

## CURRICULUM VITAE

**Kenneth Martin Rice, Ph.D.**

1. **Date**

August 22, 2018

2. **Biographical Information**

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3. **Education**

- Churchill College, Cambridge University. B.A. Hons, Mathematics, 1<sup>st</sup> 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-
- 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

## 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, 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, and for Heart; 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. **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**
2. **Lumley T, Brody J, Peloso G, Morrison A, Rice K. FastSKAT: Sequence kernel association tests for very large sets of markers. *Genetic epidemiology*. 2018; PMID: 29932245**
3. **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.**
4. **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.**
5. **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.**
6. 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
7. 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.
8. 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.
9. Rich SS, Wang ZY, Sturcke A, Ziyabari L, Feolo M, O'Donnell CJ, Rice K, Bis JC, Psaty BM. Rapid evaluation of phenotypes, SNPs and results through the dbGaP CHARGE Summary Results site. *Nature genetics*. 2016; 48(7):702-3. PMID: 27350599
10. Sitlani CM, Dupuis J, Rice KM, Sun F, Pitsillides AN, Cupples LA, Psaty BM. Genome-wide gene-environment interactions on quantitative traits using family data. *European journal of human genetics*. 2016; 24(7):1022-8. PMID: 26626313 PMCID: PMC5070904
11. Sung YJ, Winkler TW, Manning AK, Aschard H, Gudnason V, et al. An Empirical Comparison of Joint and Stratified Frameworks for Studying  $G \times E$  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.
12. 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
13. Wang S, Zhao JH, An P, Guo X, Jensen RA, Marten J, Huffman JE, Meidtnr K, Boeing H, Campbell A, Rice KM, Scott RA, Yao J, Schulze MB, Wareham NJ, Borecki IB, Province MA, Rotter JI, Hayward C, Goodarzi MO, Meigs JB, Dupuis J. General Framework for Meta-Analysis of Haplotype Association Tests. *Genetic epidemiology*. 2016; 40(3):244-52. NIHMSID: NIHMS789332 PMID: 27027517 PMCID: PMC4869684
  14. **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.**
  15. **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.**
  16. 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.
  17. Gogarten SM, Bhangale T, Conomos MP, Laurie CA, McHugh CP, Painter I, Zheng X, Crosslin DR, Levine D, Lumley T, Nelson SC, Rice K, Shen J, Swarnkar R, Weir BS, Laurie CC (2012) GWASTools: an R/Bioconductor package for quality control and analysis of Genome-Wide Association Studies. *Bioinformatics*. Oct 10. PMID:23052040
  18. **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**
  19. **Fong Y, Wakefield J, Rice K (2012) An Efficient Markov Chain Monte Carlo Method for Mixture Models by Neighborhood Pruning. *Journal of Computational and Graphical Statistics* 21(1):197-216**
  20. **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**
  21. Divers J, Redden DT, Rice KM, et al (2011) Comparing self-reported ethnicity to genetic background measures in the context of the Multi-Ethnic Study of Atherosclerosis (MESA) *BMC Genetics* 12(3) Article Number 28. PMID: 21375750 PMCID: PMC3068121
  22. Manning A, LaValley M, Liu C, Rice K, An P, Liu Y, Miljkovic I, Rasmussen-Torvik L, Harris T, Province M, Borecki I, Florez J, Meigs J, Cupples L, Dupuis J (2011) Meta-analysis of Gene-Environment interaction: joint estimation of SNP and SNPxEnvironment regression coefficients, *Genetic Epidemiology*, 35(1) 11-18. PMID: 21181894
  23. **Buzkova P, Lumley R, Rice K (2011) Permutation and parametric bootstrap tests for gene-gene and gene-environment interactions, *Annals of Human Genetics*, 75(1) 36-45. doi: 10.1111/j.1469-1809.2010.00572.x. PMID: 20384625**
  24. **Rice K (2010) A Decision-Theoretic Formulation of Fisher's Approach to Testing, *THE AMERICAN STATISTICIAN*, 64(4) 345-349**
  25. Laurie C, Doheny K, Mirel D, et al (2010) Quality control and quality assurance in genotypic data for genome-wide association studies *Genetic Epidemiology*, 34(6) 591-602. PMID: 20718045, PMCID: PMC3061487
  26. **Szpiro A, Rice K, Lumley T (2010) Model-Robust Regression and a Bayesian Sandwich Estimator, *Annals of Applied Statistics*, 4(4) 2099-2113 doi: 10.1214/10-AOAS362**
  27. **Lumley T, Rice K (2010) Potential for Revealing Individual-Level Information in Genome-wide Association Studies. *JAMA* 303(7) 659-660. PMID: 20159874**

28. **Fong Y, Wakefield J, Rice K (2009) Bayesian mixture modeling using a hybrid sampler with application to protein subfamily identification. *Biostatistics*, 11:1 18-33**
29. **Rice K (2008) Equivalence between conditional and random-effects likelihoods for pair-matched case-control studies. *Journal of the American Statistical Association* 103:481 385-396**
30. **Rice K, Spiegelhalter D (2008) 'Bayesian Statistics' entry at Scholarpedia.org, a peer-reviewed, open-access, online encyclopedia**
31. Lumley T, Rice K, Psaty B (2008) Carryover effects after cessation of drug treatment: trophies or dreams? *American Journal of Hypertension* 21:14-16
32. Mueller P, Parmigiani G, Rice K. (2007) FDR and Bayesian Multiple Comparisons Rules. *Proceedings of the Valencia/ISBA 8th World Meeting on Bayesian Statistics* (Oxford University Press)
33. **French, B; Lumley, T; Monks, SA; Rice, KM; Hindorff, LA; Reiner, AP; Psaty, BM (2006) Simple estimates of haplotype relative risks in case-control data. *Genetic Epidemiology* 30 (6): 485-494**
34. **Rice K, Spiegelhalter D (2006) A simple diagnostic plot connecting robust estimation, outlier detection, and false discovery rates. *Journal of Applied Statistics* 33 (10): 1131-1147**
35. **Rice, K.M. (2004) Equivalence between conditional and mixture approaches to the Rasch model and matched case-control studies, with applications. *Journal of the American Statistical Association*, 99(466):510-522**
36. **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**
37. **Rice, K.M. (2003) Full-likelihood approaches to misclassification of exposure in matched case-control studies. *Statistics in Medicine*, 22(20), 3177-3194**
38. Duffy S, Rohan T, Kandel R, Prevost T, Rice K. (2003) Misclassification in a matched case-control study with variable matching ratio - application to a study of c-erbB-2 overexpression and breast cancer. *Statistics in Medicine*, 22(15), 2459-2468
39. **Rice K, Holmans P. (2003) Allowing for genotyping error in analysis of unmatched case-control studies. *Annals of Human Genetics*, 67(2), 165-174**

#### **Cardiovascular Epidemiology**

(stars denote equal contributions)

40. Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Prins BP et al. *Genome biology*. 2018; 19(1):87. PMID: 30012220 PMCID: PMC6048820
41. Exome Chip Analysis Identifies Low-Frequency and Rare Variants in MRPL38 for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. Jian X et al, *Stroke*. 2018; PMID: 30002152
42. Analysis of shared heritability in common disorders of the brain. Anttila V et al *Science* 2018; 360(6395). NIHMSID: NIHMS979389 PMID: 29930110 PMCID: PMC6097237
43. Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. Feitosa MF et al, *PloS one*. 2018; 13(6):e0198166. PMID: 29912962 PMCID: PMC6005576
44. Genome-wide meta-analysis of SNP-by-9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. Irvin MR, Sitlani CM, Noordam R, Avery CL, Bis JC, Floyd JS, Li J, Limdi NA, Srinivasasainagendra V, Stewart J, de Mutsert R, Mook-Kanamori DO, Lipovich L, Kleinbrink EL, Smith A, Bartz TM, Whitsel EA, Uitterlinden

- AG, Wiggins KL, Wilson JG, Zhi D, Stricker BH, Rotter JI, Arnett DK, Psaty BM, Lange LA. The pharmacogenomics journal. 2018; PMID: 29855607
45. Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Lin H et al, *Circulation. Genomic and precision medicine*. 2018; 11(5):e002037. NIHMSID: NIHMS954034 PMID: 29748316 PMCID: PMC5951629
  46. Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Mahajan A et al, *Nature genetics*. 2018; 50(4):559-571. NIHMSID: NIHMS938867 PMID: 29632382 PMCID: PMC5898373
  47. Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Malik R et al, *Nature genetics*. 2018; 50(4):524-537. NIHMSID: NIHMS959658 PMID: 29531354 PMCID: PMC5968830
  48. Pharmacogenomics study of thiazide diuretics and QT interval in multi-ethnic populations: the cohorts for heart and aging research in genomic epidemiology. Seyerle AA et al. *The pharmacogenomics journal*. 2018; 18(2):215-226. NIHMSID: NIHMS859114 PMID: 28719597 PMCID: PMC5773415
  49. An APOO Pseudogene on Chromosome 5q is Associated with LDL-C Levels. Montasser ME, O'Hare EA, Wang X, Howard AD, McFarland R, Perry JA, Ryan KA, Rice K, Jaquish CE, Shuldiner AR, Miller M, Mitchell BD, Zaghoul NA, Chang YC. *Circulation*. 2018; PMID: 29593015
  50. A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. Sung YJ et al, *American journal of human genetics*. 2018; 102(3):375-400. PMID: 29455858 PMCID: PMC5985266
  51. Multiethnic Meta-Analysis Identifies RAI1 as a Possible Obstructive Sleep Apnea-related Quantitative Trait Locus in Men. Chen H et al, *American journal of respiratory cell and molecular biology*. 2018; 58(3):391-401.
  52. Sugar-sweetened beverage intake associations with fasting glucose and insulin concentrations are not modified by selected genetic variants in a ChREBP-FGF21 pathway: a meta-analysis. McKeown NM et al *Diabetologia*. 2017; PMID: 29098321
  53. D-Dimer in African Americans: Whole Genome Sequence Analysis and Relationship to Cardiovascular Disease Risk in the Jackson Heart Study. Raffield LM et al *Arteriosclerosis, thrombosis, and vascular biology*. 2017; 37(11):2220-2227. NIHMSID: NIHMS904717 PMID: 28912365 PMCID: PMC5658238
  54. Multi-ethnic Meta-analysis Identifies RAI1 as a Possible Obstructive Sleep Apnea Related Quantitative Trait Locus in Men. Chen H et al *American journal of respiratory cell and molecular biology*. 2017; PMID: 29077507
  55. New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. Kraja AT, et al *Circulation. Cardiovascular genetics*. 2017; 10(5). PMID: 29030403
  56. Blood Pressure and Heart Rate Measures Associated With Increased Risk of Covert Brain Infarction and Worsening Leukoaraiosis in Older Adults. Leung LY, Bartz TM, Rice K, Floyd J, Psaty B, Gutierrez J, Longstreth WT Jr, Mukamal KJ. *Arteriosclerosis, thrombosis, and vascular biology*. 2017; 37(8):1579-1586. NIHMSID: NIHMS885637 PMID: 28663254 PMCID: PMC5551454
  57. Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Wain LV, et al. *Hypertension*, 2017; PMID: 28739976
  58. Multiancestry Study of Gene-Lifestyle Interactions for Cardiovascular Traits in 610 475 Individuals From 124 Cohorts: Design and Rationale. Rao DC, Sung YJ, Winkler TW, Schwander K, Borecki I, Cupples LA, Gauderman WJ, Rice K, Munroe PB, Psaty BM. *Circulation. Cardiovascular genetics*. 2017; 10(3). NIHMSID: NIHMS864520 PMID: 28620071 PMCID: PMC5476223

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60. Haycock PC, Burgess S, Nounu A, Zheng J, Okoli GN, et al. Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. *JAMA Oncol.* 2017 May 1;3(5):636-651. PubMed PMID: 28241208.
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65. van Rooij FJ, Qayyum R, Smith AV, et al. Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. *American journal of human genetics.* 2016; PMID: 28017375
66. Floyd JS, Sitlani CM, Avery CL, et al Large-scale pharmacogenomic study of sulfonylureas and the QT, JT and QRS intervals: CHARGE Pharmacogenomics Working Group. *The pharmacogenomics journal.* 2016; PMID: 27958378d
67. Schumann G, Liu C, O'Reilly P, et al. KLB is associated with alcohol drinking, and its gene product  $\beta$ -Klotho is necessary for FGF21 regulation of alcohol preference. *Proceedings of the National Academy of Sciences of the United States of America.* 2016; 113(50):14372-14377. PMID: 27911795 PMCID: PMC5167198
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73. Cade BE, Chen H, Stilp AM et al. Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. *American journal of respiratory and critical care medicine.* 2016; 194(7):886-897. PMID: 26977737 PMCID: PMC5074655

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75. Polfus LM, Khajuria RK, Schick UM, et al. Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. *American journal of human genetics*. 2016; 99(2):481-8. PMID: 27486782  
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79. Liu CT, Raghavan S, Maruthur N, et al. Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. *American journal of human genetics*. 2016; 99(1):56-75. PMID: 27321945 PMCID: PMC5005440
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86. Yu B, et al Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. *Circ Cardiovasc Genet*. 2015 Dec 11. pii: CIRCGENETICS.115.001215. PubMed PMID: 26658788
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### Others

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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, 2<sup>nd</sup> 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
4. Rice K (2009). Review, Statistical Meta-Analysis with Applications by Joachim Hartung, Guido Knapp, and Bimal K. Sinha. *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION* (in Press)
5. Rice K, Spiegelhalter D (2008). Discussion of Efron; "Microarrays, Empirical Bayes, and the Two-Groups Model". *STATISTICAL SCIENCE* 23(1) 41-44.
6. Rice K, Kronmal R, Lumley T (2006). Analytic errors undermine conclusions of cardiovascular study. *ARCHIVES OF INTERNAL MEDICINE* Sep 166(16) 1787.

7. Rice K (2006). On Bayesian analysis of misclassified binary data from a matched case-control study with a validation sub-study, by Gordon Prescott and Paul Garthwaite. *STATISTICS IN MEDICINE* 25(3), 537-539.
8. Rice KM (2005). Discussion of Greenland, S. 'Multiple bias modelling for analysis of observational data'. *JOURNAL OF THE ROYAL STATISTICAL SOCIETY, SERIES A* 168(2): 294-29.
9. Rice KM (2004). Sprint research runs into a credibility gap, *NATURE* 432(7014): 147.
10. Rice, KM (2004). Discussion of Wakefield, J. 'Ecological Inference for 2x2 tables', *JOURNAL OF THE ROYAL STATISTICAL SOCIETY, SERIES A* 167(3): 437-438.

## 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:

Listed by grant award (PIs), start-end dates and number of calendar months

U01 HL137162-01 (K Rice & B Weir) 4/01/2017-03/31/2022 2.4 CM  
NIH \$398,416

"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 TOPMed's 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.

R01 HL120393-03S1 (B Psaty/K Rice/B Weir) 01/01/2017 5/31/2017 2.75 calendar months  
NIH/NHLBI \$1,941,748

"TOPMed Data Coordinating Center Supplement"

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.

This grant is pending replacement by the following continuation:

HHSN26817HV00001R (K Rice/B Psaty/B Weir) 9/15/2017-9/14/2020 3.0 CM  
NIH/NHLBI \$3,815,628

"Trans-Omics for Precision Medicine (TOPMed) Data Coordinating Center (DCC)" (A122283, TOPMed contract)

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.

R01 HL120393-03 (B Psaty) 4/1/2014 3/31/2018 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.

HHSN2682015000031 (R McClelland & R Kronmal) 8/15/2015 8/14/2021 0.48 CM  
NIH \$8,780,892

"Multi-Ethnic Study of Atherosclerosis (MESA)"

This is a national study to identify risk factors for sub-clinical cvd and to explore the transition from sub-clinical to overt cvd, focusing on prevention of the latter.

U01 AG049505 (S. Seshadri/sub-B Psaty) 6/15/2014 5/31/2018 0.6 CM  
NIH/NIA/Boston U. \$74,999

"Identifying Risk & Protective SNV for AD in ADSP Case-control Sample" (ADSP)

The Specific Aims of this project are as follows 1) To identify novel risk and protective variants associated with AD; 2) To replicate and characterize the genes/variants identified in Aim 1 and prior studies; 3) To test association of the genes/variants detected with established AD endophenotypes; and 4) To test for targeted gene gene (GG) and gene-environment (GE) interactions.

R01 HL105756 (B Psaty) 2/15/2011 3/31/2018 0.48 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.

R01 HL103612 (B Psaty) 8/1/2011 5/31/2017 0.075 CM  
NIH \$1,249,481

"Prospective Meta-Analyses of Drug-Gene Interactions: CHARGE GWAS Consortium" (PHG-CHARGE)

For common variants, the project will accelerate the discovery of drug-gene interactions that may affect a variety of unintended therapeutic effects.

R01HL78888 (B Psaty) 2/15/2012 1/31/2017 0.6 CM  
NIH \$543,206

"Genomics and Pharmacogenomics of statin-related rhabdomyolysis." (Rhabdo2)

This grant uses the cardiovascular branch of the HMO Research Network to conduct a population-based case-control study of statin-related rhabdomyolysis, and it includes plans for exome sequencing, collaboration with other large case-control studies, and functional validation of findings.

UH2NS100605 (S Seshadri /sub-B Psaty) 09/30/16–09/29/21 0.12 CM  
NIH/Boston U \$88,684

"Microglial, inflammatory and omics markers of cerebral small vessel disease in the CHARGE consortium" (A113598, CSVD)

This UH2 application submitted by BU on behalf of Sudha Seshadri and the CHARGE Consortium (Cohorts for Heart & Aging Research in Genomic Epidemiology) proposes to investigate immune mechanisms and small vessel disease (SVD) and dementia. The CHARGE consortium and numerous other genetic studies have implicated immune factors including microglial activation, inflammation and astroglia, in the biology of SVD and dementia. More specifically, the applicants propose to measure two circulating biomarkers of microglial inflammation (sCD-14 and YKL-40) and one marker of astroglial injury (GFAP) in approximately 17,000 persons (including 4000 minority participants, 6000 with >2 MRI scans) across 5 CHARGE population-based cohorts.

R01 HL120854 (B Psaty & R Tracy) 07/15/14-04/30/18 0.6 CM (5%)  
 NIH \$557,202  
 T-cell subsets as CVD risk factors in CHS and MESA (A122667 IAC)  
 The primary aim is to evaluate T-cell subsets as risk factors for cardiovascular events in CHS and MESA.

Pending:

Tang/ sub-Smith 04/01/2017-09/30/2020 0.3 CM  
 NIH/U of Minnesota \$96,800  
 “Whole Genome Sequencing to Identify Casual Genetic Variants Influencing Risk of Venous Thromboembolism” (A114039, TOPMed VTE)  
 We propose to leverage the considerable previous investment to follow-through with genetic association studies of VTE and investigations of underlying mechanisms in the etiology of VTE.

R01 (E Boerwinkle /sub-S Heckbert) 04/01/17–3/31/22 0.6  
 NIH/UTHSC \$78,974  
 “A Statistical Analysis Commons for HLB Locus Discovery” (A113856, CHARGE Commons)  
 This application will provide an Analysis “Commons”, an accessible data repository and computation resource enabling use of large-scale whole genome sequencing by NHLBI investigators.

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

### 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
- 22<sup>nd</sup> 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
- 4<sup>th</sup> 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-
- 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-

## 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-

## 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 45<sup>th</sup> 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 46<sup>th</sup> 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 47<sup>th</sup> 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 48<sup>th</sup> 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 49<sup>th</sup> 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 50<sup>th</sup> Annual Conference on Cardiovascular Disease Epidemiology and Prevention, San Francisco, March 2010
- AHA 51<sup>st</sup> 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 52<sup>nd</sup> 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 53<sup>rd</sup> Annual Conference on Cardiovascular Disease Epidemiology and Prevention, New Orleans, March 2013
- ASA Joint Statistical Meetings, Montreal, August 2013
- AHA 54<sup>th</sup> Annual Conference on Cardiovascular Disease Epidemiology and Prevention, San Francisco, March 2014
- ASA Joint Statistical Meetings, Seattle, August 2015
- AHA 55<sup>th</sup> 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 56<sup>th</sup> Annual Conference on Cardiovascular Disease Epidemiology and Prevention, Phoenix, March 2015
- CHARGE Consortium Meeting, Charlottesville, September 2016
- ASHG Meeting, Vancouver BC, October 2016
- Harvard Program in Quantitative Genomics, 10<sup>th</sup> 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 57<sup>th</sup> 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

## 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

## 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

### 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 Paulo, 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)

### 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

### **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, 2011-2, Bayesian interpretations of non- and semi-parametric regression methods
- Wen Wei Loh, 2012-, 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-, unifying shrinkage estimates via decision theory
- Aaron Hudson, 2017-, diagnostic for small-sample SKAT properties. A universal Bayesian LASSO

## 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)

### b) **Masters Theses, chair**

- Max Severeid (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 Bennett “Understanding Tests via Bayesian Decision Theory”, Completed, July 2018

### 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

**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

**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

**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-
- Angela Zhang 2017-