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 Epidmiology, 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: Woodroofe 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, amd 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 givento 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 Habor 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, Winipeg, 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:
March 17: Advances in Statistical and Computational Methods for the Analysis of
                Biomedical, Genetic and Omics Data:
        Conference in Honor of Shili Lin: Invited plenary speaker.
        As data density increases: from pedigrees to populations to pedigrees.
April 21: 51st 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: 64th ISI World Statistics Conference, Ottawa, Canada
        Dependence in the survival of ancestral genomes.

2024:
June 11: WNAR Annual Meeting, Fort Collins, Colorado
        The ancestry of a genome
Dec 12: XXXII International Biometric Conference, Atlanta, GA, USA
        The ancestral genome of a species survivor.

2025:
April 15: EvoHub Chalk-talk; University of Washington
        Genome ancestry and descent in small populations

June 17: WNAR Annual Meeting, Whistler, BC, Canada
            Genome ancestry and descent in small populations
Oct   6;   65th ISI World Statistics Conference, Den Haag, Netherlands
            Dependence in genome descent in small populations.
Oct 24; Statistics Department Seminar, Simon Fraser University, Burnaby, BC, Canada
            Genetic ancestry and descent in small populations

2026: (Upcoming)
June: WNAR Annual Meeting, Washington State University, Pullman, WA
            Genome ancestry and descent in population pedigrees.