

## **Seminars and research short courses 2003- 2022**

### **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 pedigree: 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: XXII International Biometric Conference, 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 International Biometric Conference, 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 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 1 million 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 PopGenLunch 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  
(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: WNAR 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: WNAR 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: XXVII International Biometric Conference, Florence, Italy (Invited session, substitute)

Estimating Relationships and Relatedness from Genetic Marker Data

July 8: XXVII International Biometric Conference, 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 individual 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: XXVIII International Biometric Conference, Victoria, Canada  
Presidential Address: History and geography of diversity in IBS and in Biometry.
- Oct 26: PopGenLunch seminar, University of Washington  
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 & 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, 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.

July 10: XXIX International Biometric Conference, Barcelona, Spain  
Realized genome sharing in heritability estimation using random effects models  
(Work with Bowen Wang: earlier versions presented by Wang, StatGen & WNAR )

### **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  
Genetic similarity between relatives: causes and consequences.

Oct 4: Invited plenary speaker; WSDS 2019, Bellevue, WA.

The true success is the journey:

A career of research and education in statistical science.

Nov 20: PIMS Lecture, University of Manitoba, Winnipeg, Manitoba, Canada.

Variation in the descent of genome: modeling and inference.

**2020.:**

Feb 5: PopGenLunch Seminar, University of Washington.

History of likelihood approaches to LD and Haplotypes

Feb 19: COMBI Seminar, University of Washington

Segments of DNA, Relatedness of Individuals, and Heritability of Traits

June 23: vISEC, Sydney, Australia (virtual, synchronous, interactive)

Detecting selection through realized relatedness in natural populations

July-August: XXX International Biometric Conference, online (Seoul, Korea):

prerecorded, interactive discussion.

A century of genotypic correlations and relatedness between individuals

**2022:**

March 4: Center for Theoretical and Applied Genetics, Berkeley, CA (Hybrid Webinar)

A century of analysis of genome descent and survival

July 11: XXXI International Biometric Conference, Riga, Latvia (in person)

Genomes surviving to and from a cloned ancestral individual

in a severely endangered species

Oct 24: 2022 Lange Symposium on Statistical Genetics. UCLA. Invited speaker.

Celebrating 100 years of inferences of and from gene identity by descent.

**2023:** (upcoming)

March 17: Advances in Statistical and Computational Methods for the Analysis of  
Biomedical, Genetic and Omics Data:

Conference in Honor of Shilli Lin: Invited plenary speaker.

As data density increases: from pedigrees to populations to pedigrees.

April 21: 51<sup>st</sup> European Mathematical Genetics Meeting, University of Surrey, Guildford, UK.

Invited speaker: celebrating 50 years since the first meeting in 1973.

I: Some history of the (E)MGM. II: Survival of founder genome in a cloned member  
of an endangered species: Equus Przewalski

July 17: 64<sup>th</sup> ISI World Statistics Conference, Ottawa, Canada

Dependence in the survival of ancestral genomes.