

Seminars 2003- 2016

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 20: NBBC, Copenhagen
- June 28: Seminar for the RSS Highlands Group, Aberdeen, Scotland UK
Mapping causal DNA through the shared descent of genome
in population samples
- July 20: ISI WSC–2017 Marrakech; 3 sessions
- 1) Chair/discussant: IBS invited special session (ISP 123)
 - 2) Session for society presidents,
 - 3) Contributed paper:
Two, three, or many? Estimation of the shared descent of
genome