics Program Project Webinar
Identity by descent: definition, and distribution, and models for inference

2013:

Feb 17: UW Statistical Genetics Program Project Annual review Meeting
Identity by descent: jointly among individuals and jointly across loci
Apr 30: STAT 534 class
Latent variables, conditional independence, and Hidden Markov Models
June 15; IPAM High throughput Genomics Reunion Workshop (invited)
Coalescents, Ewens' sampling formula, Identity by descent, and rare variants in the analysis of genetic traits in population samples.
June 21: WVAR Annual Meeting, UCLA (Contributed paper)
With Chensheng Kuang, Cecelia Laurie, and Chaozhi Zheng.
Models for the coancestry of DNA in extant individuals
Aug 5: JSM, Montreal, Canada. (Special Topic Contributed Session)
With Chris Glazner, Mary Kuhner, and Chaozhi Zheng.
MCMC for coancestry in pedigrees and populations
Nov 26: SQG Conference, UW Tower, Seattle, Washington.
Coancestry of genome in pedigrees and populations
Dec 12: SMEEG conference, Angers, France.
Models for the use and inference of identity-by-descent in populations
(Also given to UW PopgenLunch group, Dec 6.)

2014:

Feb 1: Workshop on Computation-Intensive Probabilistic and Statistical Methods
for Large-Scale Population Genomics. Simons Institute, Berkeley.
Coancestry in the analysis of complex traits.
Mar 7: UW PopgenLunch seminar
Computations and Monte Carlo on Pedigrees, IBD graphs, and BEAGLE DAGs:
Towards an LD-adjusted pedigree-free lod-score
June 9: IPAM Genomics Reunion Workshop: Lake Arrowhead.
Haplotypic variation and inference of coancestry:
Two related incomplete projects
(Also given to UW PopgenLunch group, June 6.)
July 7: IBC, Florence, Italy (Invited session, substitute)
Estimating Relationships and Relatedness from Genetic Marker Data
July 8: IBC, Florence, Italy (Contributed session)
Inference of coancestry in admixed populations.
(Joint work with Mary K. Kuhner)

2015:

March 26: Rustagi Lecture, Dept. Statistics, Ohio State University.
Gene mapping in the absence of pedigree information.
April 17: UW PopgenLunch seminar
Gene mapping from inferred identity by descent
May 4-15: Vietnam National University; University of Science. Hanoi, Vietnam.
Probability models and statistical inference procedures

- arising in population genetics.
 Fifteen lectures for final honors mathematics students.
- May 8; Opening Speaker; Statistics Day, VNU, University of Science (Hanoi),
 Statistics for Genetics and Genomics: Past, Present and Future.
- July 6: Invited Keynote speaker, iEOS 2015, St. Andrews. Scotland
 Genomics and inheritance
- July 30: Invited Speaker, WEHI Centenary Symposium, Melbourne, Australia.
 Inheritance of genomes: across chromosomes and among individuals
- Oct 16 : Invited speaker; Cold Spring Harbor Laboratory Symposium in
 Probabilistic Modeling in Genomics
 Modeling and inferring coancestry among multiple individuals
 across a chromosome.
 (Also given to UW PopGenLunch group, Oct 7)
- 2016:
- May 23: Keynote speaker, IBS--RBras, Salvador Brazil. (May 22--25)
 Across and among genomes: models and metrics for the
 genetic mapping of quantitative traits
 (Preliminary version given to UW PopGenLunch group, May 6)
- June 30: Invited Distinguished Lecture, 4th IMS-APRM, Hong Kong
 Mapping quantitative traits through the inference of coancestry
 in populations
- July 11: Presidential Address, IBC, Victoria, Canada
 History and geography of diversity in IBS and in Biometry.
- Oct 26: UW PopgenLunch seminar
 Finding genes via the co-ancestry of genome.
- Nov 9: MBI online National Colloquium webinar
 Finding genes via relatedness and the co-ancestry of genome.
- 2017:
- Jan 25: Statistics department, CREEM, University of St Andrews, UK.
 Dependence among individuals and across genomes: using shared
 descent in the genetic mapping of quantitative traits.
- Feb 17: Roslin Institute, University of Edinburgh, UK
 Two, three, or many? Estimation of the shared descent of genome.
- Feb 25; Statistics Department, University of Leeds, UK
 Finding genes via shared ancestry of genome
- March 17: E-ACTG meeting Edinburgh; invited talk.
 Mapping QTL using shared descent of genome
- March 29: QBDG seminar, CBD ST. Andrews
 Relationships, relatedness, and estimation of the shared
 descent of genome
- April 5; European Mathematical Genetics meeting, Tartu, Estonia
 Estimation of realized relatedness: contiguity matters.
- April 21: Statistics Department, University of Edinburgh, Scotland, UK
 Models and methods for the estimation of the shared descent
 of genomes
- April 24: Carnegie Lecture, School of Biological Sciences,
 University of St. Andrews, UK
 Variation in inheritance among individuals and across genomes
- May 3: Brazil at St Andrews: Workshop on Amazonian Biodiversity
 Genetic variation in Amerindian Populations: 1976-1998
- May 18: Mitchell Lecture, School of Mathematics and Statistics,
 University of Glasgow, UK
 Inference and application of the shared descent of genome
 in population samples
- June 28: RSS Highlands meeting, Aberdeen, Scotland, UK
 Mapping causal DNA through the shared descent of genome in
 population samples
- June 19: Nordic-Baltic Biometric Conference, Copenhagen, Denmark
 Biometry and the International Biometric Society
- June 20: Nordic-Baltic Biometric Conference, Copenhagen, Denmark

- Estimation of realized relatedness and joint identity by descent
(Work joint with Bowen Wang)
- July 18: World Statistics Congress of the ISI, Marrakech, Morocco
Two, three, or many? Estimation of the shared descent of genome.
(Contributed paper: Joint work with Bowen Wang)
- July 19: World Statistics Congress of the ISI, Marrakech, Morocco
Presentation as President of the International Biometric Society
- Nov 3: PopGenLunch Seminar, University of Washington.
Detecting inbreeding depression and recessive lethals from data on survivors
- Nov 27: Australasian region of the IBS, Kingscliff, New South Wales, Australia
Biometry and the International Biometric Society
- 2018:
- Feb 28: PopGenLunch Seminar, University of Washington
Likelihood and latent variables in genetic inference.
- March 22: Genome Sciences Training Program, University of Michigan, Ann Arbor,
Mapping causal DNA through the shared descent of genome in population samples
- April 6: Workshop in honor of Charlie Geyer, i
University of Minnesota, Minneapolis, MN
Information in uncertainty:
Likelihood inference in latent variable problems.
- June 1: PopGenLunch Seminar, University of Washington,
Detecting causal regions for inbreeding depression
Pedigree information in contrast to population-inferred descent.
- 2019:
- January 30: PopGenLunch Seminar, University of Washington.
Fools step in where angels fear to tread: perils of model mis-specification in heritability estimation (work with Bowen Wang)
- May 29: StatDay, University of Washington,
The huge variance of genome descent: I met my distant cousin and she looks just like me.
- June 5: PopGenLunch Seminar, University of Washington.
Computation of pedigree-based kinship coefficients:
a challenge of 59K individuals, 393 founders, 66 generations.
Plus ca change, plus c'est la meme chose.
- June 24-26; WNAR Contributed Paper: Portland, Oregon.
Segments of genome: identity by descent, state, or function.
- July 12-14: CNC-7 Contributed Paper: Harpenden, UK.
Effects of mis-specification of genotypic covariance matrices
- Sept 27: Invited talk, RTG Workshop, Goettingen, Germany
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- Oct 3-5: Invited plenary speaker; WSDS, Bellevue, WA.
The true success is the journey: A career of research and education in statistical science.