CURRICULUM VITAE

Kenneth Martin Rice, Ph.D.

1. **Date**

   September 29, 2020

2. **Biographical Information**

   - Kenneth Martin Rice
   - University of Washington
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3. **Education**

   - Churchill College, Cambridge University. B.A. Hons, Mathematics, 1st class, 1995
   - Churchill College, Cambridge University. Diploma in Mathematical Statistics,
     with distinction, 1998 ("Analysis of phenotypic variation in Von Hippel Lindau Disease",
     supervised by D Easton)
   - Churchill College, Cambridge University. Ph.D, Biostatistics, 2001 ("Models for
     misclassification of covariables in epidemiology", supervised by D Spiegelhalter, PME Altham)

4. **Licensure:**

   Not applicable

5. **Professional Positions**

   - Research Associate, MRC Biostatistics Unit, Cambridge, 2001-2004
   - Assistant Professor, University of Washington, Seattle WA, 2004-2010
   - Associate Professor, University of Washington, Seattle WA, 2010-2018
   - Professor, University of Washington, Seattle WA, 2018-

6. **Honors, Awards, Scholarships**

   - Scholarship award, Churchill College, Cambridge University, 1995
   - Cambridge University Wishart Prize for Statistics, 1998
   - Cambridge University Smith-Knight and Rayleigh-Knight Prize for Applied Mathematics Essay,
     "Misclassification of Exposure in Case-Control Studies", 2000
   - European Young Researcher Award to attend International Workshop on Statistics with Deficient
     Data, Munich, 2000

- European Young Researcher Award to attend Inaugural Meeting of the International Biometric Society, Eastern Mediterranean Region, Athens, 2001
- European Young Researcher Award to attend Valencia International Meeting on Bayesian Statistics, Tenerife, 2002
- MRC Additional Salary Progression Award, 2003
- American Statistical Association's Section on Epidemiology in Statistics, Young Scholar Award for best paper presented by a 'Young Investigator' at the Joint Statistical Meetings, "A full-likelihood derivation of conditional methods for matched case-control studies, with application to misclassification of exposure", 2003
- Best Talk, Royal Statistical Society Young Statisticians' Meeting, "When is an outlier not an outlier?", 2004
- Young Researcher Award, to attend Fifth International Workshop on Objective Bayesian Statistics, 2005
- Poster Prize, Fifth International Workshop on Objective Bayesian Statistics, 2005, "Towards reference priors for alternative distributions, with applications"
- UW Biostatistics Retreat: Best Faculty Presentation; 2006 (as voted by student attendees)
- UW Biostatistics Retreat: Best Faculty Presentation; 2007 (as voted by student attendees)
- UW Biostatistics Retreat: Best Faculty Presentation; 2008 (as voted by student attendees)
- CHARGE consortium "Tiger" award, 2016, for contributions since its inception
- Fellow of the American Statistical Association, 2018
- Prentice Professorship, 2019-2020

7. **Professional Activities (outside of UW)**

External Consulting:

None

Reviewer:

Annals of Applied Statistics, American Journal of Kidney Diseases, Archives of General Psychiatry, Bayesian Analysis, BioMedCentral Genetics, Biometrical Journal, Biometrics, Biometrika, Biostatistics, Blood, Circulation, Computational Statistics and Data Analysis, Epidemiology, Human Genetics, Genetic Epidemiology, International Journal of Epidemiology, Journal of Clinical Epidemiology, Journal of the American Society of Echocardiography, Journal of the American Statistical Association (Theory & Methods, and Applications & Case Studies), Journal of the Royal Statistical Society Series A, Journal of the Royal Statistical Society Series C, Journal of Statistical Planning and Inference, Lancet, Nature, Nature Genetics, New England Journal of Medicine, Nicotine & Tobacco Research, PLoS ONE, Psychometrika, Statistical Science, Statistics and Computing, Statistics in Medicine, The American Statistician

I am a 'dedicated statistical referee' for the Circulation group of journals, including a role as Statistical Editor for the Journal of the American Heart Association; these are paid, regular commitments.

I have served as an Associate Editor for Statistics in Medicine, and for the Journal of the Royal Statistical Society Series A.

Professional Societies:

American Statistical Association, 2002-
Royal Statistical Society, 2002-

Other:

Organizer, Royal Statistical Society Young Statisticians' Meeting 2003, Cambridge University

8. **Bibliography**

Refereed research articles (by area)

See also my bibliography on myNCBI and my profile on Google Scholar

> **Methods** (bold denotes work as a first or senior author, or with a student or mentee as first author)

1. Li et al (2020) Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nat Genet. Sep;52(9):969-983. doi: 10.1038/s41588-020-0676-4. PubMed PMID: 32839606; PubMed Central PMCID: PMC7483769.
2. **Qijun Li K, Rice K. Improved inference for fixed-effects meta-analysis of 2 × 2 tables. Res Synth Methods. 2020 May;11(3):387-396. doi: 10.1002/jrsm.1401. PubMed PMID: 32092228.**
3. Sitlani CM, Lumley T, McKnight B, Rice KM, Olson NC, Doyle MF, Huber SA, Tracy RP, Psaty BM, C Delaney JA. Incorporating sampling weights into robust estimation of Cox proportional hazards regression model, with illustration in the Multi-Ethnic Study of Atherosclerosis. BMC Med Res Methodol. 2020 Mar 14;20(1):62. doi: 10.1186/s12874-020-00945-9. PubMed PMID: 32169052; PubMed Central PMCID: PMC7071747.
4. **Rice K, Bonnett T, Krakauer C. Knowing the signs: a direct and generalizable motivation of two-sided tests (with discussion). Journal of the Royal Statistical Society: Series A (Statistics in Society). 2019/12; doi: 10.1111/rssa.12496.**
5. Gogarten SM, Sofer T, Chen H, Yu C, Brody JA, Thornton TA, Rice KM, Conomos MP. Genetic association testing using the GENESIS R/Bioconductor package. Bioinformatics. 2019 Jul 22;. doi: 10.1093/bioinformatics/btz567. [Epub ahead of print] PubMed PMID: 31329242.
6. **Sofer T, Zheng X, Gogarten SM, Laurie CA, Grinde K, Shaffer JR, Shungin D, O'Connell JR, Durazo-Arvizo RA, Raffield L, Lange L, Musani S, Vasan RS, Cupples LA, Reiner AP; NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Laurie CC, Rice KM. A fully adjusted two-stage procedure for rank-normalization in genetic association studies. Genet Epidemiol. 2019 Apr;43(3):263-275. doi: 10.1002/gepi.22188. Epub 2019 Jan 17. PMID: 30653739**
7. **Chen H, Huffman JE, Brody JA, Wang C, Lee S, Li Z, Gogarten SM, Sofer T, Bielak LF, Bis JC, Blangero J, Bowler RP, Cade BE, Cho MH, Correa A, Curran JE, de Vries PS, Glahn DC, Guo X, Johnson AD, Kardia S, Kooperberg C, Lewis JP, Liu X, Mathias RA, Mitchell BD, O'Connell JR, Peyser PA, Post WS, Reiner AP, Rich SS, Rotter JI, Silverman EK, Smith JA, Vasan RS, Wilson JG, Yanek LR; NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium; TOPMed Hematology and Hemostasis Working Group, Redline S, Smith NL, Boerwinkle E, Borecki IB, Cupples LA, Laurie CC, Morrison AC, Rice KM, Lin X. Efficient Variant Set Mixed Model Association Tests for Continuous and**

Binary Traits in Large-Scale Whole-Genome Sequencing Studies. Am J Hum Genet. 2019 Feb 7;104(2):260-274. doi: 10.1016/j.ajhg.2018.12.012. Epub 2019 Jan 10. PMID: 30639324

8. **Domínguez Islas C, Rice KM. Addressing the estimation of standard errors in fixed effects meta-analysis. Statistics in medicine. 2018; 37(11):1788-1809. PMID: 29574827 PMCID: PMC6001579**

9. **Lumley T, Brody J, Peloso G, Morrison A, Rice K. FastSKAT: Sequence kernel association tests for very large sets of markers. Genetic epidemiology. 2018; NIHMSID: NIHMS972871 PMID: 29932245 PMCID: PMC6129408**

10. **Sondhi A, Rice KM. Fast permutation tests and related methods, for association between rare variants and binary outcomes. Ann Hum Genet. 2017 Dec 18;PubMed PMID: 29250767.**

11. **Rice KM, Higgins JP, Lumley T. A re-evaluation of fixed effect(s) meta-analysis. Journal of the Royal Statistical Society. Series A, (Statistics in Society). 2018 January; 181(1):205-227.**

12. **Keller JP, Rice KM. Selecting Shrinkage Parameters for Effect Estimation: the Multi-Ethnic Study of Atherosclerosis. Am J Epidemiol. 2017 Jun 12;PubMed PMID: 28992037.**

13. Brody JA, et al. Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature genetics. 2017; 49(11):1560-1563. PMID: 29074945

14. Sofer T, Heller R, Bogomolov M, Avery CL, Graff M, et al. A powerful statistical framework for generalization testing in GWAS, with application to the HCHS/SOL. Genet Epidemiol. 2017 Apr;41(3):251-258. PubMed PMID: 28090672; NIHMSID: NIHMS829142; PubMed Central PMCID: PMC5340573.

15. Castaldi PJ, Cho MH, Liang L, Silverman EK, Hersh CP, et al. Screening for interaction effects in gene expression data. PLoS One. 2017;12(3):e0173847. PubMed PMID: 28301596; PubMed Central PMCID: PMC5354413.

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18. Sung YJ, Winkler TW, Manning AK, Aschard H, Gudnason V, et al. An Empirical Comparison of Joint and Stratified Frameworks for Studying G × E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. Genet Epidemiol. 2016 Jul;40(5):404-15. PubMed PMID: 27230302; NIHMSID: NIHMS781298; PubMed Central PMCID: PMC4911246.

19. Chen H, Wang C, Conomos M, Stilp A, Li Z, Sofer T, Szpiro A, Chen W, Brehm J, Celedon J, Redline S, Papanicolaou G, Thornton T, Laurie C, Rice K, Lin X: Control for population structure and relatedness for binary traits in genetic association studies using logistic mixed models. American journal of human genetics. 2016; 98(4):653-66. PMID: 27018471 PMCID: PMC4833218

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21. **Rice K, Lumley T. Graphics and statistics for cardiology: comparing categorical and continuous variables. Heart. 2016 Mar 1;102(5):349-55. doi: 10.1136/heartjnl-2015-308104. Epub 2016 Jan 27. Review. PubMed PMID: 26819235.**

22. **Sitlani CM, Rice KM, Lumley T, McKnight B, Cupples LA, Avery CL, Noordam R, Stricker BH, Whitsel EA, Psaty BM. Generalized estimating equations for genome-wide**

association studies using longitudinal phenotype data. Stat Med. 2015 Jan 15;34(1):118-30. doi: 10.1002/sim.6323. Epub 2014 Oct 9. PubMed PMID: 25297442.

23. Li S, Mukherjee B, Taylor JM, Rice KM, Wen X, Rice JD, Stringham HM, Boehnke M. The role of environmental heterogeneity in meta-analysis of gene-environment interactions with quantitative traits. Genet Epidemiol. 2014 Jul;38(5):416-29. doi: 10.1002/gepi.21810. Epub 2014 May 6. PubMed PMID: 24801060; PubMed Central PMCID: PMC4108593.

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25. **Voorman A, Rice K, Lumley T. (2012) Fast computation for genome-wide association studies using boosted one-step statistics. Bioinformatics. Jul 15;28(14):1818-22. PMID: 22592383 PMCID: PMC3389774**

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27. **Voorman A, Lumley T, McKnight B, Rice K (2011) Behavior of QQ-Plots and Genomic Control in Studies of Gene-Environment Interaction. PloS ONE 6(5): e19416. doi:10.1371/journal.pone.0019416 PMID: 21589913 PMCID: PMC3093379**

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43. **Rice, K. M. (2004) A full-likelihood derivation of conditional methods for matched case-control studies, with application to misclassification of exposure, Proceedings of the American Statistical Association 2003, Section on Statistics in Epidemiology [CD-ROM], Alexandria, VA: American Statistical Association**

44. **Rice, K.M. (2003) Full-likelihood approaches to misclassification of exposure in matched case-control studies. Statistics in Medicine, 22(20), 3177-3194**

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Cardiovascular Epidemiology
(stars denote equal contributions)

47. Ntalla et al (2020) Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nat Commun. May 21;11(1):2542. doi: 10.1038/s41467-020-15706-x. PubMed PMID: 32439900; PubMed Central PMCID: PMC7242331.

48. De Las Fuentes et al (2020) Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Mol Psychiatry. May 5;. doi: 10.1038/s41380-020-0719-3. PubMed PMID: 32372009; NIHMSID:NIHMS1579455.

49. Shah et al (2020 Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nat Commun. Jan 9;11(1):163. doi: 10.1038/s41467-019-13690-5. PubMed PMID: 31919418; PubMed Central PMCID: PMC6952380.

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51. Noordam R et al (2019) Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nat Commun. 2019 Nov 12;10(1):5121. doi: 10.1038/s41467-019-12958-0. PubMed PMID: 31719535; PubMed Central PMCID: PMC6851116.

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Books and Book Chapters

1. **Rice, K.M. Bayesian methods for model comparison. In Armitage and Colton, eds, Encyclopedia of Biostatistics, 2nd Edition, Wiley, February 2005.**
2. **Rice, K.M. Bayesian measures of goodness of fit. In Armitage and Colton, eds, Encyclopedia of Biostatistics, 2nd Edition, Wiley, February 2005.**

Other Non-Refereed Scholarly Publications

1. **Dukić V and Rice K (2011) Discussion of Louis et al, 'Association Tests that Accommodate Genotyping Uncertainty', BAYESIAN STATISTICS 9 pp. 413-417. J. M. Bernardo, M. J. Bayarri, J. O. Berger, A. P. Dawid, D. Heckerman, A. F. M. Smith and M. West (Eds.) Oxford University Press**
2. **Rice K (2009). Review, Random Effect and Latent Variable Model Selection, edited by Dunson *BIOMETRICS* 65(3) 993**
3. **Rice K (2010) Review, The Handbook of Research Synthesis and Meta-Analysis (2nd ed.) edited by Hedges et al (ed) *JASA* 2010, 1627**
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9. **Patents and Other Intellectual Property**

1. Rice, K.M., 'EmbedBugs' R/S library for remote running of the WinBugs software, MRC Biostatistics Unit, Nov 2001.
2. Kloster M and Rice K, 'huber.lm' R package for outlier-robust inference, implementing methods described by Rice and Spiegelhalter, May 2006.

10. **Current Other Support:**

Active

U01 HL120393-04   (B Psaty)   4/1/2014 - 3/31/2019 NCE   0.6 CM
NIH $652,895
"Rare Variants and NHLBI Traits in Deeply Phenotyped Cohorts" (ECA)
Using jointly-called ExomeChip genotype data from over 50,000 subjects, the primary aim of this application is to discover novel candidate genes and putative functional variants for high-priority heart, lung and blood phenotypes in multi-ethnic cohorts.

U01 HL120393-04S2 (B Psaty/K Rice/B Weir)   01/01/2017 - 3/31/2019 NCE
                              0.27 CM
NIH/NHLBI $618,708
"TOPMed Data Coordinating Center Supplement" (Data Commons)
Heart, lung and blood-related diseases pose an increasingly large burden on our public's health as the population ages. The main goal of this study is to identify genetic risk factors for these diseases.

Understanding these risk factors is likely to lead ultimately to increased disease prevention and new approaches to treatment.

U01 HL137162 (K Rice & B Weir) 4/21/2017 - 03/31/2020
2.4 CM
NIH
$362,712
"From gene regions to whole chromosomes: scaling up association-finding for disease and omics outcomes in TOPMed" (A114244, TOPMed U01)
This application will bring unprecedented forms of analysis to the Trans-Omics for Precision Medicine (TOPMed) already-rich data resources. By using new computational methods, and collaborating with TOPMeds Working Groups, it will address scientific questions that are currently out of reach. The application's investigators are already known in TOPMed for their wealth of technical skill and commitment to the overall project.

HHSN268201800001I (Rice, Psaty, Weir)
05/01/2018 - 04/30/2019 3.0 CM
NIH/NHLBI $3,202,542
Trans-Omics for Precision Medicine (TOPMed) Data Coordinating Center (DCC)" (A133235 TOPMed DCC contract)
The DCC will provide administrative and technical support for the TOPMed project. Technical tasks include data cleaning of sequence data and harmonization of phenotype data. There is not support for methodology development.

R01 HL105756 (B Psaty) 2/15/2011 - 3/31/2019 NCE 1.63 CM
NIH $577,477
"CHARGE Consortium: Gene Discovery for CVD and Aging Phenotypes" (CCG)
The proposed project provides Coordinating Center assistance to the CHARGE consortium and provides for exchanges for students, fellows and junior faculty.

Pending

R01 HL118305 (DC Rao sub-B Psaty) 12/01/2019-11/30/2023 0.6 CM
NIH/Washington U $34,998
A Multi-Ethnic Study of Gene-Lifestyle Interactions in Cardiovascular Traits (A142683 Cardio Traits 2)
The primary goal of the proposed research is to leverage existing GWAS and Exome Chip data in 25 large multi-ethnic cohorts to discover additional genetic loci for cardiovascular traits by modeling gene-lifestyle interactions.

R01 (Sofer, sub-K Rice) 07/01/2019-06/30/2023
1.2 CM
NIH/Brigham and Women's Hospital $21,264
"Analysis of large and diverse whole genome sequencing data sets" (A139939 Sofer BWH R01)
We will develop approaches that will satisfy multiple goals at the same time: test rare variant associations in a pooled sample, account for heterogeneity, and be computationally at least as efficient as existing methods that do not properly account for such heterogeneity.

In addition, I have acted as PI and director for NHLBI T32 HL007138-35, "Cardiovascular Biostatistics Training" (finished 12/31/2012).

11. **Public Health Practice Activities**

Not applicable

12.   **Conferences and Symposiums**

Invited Oral Presentations

- Invited Speaker, Royal Statistical Society Young Statisticians' Meeting, Liverpool, to talk on; Rice, K.M. Misclassification of Exposure in Matched Case-Control Studies, April 2001
- Invited Probability and Statistics Seminar, Institute of Mathematics and Statistics at the University of Kent at Canterbury, Nov 2003
- "Equivalence of random-effects and conditional likelihoods for matched case-control studies", University of Washington, Department of Biostatistics, Jan 2004
- Cardiovascular Health Research Unit Seminar Series, Lies, damned lies, and what to do with them (introduction to methods which allow for misclassification), March 2005
- Department of Statistics Seminar Series, University of Washington, "Connections between robust inference, outlier detection and false discovery rates", April 2005
- Cardiovascular Health Study Seminar Series, University of Washington, "Connections between robust inference, outlier detection and false discovery rates", May 2005
- Invited Discussant, OBayes5 – Fifth International Workshop on Objective Bayes Methodology, session on Multiple Comparisons, June 2005
- NHLBI meeting on pharmacogenomics; 'Analysis plan for multi-SNP association studies', Sept 2005
- Faculty interest seminar, Departmental Seminar Series, 'Connections between likelihood and model-free methods', October 2005
- "Models with robustness to outliers", Fred Hutchison Cancer Research Center, Biostatistics Seminar Series, Feb 2006
- "Models with robustness to outliers", UW Biostatistics Informal Seminar, Feb 2006
- "Models with robustness to outliers" University of Florida, Department of Statistics, March 2006
- "Connections between local FDR and alternative hypotheses" Invited talk, SAMSI Program on Multiplicity and Reproducibility in Scientific Studies, July 2006
- "Connections between Bayesian and Conditional Inference in Matched Studies", Invited Session on Highly Stratified Data, JSM 2006
- "FDR and Bayesian Multiple Comparisons Rules", Invited Presentation, Valencia/ISBA 8th World Meeting on Bayesian Statistics, June 2006. (with Peter Mueller and Giovanni Parmigiani)
- "Connections between local FDR and alternative hypotheses" SAMSI Program on Multiplicity and Reproducibility in Scientific Studies, July 2006
- "Decision-theoretic multiple comparisons" SAMSI Program on Multiplicity and Reproducibility in Scientific Studies, July 2006
- "Bonferroni for Bayesians"; UW Biostatistics Department Retreat, Oct 2006
- "Models with robustness to outliers", Insightful Corporation, Nov 2006
- "Looking Silly with Statistics: some Modifiable Risk Factors"; VA Biostatistics discussion group, Jan 2007
- "Models with Robustness to Outliers"; University of Chicago, Feb 2007
- "Decision Theory for Multiple Comparisons"; ENAR, Invited Session, March 2007
- "Decision Theory for Multiple Comparisons"; UW Center for Statistics in the Social Sciences, June 2007
- "Decision Theory for Multiple Comparisons"; JSM, Invited Session, July 2007
- "New Frequentist ways to make old Bayesian mistakes"; UW Biostatistics Department Retreat, Sept 2007

- "Analysis Guidelines for Genome-wide Association Studies ", CHARGE consortium meeting, Framingham, July 2008
- "Optimal inference from intervals: a decision-theoretic approach", Portland State University, Jan 2008
- "Novel Bayesian approaches to model-robust inference", Invited Session on Bayesian Methods in Epidemiology, ENAR, March 2008
- "Inference with Robustness to Modeling Assumptions; A Decision Theoretic Approach", Invited Session on Connections Between Bayesian and Frequentist Methods, WNAR, June 2008
- "Model-robust inference: a decision-theoretic approach" (Selected Oral Presentation) International Society for Bayesian Analysis, 9th World Meeting, Hamilton Island, Australia, July 2008
- "Analysis for Genome-wide Association Studies; some Frequently Asked Questions", CHARGE consortium meeting, Seattle, July 2008
- "Bayesian model-robustness: novel approaches that avoid multiplicities", Invited Session on Challenges of Multiplicities In Statistical Analysis, JSM, August 2008
- "Taking the shine off a TROPHY", UW Biostatistics Department Retreat, Sept 2008
- "David Duncan: Recent perspectives on his Decision Theory work" ENAR, March 2009
- "Lessons from CHS genome-wide studies; how they work - and what causes problems" Cardiovascular Health Study Co-ordinating Center, March 2009
- "Correlated Phenotypes in Genome-wide Association Studies ", CHARGE consortium meeting, Rotterdam, April 2009
- "Intuition 'out in the tail': Why the usual rules don't apply" University of Montana, invited seminar, Jan 2010
- "Chasing Tail(s): Statistical Intuition for High-throughput Studies" UW Biostat April 2010
- "Making peace with p's: Bayesian tests with straightforward frequentist properties" CSSS seminar, Nov 2010
- "Chasing Tail(s): Statistical Intuition for High-throughput Studies" University of Utah, invited seminar, Dec 2010
- "Why intuition fails in GWAS": Workshop on Computational Statistical Methods for Genomics and Systems Biology, Université de Montréal, April 2011
- "Making peace with p's: Bayesian tests with straightforward frequentist properties", seminar, Institute for Health Metrics Evaluation, Seattle, April 2011
- "Analysis for GxE: experience from the CHARGE consortium": GENEVA steering committee meeting, Washington DC, May 2011
- "Making peace with p's: Bayesian tests with straightforward frequentist properties": Association of Clinical and Translational Statisticians Annual Meeting, Miami, August 2011
- "Genome-wide analysis of interactions – experiences from CHARGE": Joint Statistical Meetings, Miami, August 2011
- "When is a large sample not so large? Non-intuitive Behavior in High-Throughput Association Analyses" NHLBI Symposium on Genomics, Gene Discovery and Clinical Applications for Cardiovascular, Lung and Blood Diseases, Washington DC, September 2011
- "QQ Plots in CHARGE-S", CHARGE consortium meeting, Rotterdam, Los Angeles, October 2011
- "When is a Large Sample not so Large? Non-Intuitive Behavior in High-Throughput Association Analyses", NCI Biostatistics Seminar, Washington DC, February 2012
- "Extreme Statistics: Non-Intuitive Behavior in High-Throughput Association Analyses", Texas A&M University, Department of Statistics Seminar, February 2012
- "Efficient Design and Inference for Gene x Environment Interaction, using Sequencing Data", ENAR Invited Session on Survey Methods, Washington DC, April 2012

- "Making peace with p's: Bayesian tests with straightforward frequentist properties" University of Auckland, Department of Statistics Seminar, April 2012
- "Exome Chip Analysis Guidelines", CHARGE consortium meeting, Reykjavik, Iceland, May 2012
- "When is a large sample not so large? Problems with inference in high-throughput studies, with some solutions" NIEHS Symposium on Emerging Issues in Analysis and Design of Large Scale Genetic Studies, North Carolina, May 2012
- "Interpreting tests which are both Bayesian and frequentist", ISBA World Meeting, Kyoto, Japan, June 2012
- "Asymptotics in GWAS: When Do We Need Non-standard Methods?" IMS Asia-Pacific Regional Meeting, Tsukuba, Japan, July 2012.
- "Understanding Shrinkage in a Decision Theoretic Framework", JSM Invited Session, San Diego, August 2012
- "When is a large sample not so large? Analytic problems (and solutions) in GWAS", Washington University St Louis, Department of Biostatistics Seminar, September 2012
- "Shrinkage, as a simple decision", International Society for Bayesian Analysis Regional Meeting and Workshop/Conference on Theory and Applications, Varanasi, India, January 2013
- "A Unified Approach to Shrinkage", New Zealand Statistical Association, Hamilton New Zealand, November 2013
- "A Unified Approach to Shrinkage", Research School of Finance, Actuarial Studies and Applied Statistics Summer Camp, Canberra Australia, December 2013
- "A Unified Approach to Shrinkage", University of New South Wales Department of Statistics, Sydney Australia, December 2013
- "A Unified Approach to Shrinkage", University of Washington Department of Biostatistics, January 2014
- "Sharing Individual Participant Data (IPD); how might it help?", CHARGE meeting, Redondo Beach CA, January 2014
- "Meta/Mega Analysis of G x E Interactions with Complex Disease Outcomes: Experience and Insights from the CHARGE Consortium", ENAR, Washington DC, March 2014
- "Fixed-effects meta-analysis: it's what data want to tell you about", Bayesian Biostatistics Workshop, Zurich, Switzerland, July 2014
- "Bayesian Score Tests", International Indian Statistical Association Meeting, Riverside CA, July 2014
- "Meta-analysis: mega-analysis and pooling", NCI Data Harmonization Workshop, Bethesda, Oct 2014
- "Performance of score tests for binary outcomes", CHARGE meeting, Washington DC, November 2014
- "The truth about meta-analysis" Cardiovascular Health Studies Coordinating Center, Seattle, January 2015
- "Robust Standard Errors and Controlling Inflation", Gene-Lifestyle Working Group Meeting, St Louis, January 2015
- "The truth about meta-analysis" Cardiovascular Health Research Unit, Seattle, February 2015
- "Association tests for the rarest variants", WNAR, Boise, June 2015
- "fastSKAT: Sequence Kernel Association Tests for large sets of markers" at ASHG 2016, October 2016
- "fastSKAT: Sequence Kernel Association Tests for large sets of markers" at TOPMed/NHGRI analysis satellite meeting to Boston PQG, November 2016
- "Why does my QQ plot look weird?" TOPMed Steering Committee in-person meeting, Washington DC, December 2016

- "Issues arising in early WGS analysis": CHARGE consortium in-person meeting, New York, March 2016
- "fastSKAT: Sequence Kernel Association Tests for large sets of markers" at JSM, Baltimore, July 2017
- "We didn't see this in GWAS: Understanding and Fixing Unfamiliar Problems in Association Analyses, when Pooling Whole Genome Sequence Data from Multiple Studies", ENAR, Atlanta, March 2018
- "Knowing the Signs: Decision theory for significance tests", ISBA World Meeting, Edinburgh, June 2018
- "A re-appraisal of fixed-effect(s) meta-analysis", JSM 2018, Vancouver, August 2018
- "A re-appraisal of fixed-effect(s) meta-analysis", University of Edinburgh Department of Statistics Seminar, September 2018
- "A re-appraisal of fixed-effect(s) meta-analysis", Joint RSS/PSI webinar, with discussion, September 2018
- "A re-appraisal of fixed-effect(s) meta-analysis", University of Michigan Department of Biostatistics Seminar, November 2018
- "A re-appraisal of fixed-effect(s) meta-analysis", Ohio State University Department of Statistics Seminar, February 2019
- "Analysis of Whole Genome Sequence Analysis in >100k Individuals: Experience in the TOPMed Program", ASA Symposium on Data Science and Statistics, Bellevue, May 2019
- "Knowing the Signs: Decision theory for significance tests (with discussion)", Ordinary Meeting of the Royal Statistical Society, held at its annual conference, Belfast, September 2019

Meeting Oral Abstracts

- Royal Statistical Society Young Statisticians' Meeting, Liverpool, to talk on; Rice, K.M. Misclassification error in genotyping, April 2001
- Bayesian measures of model complexity and fit, Ordinary Meeting of the Royal Statistical Society, March 2002
- Statistical modeling and analysis of genetic data, Ordinary Meeting of the Royal Statistical Society, May 2002
- Monitoring and comparing clinical performance - do we need 'clever' statistical methods?, Medical Section of the Royal Statistical Society, May 2002
- Royal Statistical Society Young Statisticians' Meeting, Cambridge, (as organizer), April 2003
- Performance Monitoring and Surveillance, Medical Section of the Royal Statistical Society, Jan 2003
- Ecological Inference for 2x2 tables, Ordinary Meeting of the Royal Statistical Society, Nov 2003
- University of Washington Department of Biostatistics Seminar Series, Equivalence of random-effects and conditional likelihoods for matched case-control studies, Jan 2004
- 22nd International Biometric Conference, Cairns, Having your cake and eating it: Equivalence of random-effects and conditional methods for matched case-control studies, July 2004

Meeting Posters

- Santa Cruz Bayesian Data Analysis Workshop, "A Bayesian derivation of conditional methods
- for case-control studies, with applications", August 2003
- 4th Workshop on Bayesian Nonparametrics, Universita di Roma "La Sapienza", "A Bayesian semi-parametric derivation of conditional likelihoods, with applications to case-control studies", June 2004

- Fifth International Workshop on Objective Bayesian Statistics, "Towards reference priors for alternative distributions, with applications", 2005
- "Models with robustness to outliers" Contributed Poster, Valencia/ISBA 8th World Meeting on Bayesian Statistics, June 2006
- "We didn't see this in GWAS: Understanding and fixing unfamiliar problems in association analyses, when pooling whole genome sequence data from multiple studies", ASHG Orlando, October 2017

13. **University Service**

- University of Washington, Department of Biostatistics, Biostatistics Strategic Planning Committee member, 2008-2010
- University of Washington, Department of Biostatistics, Biostatistics Admissions Committee member, 2004-2006, 2010-11
- University of Washington, Faculty Field Tour Recruitment Session Participant, March 2006
- University of Washington, Department of Biostatistics, Seminars 2006-2010 ; chaired seminar committee, invited speakers, managed visits for external speakers, introduced speakers
- Member, University of Washington, Department of Biostatistics Educational Policy and Teaching Evaluation Committee, 2010-2019, 2020-
- Member, University of Washington, Department of Biostatistics Training Grant Directors Committee, 2012-14
- Chair, University of Washington, Department of Biostatistics PhD Review Committee, 2013-2014
- Faculty Senator, 2015-2019

14. **Professionally-Related Service**

- Session Chair, "Recent Advances in the Design and Analysis of Clinical Trials", Invited Session, JSM 2006
- Member, MESA Genetics P&P Committee; (Jan 2007- 2013) Statistical appraisal and review of ancillary study proposals
- Chair, Contributed Papers Session on Multiple Comparisons, ENAR 2007
- Organizer, Contributed Papers Session on Connections between Bayesian and Frequentist Methods, WNAR 2008
- Chair, Analysis Committee, CHARGE consortium of Genome-Wide Association Studies, 2007-
- Organizer and Chair, Contributed Papers Session on Meta-Analysis, ENAR 2009
- Organizer, Contributed Session on "Analysis of Genome-Wide Association Studies: Methods from the CHARGE Consortium of Cohort Studies", JSM 2011
- Member, Savage Award committee (thesis prize, International Society for Bayesian Analysis) 2011-12
- General Methodology Chair, JSM Program Committee 2012-13
- Session Organizer and Chair, "Twenty Years of Gibbs Sampling/MCMC", Introductory Overview Lecture Session, JSM 2013
- Session Chair "Next-Generation Bioinformatics and Beyond", Introductory Overview Lecture Session, JSM 2013
- JSM Program Chair for WNAR, 2015-16, 2016-17 and 2017-18
- Member, UW CSSS executive committee, 2015-
- Member, External Executive Committee, The Environmental Determinants of Diabetes in the Young (TEDDY) Study, 2014-

- Chair, Analysis Committee, TOPMed Whole Genome Sequencing program, 2015-
- Member, Observational Study Monitoring Board Member, Pediatric Cardiac Genetics Consortium, 2015-
- Member, The Infectious, Reproductive, Asthma and Pulmonary Conditions (IRAP) Study Section, October 2018
- Member, NIEHS Board of Scientific Counselors, Review of the Immunity, Inflammation and Disease Laboratory, Translational Clinical Research Unit and the Environmental Polymorphisms Registry November 2019

15. **Other Pertinent Information**

Online Educational Programs

- WinBUGS – The Movie! A Flash guide to where to point and click when using the WinBUGS software.

Meetings attended (see also Invited Presentations)

- Ninth Annual Public Health Forum, 'Poverty, Inequality and Health', London School of Hygiene and Tropical Medicine, April 1999
- Brain Connectivity Workshop, University of Cambridge, May 2003
- Inaugural meeting of Leducq International Network Against Thrombosis (LINAT) Vermont, December 2004
- AHA 45th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Washington DC, May 2005
- Second international LINAT meeting, Leiden, The Netherlands, July 2005
- Third Seattle Symposium in Biostatistics: Statistical Genetics and Genomics, Seattle, Nov 2005
- AHA 46th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Phoenix, May 2006
- ISM Workshop on Recent Advances on Stochastic Computation and Bioinformatics, Vancouver, August 2006
- Conference on Statistical Methods in Epidemiology and Observational Studies, Seattle, August 2006
- AHA 47th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Florida, May 2007
- Fourth international LINAT meeting, Seattle, June 2007
- CHARGE Consortium, Steering Committee Meeting, Framingham, Jan 2008
- Multi-Ethnic Study of Atherosclerosis, Steering Committee Meeting, Washington DC, Feb 2008
- AHA 48th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Colorado, March 2008
- GENEVA project, Steering Committee Meeting, Washington DC, May 2008
- Fifth international LINAT meeting, Oklahoma, May 2008
- CHARGE Consortium, Steering Committee Meeting, Framingham, July 2008
- AHA 49th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Tampa, March 2009
- CHARGE Consortium, Steering Committee Meeting, Rotterdam, April 2009
- GENEVA project, Steering Committee Meeting, Washington DC, April 2009
- Sixth international LINAT/MISTRAL meeting, Leuven, Belgium, May 2009

- AHA 50th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, San Francisco, March 2010
- AHA 51st Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Atlanta, March 2011
- Exome Sequencing Project, Progress Meeting, Washington DC, June 2011 and September 2011
- Prentice Symposium, Fred Hutchison Cancer Research Center, Seattle, October 2011
- AHA 52nd Annual Conference on Cardiovascular Disease Epidemiology and Prevention, San Diego, March 2012
- Exome Sequencing Project, Progress Meeting, Washington DC, March 2012
- CHARGE Consortium, Steering Committee Meeting, Houston, December 2012
- AHA 53rd Annual Conference on Cardiovascular Disease Epidemiology and Prevention, New Orleans, March 2013
- ASA Joint Statistical Meetings, Montreal, August 2013
- AHA 54th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, San Francisco, March 2014
- ASA Joint Statistical Meetings, Seattle, August 2015
- AHA 55th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Baltimore, March 2015
- ENAR Meeting, Miami, March 2015
- CHARGE Consortium Meeting, Jackson, July 2015
- ASHG Meeting, Baltimore 2015
- CHARGE Gene-Lifestyle Working Group meeting, December 2015
- AHA 56th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Phoenix, March 2015
- CHARGE Consortium Meeting, Charlottesville, September 2016
- ASHG Meeting, Vancover BC, October 2016
- Harvard Program in Quantitative Genomics,10th annual conference, "Whole Genome Sequencing Analysis: Comprehensive Capture of Genetic Variants", Boston, November 2016
- TOPMed Steering Committee in-person meeting, Washington DC, December 2016
- Alzheimer's Disease Sequencing Project in-person meeting, Washington DC, January 2017
- AHA 57th Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Portland OR, March 2017
- CHARGE Consortium Meeting, Boston, September 2017
- TOPMed Steering Committee in-person meeting, Washington DC, December 2017
- NIH Data Commons Pilot Program in-person meeting, Washington DC, December 2017
- Joint Genome Sequencing Project/TOPMed analysis workshop, Nashville, January 2018
- NIH Data Commons Pilot Project in-person meetings, February, August, September & October 2018
- NIH "All of Us" in-person planning meeting, March 2018
- CHARGE Consortium Meeting, Rotterdam, April 2018
- TOPMed analysis workshop, Ann Arbor, April 2018
- TOPMed Steering Committee in-person meeting, Washington DC, December 2018
- NHLBI DataSTAGE in-person meeting, Washington DC, December 2018
- Joint GSP-TOPMed analysis workshop, Ann Arbor, February 2019
- NHLBI DataSTAGE in-person meeting, Chapel Hill NC, March 2019
- TOPMed Steering Committee in-person meeting, Washington DC, April 2019
- TOPMed 2.0 Brainstorming meeting, Washington DC, April 2019
- NHLBI DataSTAGE in-person meeting, Washington DC, June 2019

- CHARGE Consortium Meeting, St Louis MO, June 2019
- TOPMed Steering Committee in-person meeting, Washington DC, December 2019

16. **Teaching History**

Formal Courses

- Biostatistics 578, R and 'extras' for 518, second quarter, Winter 2005
- Biostatistics 590, Consulting, Winter 2006
- Biostatistics 578, Special Topics: Covariate Measurement Error, Spring 2006
- Biostatistics 580, Departmental Seminar, Autumn/Winter/Spring 2006/7
- Statistics/Biostatistics 570, Regression models for independent data, Autumn 2006
- Biostatistics 578, R and 'extras' for 518, second quarter, Winter 2007
- Biostatistics 599, Consulting, Winter 2007
- Biostatistics 580, Departmental Seminar, Autumn/Winter/Spring 2007/8
- Statistics/Biostatistics 570, Regression models for independent data, Autumn 2007
- Biostatistics 578, R and 'extras' for 518, first quarter, Autumn 2007
- Biostatistics 578, R and 'extras' for 518, second quarter, Winter 2008
- Biostatistics 578, Special Topics: Association Mapping (team-taught), Spring 2008
- Biostatistics 580, Departmental Seminar, Autumn/Winter/Spring 2008/09
- Biostatistics 578, Human Association Mapping (Multiplicities, Meta-Analysis), Spring 2008
- Statistics/Biostatistics 570, Regression models for independent data, Autumn 2008
- Biostatistics 578, R and 'extras' for 518, first quarter, Autumn 2008
- Biostatistics 578, R and 'extras' for 518, second quarter, Winter 2009
- Biostatistics 578, Human Association Mapping (Multiplicities, Meta-Analysis), Spring 2009
- Statistics/Biostatistics 570, Regression models for independent data, Autumn 2009
- Statistics/Biostatistics 572, Advanced Regression Methods, Spring 2010
- Statistics/Biostatistics 533, Theory of Linear Models, Spring 2010
- Statistics/Biostatistics 571, Regression models for dependent data, Winter 2011
- Statistics/Biostatistics 572, Advanced Regression Methods, Spring 2011
- Statistics/Biostatistics 570, Regression models for independent data, Autumn 2011
- Statistics/Biostatistics 571, Regression models for dependent data, Winter 2012
- Biostatistics 578, Computing and Research, Summer 2012
- Statistics/Biostatistics 590, Statistical Consulting, Winter 2013
- Biostatistics 540, Correlated Data Analysis, Spring 2013
- Statistics/Biostatistics 590, Statistical Consulting, Winter 2014
- Biostatistics 540, Correlated Data Analysis, Spring 2014
- Biostatistics 563, Computing for Research, Summer 2014
- Statistics/Biostatistics 590, Statistical Consulting, Winter 2015
- Biostatistics 513, Medical Biometry III, Spring 2015
- Statistics/Biostatistics 571, Regression models for dependent data, Winter 2016
- Statistics/Biostatistics 572, Advanced Regression Methods, Spring 2016
- Biostatistics 514/517, Biostatistics I, Autumn 2016
- Biostatistics 561, Computational Skills for Biostatistics I, Autumn 2016
- Statistics/Biostatistics 572, Advanced Regression Methods, Spring 2017
- Biostatistics 514/517, Biostatistics I, Autumn 2017
- Statistics/Biostatistics 590, Statistical Consulting, Winter 2018

- Biostatistics 514/517, Biostatistics I, Autumn 2018
- Statistics/Biostatistics 590, Statistical Consulting, Winter 2019
- Statistics/Biostatistics 590, Statistical Consulting, Spring 2020

Other Teaching

Guest Lectures

- Student Journal Club (Bayesian Interpretation of Conditional Likelihoods), Summer 2005
- Biostatistics 536, Fall 2005, guest lecture (Introduction to misclassification)
- Biostatistics 578, Research in Biostatistics, (Introduction to haplotype inference), Summer 2006
- Epidemiology/Health Services 548, guest lecture (Structural Equation Models), Winter 2006
- Biostatistics Informal Seminar Series, 'Models with robustness to outliers', Feb 2006
- Epidemiology 519, guest lecture (Looking Silly with Statistics), Autumn 2006
- Biostatistics 578 (Bayesian Biostatistics), guest lecture, Spring 2007
- Biostatistics 111, Introduction to Biostatistics (Looking Silly with Statistics), Spring 2007
- Biostatistics 578 (Measurement, Design and Analysis in Behavioral or Mental Health Research), guest lecture, Winter 2007
- Epidemiology/Health Services 548, guest lecture (Structural Equation Models), Winter 2007
- Epidemiology/Health Services 590N, guest lecture (Structural Equation Models), Winter 2007
- Epidemiology 519, guest lecture (Looking Silly with Statistics), Autumn 2008
- Biostatistics 111, Introduction to Biostatistics (Guest Lecture), Spring 2009
- Epidemiology/Health Services 590N, guest lecture (Analyzing Multilevel Data), Winter 2009
- Epidemiology 519, guest lecture (Looking Silly with Statistics), Autumn 2009
- Epidemiology/Health Services 590N, guest lecture (Analyzing Multilevel Data), Winter 2010
- Epidemiology 519, guest lecture (Looking Silly with Statistics), Autumn 2010
- Epidemiology/Health Services 590N, guest lecture (Analyzing Multilevel Data), Winter 2011
- Epidemiology 519, guest lecture (Looking Silly with Statistics), Autumn 2011
- Epidemiology 519, guest lecture (Looking Silly with Statistics), Autumn 2012
- Biostatistics 563, Computing and Research in Biostatistics (How To Make a Poster), Summer 2013
- Epidemiology 519, guest lecture (Introduction to Mendelian Randomization), Autumn 2013
- Biostatistics 519/Epi 515, guest lecture (Introduction to Bayesian Statistics), April 2014
- Human Biology 530, guest lecture (Visualizing and summarizing data), January 2015
- Biostatistics 519/Epi 515, guest lecture (Introduction to Bayesian Statistics), April 2015
- Biostatistics 519/Epi 515, guest lecture (Introduction to Bayesian Statistics), April 2016
- Biostatistics 519/Epi 516, guest lecture (Introduction to Bayesian Statistics), April 2017
- Biostatistics 519/Epi 516, guest lecture (Introduction to Bayesian Statistics), April 2018
- Biostatistics 519/Epi 516, guest lecture (Introduction to Bayesian Statistics), April 2019

Continuing Education

- Computing for Statistical Genetics (R and Bioconductor), Summer Institute for Statistical Genetics, 2007 (Seattle and Liege, Belgium)
- Computing for Statistical Genetics (R and Bioconductor), Summer Institute for Statistical Genetics, 2008 (Seattle and Auckland, New Zealand)
- Computing for Statistical Genetics (R and Bioconductor), Summer Institute for Statistical Genetics, 2009 (Seattle and Liege, Belgium)

- Using R for Data-Cleaning and Data-Analysis in Genome-Wide Association Studies, Bioconductor Workshop, July 2009
- Computing for Statistical Genetics (R and Bioconductor), Summer Institute for Statistical Genetics, 2010 (Seattle and Beijing, China)
- Advanced R Programming for Bioinformatics, Summer Institute for Statistical Genetics, 2010 (Seattle)
- Computing for Statistical Genetics (R and Bioconductor), Summer Institute for Statistical Genetics, 2011 (Seattle and Liege, Belgium)
- Advanced R Programming for Bioinformatics, Summer Institute for Statistical Genetics, 2011 (Seattle)
- Computing for Statistical Genetics (R and Bioconductor), Summer Institute for Statistical Genetics, 2012 (Seattle)
- Advanced R Programming for Bioinformatics, Summer Institute for Statistical Genetics, 2012 (Seattle)
- Advanced R Programming for Bioinformatics, Summer Institute for Statistical Genetics, 2012 (Seattle Edinburgh)
- Introduction to R, Summer Institute for Statistical Genetics, Summer Institute in Statistics and Modeling in Infectious Disease, 2013 (Seattle)
- Elements of R, Summer Institute for Statistical Genetics, 2013 (Seattle)
- Advanced R Programming for Bioinformatics, Summer Institute for Statistical Genetics, 2013 (Seattle)
- Elements of R for Bioinformatics, 2013 (University of Auckland, New Zealand)
- Elements of R, South American Institute for Statistical Genetics, 2014 (Sao Paolo, Brazil)
- Introduction to R, Summer Institute for Statistical Genetics, Summer Institute in Statistics and Modeling in Infectious Disease, 2014 (Seattle)
- Elements of R, Summer Institute for Statistical Genetics, 2014 (Seattle)
- Advanced R Programming for Bioinformatics, Summer Institute for Statistical Genetics, 2014 (Seattle)
- Elements of R, Swiss Institute for Statistical Genetics, 2014 (Laussane, Switzerland)
- Introduction to R, Summer Institute for Statistical Genetics, Summer Institute in Statistics and Modeling in Infectious Disease, 2015 (Seattle)
- Elements of R, Summer Institute for Statistical Genetics, 2015 (Seattle)
- Advanced R Programming for Bioinformatics, Summer Institute for Statistical Genetics, 2015 (Seattle)
- Introduction to R, Summer Institute for Statistical Genetics, Summer Institute in Statistics and Modeling in Infectious Disease, 2016 (Seattle)
- Elements of R, Summer Institute for Statistical Genetics, 2016 (Seattle)
- Bayesian Statistics for Genetics, Summer Institute for Statistical Genetics, 2016 (Seattle)
- Introduction to R, Winter Institute for Statistical Genetics, 2017 (Abu Dhabi)
- Introduction to R, Summer Institute for Statistical Genetics, Summer Institute in Statistics and Modeling in Infectious Disease, 2017 (Seattle)
- Advanced R Programming for Bioinformatics, Summer Institute for Statistical Genetics, 2017 (Seattle)
- Bayesian Statistics for Genetics, Summer Institute for Statistical Genetics, 2017 (Seattle)
- Bayesian Statistics for Genetics, Swiss Institute for Statistical Genetics, 2017 (Laussane, Switzerland)
- Introduction to R, Summer Institute for Statistical Genetics, Summer Institute in Statistics and Modeling in Infectious Disease, 2018 (Seattle)
- Bayesian Statistics for Genetics, Summer Institute for Statistical Genetics, 2018 (Seattle)

- Computational Pipeline for WGS, Data Summer Institute for Statistical Genetics, 2018 (Seattle)
- Session on "Statistical Methods: Advanced Common Sense" for AHA Research Leaders Academy, August 2018, Salt Lake City
- Introduction to R, Winter Institute for Statistical Genetics, January 2019 (Abu Dhabi)
- Computational Pipeline for WGS, Winter Institute for Statistical Genetics, 2019 (Abu Dhabi)
- Introduction to R, Summer Institute for Statistical Genetics, Summer Institute in Statistics and Modeling in Infectious Disease, 2019 (Seattle)
- Bayesian Statistics for Genetics, Summer Institute for Statistical Genetics, 2019 (Seattle)
- Computational Pipeline for WGS, Data Summer Institute for Statistical Genetics, 2019 (Seattle)
- Introduction to R, Summer Institute for Statistical Genetics, Summer Institute in Statistics and Modeling in Infectious Disease, 2020 (Seattle)
- Bayesian Statistics for Genetics, Summer Institute for Statistical Genetics, 2020 (Seattle)
- Computational Pipeline for WGS, Data Summer Institute for Statistical Genetics, 2020 (Seattle)

Other teaching

- University of Cambridge, 1997-2004: supervising mathematics and economics undergraduates (first-year through third) for Cambridge University statistics and probability courses;
  - Probability IA – introductory probability for first year mathematics students
  - EQEM – qualifying exam in mathematics for first year economics students
  - Statistics IB – introductory statistics for second year mathematics students
  - Principles of Statistics II – advanced statistical theory for final year math students
- - Computational Stats and Statistical Modelling – applications of generalized linear   -Modelling for final year mathematics students, with applications using R and S-Plus
- One-day meeting on Introductory Genetics for Statisticians, aimed at statisticians not working in the field, MRC Biostatistics Unit, Dec 2002
- Informal session on control of False Discovery Rates in non-standard situations, MRC Biostatistics Unit, June 2003
- Introductory session on Mathematica for Statisticians, MRC Biostatistics Unit, Nov 2003
- 'Masterclass' in Biostatistics, international LINAT meeting, Leiden, The Netherlands, July 2005
- Faculty interests poster presentation, departmental retreat, October 2005
- Faculty interests seminar, for applicant students, February 2006
- Biostatistics summer computing sessions (Introduction to WinBUGS), Summer 2006
- Microteaching session on scientific presentations, New Student Orientation, September 2006
- Faculty interests seminar, for applicant students, January, February 2007
- Leading a discussion on participants research results, and on presentation in talk and poster formats, summer undergraduate program, Summer 2007
- Biostatistics summer computing sessions (Introduction to WinBUGS), Summer 2007
- 'Masterclass' in Biostatistics, international LINAT meeting, Paris, July 2007
- Faculty interests seminar, for applicant students, January, February 2008
- Introduction to Analysis of Whole Genome Association Studies – CHARGE Consortium, Jan 2008
- Tutorials: introduction to Bayesian inference, introduction to meta-analysis, at Statistical and Applied Mathematical Sciences Institute (SAMSI), June 2008
- 'Masterclass' in Biostatistics, international LINAT meeting, Oklahoma, July 2008
- Faculty interests seminar, for applicant students, January, February 2009
- Summer Sessions on poster presentation, July/August 2010
- Faculty interests seminar, for applicant students, January, February 2011

- "Privacy issues in GWAS" for online Oregon Health Science course on ethics in modern genetic studies, February 2011
- Summer Sessions on poster presentation, July/August 2011
- Departmental Retreat presentation on "Research Topics in Genome-Wide Association Studies", September 2011
- Organized and taught in short course on Exome Chip analysis, for the CHARGE Consortium, Boston, September 2012
- Departmental Retreat presentation on "Pointless debates about meta-analysis (and how to not have them)", September 2012
- Departmental Retreat presentation on "Biostatistics for Cardiovascular Health Research", September 2013

Qualifying Exam Committees

- Second Year applied exam oral examiner, Summer 2005
- Second Year applied exam oral examiner, Summer 2006
- Advanced Statistical Theory PhD Qualifying Examination, Summer 2006
- Second Year applied exam oral examiner, Summer 2007
- Advanced Statistical Theory PhD Qualifying Examination, Summer 2008
- Advanced Statistical Theory PhD Qualifying Examination, Summer 2009 (chair)
- Second Year applied exam oral examiner, Summer 2009
- Advanced Statistical Theory PhD Qualifying Examination, Summer 2011 (chair)
- First Year Theory Examination, Summer 2012 (chair)
- Second Year applied exam oral examiner, Summer 2012
- First Year Theory Examination, Summer 2013 (chair)
- Advanced Statistical Theory PhD Qualifying Examination, Summer 2014 (chair)
- Second Year applied exam oral examiner, Summer 2016
- First Year Theory Examination, Summer 2018 (chair)
- First Year Theory Examination, Summer 2019
- First Year Theory Examination, Summer 2020 (chair)

Independent Study

- Bharat Rajan 2005-6, relationships between bootstrap and sandwich variance estimates
- Daryl Morris 2007, multiplicity adjustments with hierarchical structures
- Sangsoon Woo 2008, efficient replication versus meta-analysis in settings of multiplicity
- Takumi Saegusa 2008-2009, efficient simulation of genome-wide testing data
- Luis Crouch 2010-12, decision theoretic justification of Bayes Factors
- Clara Dominguez Islas 2011, reconciling fixed and random effects meta-analyses
- Kevin Rubinstein, 2011-14, Bayesian interpretations of shrinkage methods
- David Benkeser, 2011-12, Bayesian interpretations of non- and semi-parametric regression methods
- Wen Wei Loh, 2012-14, Bayesian Score tests
- Joshua Keller, 2013-14, Methods for Confounding Adjustment and High-Dimensional Environmental Exposures
- Jean Morrison, 2013-14, small-sample properties of SKAT for binary outcomes
- Allison Meisner, 2013-14, implementing leverage and influence diagnostics for GEE analyses
- Arjun Sondhi, 2014-16, small sample properties of association tests for binary outcomes

- Parker Xie, 2018-2019, unifying shrinkage estimates via decision theory
- Aaron Hudson, 2017-, diagnostic for small-sample SKAT properties. A universal Bayesian LASSO
- Chloe Krakauer, 2019 Decision-theoretic assessments of binary testing decisions
- Kendrick Li, 2019 Exact Bayesian and frequentist analysis of highly stratified binary data
- Spencer Hansen, 2019-, small sample issues and exact inference in meta-analysis

17. **Advising and Formal Mentoring**

a) PhD Dissertations, chair

- Youyi Fong "Algorithms and inference for mixture models with application to protein sequence analysis" (jointly with Jon Wakefield) Completed August 2010
- Clara Dominguez Islas 2011-2015, reconciling fixed and random effects meta-analyses. Completed July 2015
- Joshua Keller, 2013-2016, Methods for Confounding Adjustment and High-Dimensional Environmental Exposures (jointly with Adam Szpiro)
- Chloe Krakauer, 2019- , Uses of loss estimation for assessment of inferential methods
- Kendrick Li, 2019- , shrinkage and higher-order asymptotics for meta-analysis and network meta-analysis

b) Masters Theses, chair

- Max Sevareid (Health Services MPH) "Comparison of ultrasound and angiogram measures of stroke predictors" Completed, July 2008
- Carolyn Hutter "Mendelian Randomization: A Simulation Study Evaluating Violations of the Underlying Core Conditions" Completed, January 2009 (Winner of the 2008 Gilbert S. Omenn Award for Academic Excellence, UW School of Public Health and Community Medicine, also the American College of Epidemiology Best Poster Prize, 2008)
- Laina Mercer "Regression methods using parametric two-part models, with application to Coronary Artery Calcium progression" (jointly with Robyn McClelland) Completed August 2011
- Sooraj Kuttykrishnan "Sensitivity of Structural Equation Modeling to model mis-specification, with application to kidney disease" Completed, July 2014
- Tyler Bonnett "Understanding Tests via Bayesian Decision Theory", Completed, July 2018
- Ljubomir Miljacic "Performance of the "NCI method" of assessing nutritional intake, with application to fish intake in tribal communities", 2018-2019
- Zora Yang "Accuracy and computational efficiency of power calculations for logistic regression" 2018-2019

c) Mentored Scientists and Postdocs

- Collaboration with Adam Szpiro (as postdoc) - see Submitted Manuscripts
- Daniella Witten (as Assistant Professor)

d) MS and PhD committees in non chair role;

Member, Doctoral Committee

- Sierra Li (General Exam, July 2005)

- Pam Shaw (Final Exam, August 2006)
- Greg Strylewicz (GSR - Medical Education and Biomedical Informatics, Final Exam June 2007)
- Daniel Enquorabie (Epidemiology, Final Exam June 2007)
- Elisabeth Rosenthal (Final Exam, March 2008)
- Ben French (Final Exam, May 2008)
- Paramita Saha (Final Exam, June 2009)
- Catherine Johnson (Epidemiology, Final Exam June 2009)
- Siobhan Everson-Stewart (Final Exam June 2010)
- Abigail Shoben (Final Exam June 2010)
- Yoonha Choi (Final Exam August 2010)
- Jane Lange
- Charles Cheung (Final Exam Spring 2013)
- Peter Chi (Final Exam February 2013)
- Michelle Ross (Final Exam December 2012)
- Erin O'Brien (Epidemiology, Final Exam June 2012)
- Stephen Maley (Epidemiology, Final Exam October 2013)
- Erin Bouldon (Health Services, Final Exam October 2014)
- Jason Liang (Final Exam August 2015)
- Arend Voorman (Final Exam May 2014)
- Veronika Skrivankova
- Arjun Sondhi (Final Exam August 2019)
- William Tressel
- Xian Zhang (Final Exam 2019)
- Phuong Vu (Final Exam, September 2019)

Member, Masters Committee

- April Slee (Completed, January 2006)
- Allen de Camp (Completed, September 2006)
- Joe Rothstein (Completed, August 2006)
- Mark Giganti (Completed, August 2007)

e) Other Mentoring

Research Assistant Supervision

- Margaret Kloster, 2005-2006
- Kim Young, 2006-2007
- Veronica Skrivankova, 2008-2010
- Megan Smith, 2010-2011
- Alison Kosel, 2010-2012
- Arend Voorman, 2010-13
- Arjun Sondhi, 2014-16
- Chaoyu Yu, 2017-18
- Tianyu Zhang, 2018-2019

Teaching Assistant Supervision

- Daryl Morris, Autumn 2006
- Cecilia Cotton, Autumn 2007
- Youyi Fong, Autumn 2008
- Michelle Ross, Autumn 2009
- Liz Thomas, Spring 2010
- Erin Gabriel and Yates Coley, Winter 2011
- Leila Zelnick and Matt Conomos, Autumn 2011
- Silas Bergen and Jason Liang, Winter 2012
- Bob Salim, Spring 2013
- Jean Morrison, Spring 2014
- Jon Fintzi, Joo Yoon Han, LaNae Schaal, Qian Zhang, Spring 2015
- Yunqi Bu, Xinyuan Dong, Travis Hee Wai, Xiaowen Tian, Michael Flanagan, Autumn 2016
- Tyler Bonnett, Yunqi Bu, David Clausen, Arash Tarkhan, Parker Xie, Autumn 2017
- Austin Schumacher, David Whitney, Hyunju Son, Autumn 2018

Biology Project committee (other than as Doctoral committee member)

- Bharat Rajan (2007)
- Veronika Skrivankova (2011)

f) Academic Advising

- Bharat Rajan, 2005-2007
- Carolyn Hutter 2006-2008
- Daryl Morris 2007-2008
- Takumi Saegusa 2006-2010
- Patrick Danaher 2007-2010
- Luis Crouch 2008-2012
- Jennifer Kirk 2011-2014
- Allison Meisner 2012-2014
- Katherine Tan 2013-2016
- Yichen Jia 2015-2016
- Yuqi Ren 2015-2016
- Cooper Schumacher 2015-2016
- Xiudi Li 2017-
- Steve Wang 2017-2019
- Angela Zhang 2017-
- Maria Valdez 2018-