CURRICULUM VITAE
Sharon R. Browning, PhD

1. Date: January 4, 2023

2. Biographical Information

- Work address: Department of Biostatistics, Campus Box 357232
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3. Education

- University of Auckland, Auckland, New Zealand. BScHons in Mathematics with 1st class honors, 1995.
- University of Washington, Seattle, WA. PhD in Statistics, 1999.

4. Licensure N/A

5. Professional Positions (e.g., Medical Residency, Fellowships, Faculty Appointments, etc)

- Visiting Assistant Professor, Department of Statistics, Texas A&M University, 1999-2000.
- Assistant Professor, Department of Statistics, North Carolina State University, 2000-2002.
- Principal Scientist, Genetics Research, GlaxoSmithKline, 2002-2005.
- Lecturer, Department of Statistics, University of Auckland, 2005-2007.
- Senior Lecturer, Department of Statistics, University of Auckland, 2008-2010.
- Research Associate Professor, Department of Biostatistics, U. of Washington, 2010-2017.
- Research Professor, Department of Biostatistics, University of Washington, 2017-

6. Honors, Awards, Scholarships

- Annual Prize in Statistics, University of Auckland, 1994.
- Dean of Science Prize, University of Auckland, 1995.
- William Georgetti PhD Scholarship, New Zealand Vice Chancellors' Committee, 1995.
- Z.W. Birnbaum Fellowship for PhD study in the Department of Statistics at the University of Washington, 1995.
- PMMB (Program in Mathematics and Molecular Biology) Fellow, 1997.
- Research Starter Grant in Informatics awarded by PhRMA foundation, 2002.
- University of Auckland Research Committee new staff research grant, 2006.
- Marsden Fund FastStart award, 2007.
- Best Paper Award from International Genetic Epidemiology Society for best paper published in Genetic Epidemiology in 2007 (BL Browning and SR Browning. Efficient multilocus association mapping for whole genome association studies using localized haplotype clustering. Genetic Epidemiology, 31: 365-375), 2008.

7. Professional Activities (outside of UW)

- Reviewing for journals including Science, Cell, Nature Genetics, Nature Communications, American Journal of Human Genetics, Genetic Epidemiology, Human Genetics, Genetics, Genome Research, Molecular Biology and Evolution, Bioinformatics, and PLoS Genetics.
- Associate editor for Statistical Applications in Genetics and Molecular Biology (Berkeley Electronic Press), 2007-2012.
- Editorial board for Human Genetics (Springer), 2009-present.
- Associate editor for American Journal of Human Genetics, 2011-2013.

- Guest editor for PLoS Genetics 2011, 2013, 2015, 2017, 2018, 2020, 2022.
- Guest editor for PLoS Computational Biology 2012.
- Associate editor for Genetics, 2019-2021.
- Acting senior editor for Genetics, 2020.
- Senior editor for Genetics, Statistical Genetics and Genomics section, 2021-present
- Member of 1000 Genomes Analysis Group, 2008-2015.
- Member of NIH grant review panel: Genetic Variation and Evolution (GVE) Study Section 2012-2018.
- Ad hoc NIH grant review: NIDCR 2011, GVE 2011, GCAT 2019, GGG 2021.
- Ad hoc NSF grant review: 2020.
- Member, Hispanic Community Health Study / Study of Latinos, 2013-present.
- Member, Population Genetics working group, NHLBI Trans-Omics for Precision Medicine (TOPMed) Whole Genome Sequencing Program, 2016-present.

8. Bibliography

a) Refereed Research Articles

1. **Browning, S.,** 1998 Relationship information contained in gamete identity by descent data. J Comput Biol **5:** 323-334.
2. **Browning, S. G.,** 1998 Tandem queues with blocking: A comparison between dependent and independent service. Operations Research **46:** 424-429.
3. **Browning, S.,** 2000 A Monte Carlo approach to calculating probabilities for continuous identity by descent data. Journal of Applied Probability **37:** 850-864.
4. **Browning, S.,** 2000 The relationship between count-location and stationary renewal models for the chiasma process. Genetics **155:** 1955-1960.
5. **Browning, S.,** and B. L. Browning, 2002 On reducing the statespace of hidden Markov models for the identity by descent process. Theoretical Population Biology **62:** 1-8.
6. **Browning, S.,** 2003 Pedigree data analysis with crossover interference. Genetics **164:** 1561-1566.
7. **Browning, S. R.,** J. D. Briley, L. P. Briley, G. Chandra, J. H. Charnecki, M. G. Ehm, K. A. Johansson, B. J. Jones, A. J. Karter, D. P. Yarnall and M. J. Wagner, 2005 Case-control single-marker and haplotypic association analysis of pedigree data. Genet Epidemiol **28:** 110-122.
8. **Browning, S. R.,** 2006 Multilocus association mapping using variable-length Markov chains. Am J Hum Genet **78:** 903-913.
9. Browning, B. L., and **S. R. Browning,** 2007 Efficient multilocus association mapping for whole genome association studies using localized haplotype clustering. Genetic Epidemiology **31:** 365-375.
10. **Browning, S. R.,** and B. L. Browning, 2007 Rapid and accurate haplotype phasing and missing data inference for whole genome association studies by use of localized haplotype clustering. American Journal of Human Genetics **81:** 1084-1097.
11. **Browning, S. R.,** and J. Thomas, 2007 Multilocus analysis of GAW15 NARAC chromosome 18 case-control data. BMC Proc **1 Suppl 1:** S11.
12. Black, J., **S. R. Browning,** A. V. Collins and J. R. Phillips, 2008 A Canine Model of Inherited Myopia: Familial Aggregation of Refractive Error in Labrador Retrievers. Investigative Ophthalmology & Visual Science **49:** 4784-4789.
13. Browning, B. L., and **S. R. Browning,** 2008 Haplotypic analysis of Wellcome Trust Case Control Consortium data. Human Genetics **123:** 273-280
14. **Browning, S. R.,** 2008 Estimation of pairwise identity by descent from dense genetic marker data in a population sample of haplotypes. Genetics **178:** 2123-2132.

15. **Browning**, **S. R.,** 2008 Missing data imputation and haplotype phase inference for genome-wide association studies. Human Genetics **124:** 439-450.
16. **The Australia and New Zealand Multiple Sclerosis Genetics Consortium**, 2009 Genome-wide association study identifies new multiple sclerosis susceptibility loci on chromosomes 12 and 20. Nature Genetics **41:** 824-828.
17. Browning, B. L., and **S. R. Browning,** 2009 A Unified Approach to Genotype Imputation and Haplotype-Phase Inference for Large Data Sets of Trios and Unrelated Individuals. American Journal of Human Genetics **84:** 210-223.
18. *Madsen, B. E., and **S. R. Browning,** 2009 A Groupwise Association Test for Rare Mutations Using a Weighted Sum Statistic. Plos Genetics **5:** e1000384.
19. *Zeng, I. S. L., **S. R. Browning,** P. Gladding, M. Jullig, M. Middleditch and R. A. H. Stewart, 2009 A Multi-feature Reproducibility Assessment of Mass Spectral Data in Clinical Proteomic Studies. . Clinical Proteomics **5:** 170-177.
20. **Browning**, **S. R.,** and B. L. Browning, 2010 High Resolution Detection of Identity by Descent in Unrelated Individuals. American Journal of Human Genetics **86:** 526-539.
21. Girirajan, S., J. A. Rosenfeld, G. M. Cooper, F. Antonacci, P. Siswara, A. Itsara, L. Vives, T. Walsh, S. E. Mccarthy, C. Baker, H. C. Mefford, J. M. Kidd, **S. R. Browning,** B. L. Browning, D. E. Dickel, D. L. Levy, B. C. Ballif, K. Platky, D. M. Farber, G. C. Gowans, J. J. Wetherbee, A. Asamoah, D. D. Weaver, P. R. Mark, J. Dickerson, B. P. Garg, S. A. Ellingwood, R. Smith, V. C. Banks, W. Smith, M. T. Mcdonald, J. J. Hoo, B. N. French, C. Hudson, J. P. Johnson, J. R. Ozmore, J. B. Moeschler, U. Surti, L. F. Escobar, D. El-Khechen, J. L. Gorski, J. Kussmann, B. Salbert, Y. Lacassie, A. Biser, D. M. Mcdonald-Mcginn, E. H. Zackai, M. A. Deardorff, T. H. Shaikh, E. Haan, K. L. Friend, M. Fichera, C. Romano, J. Gecz, L. E. Delisi, J. Sebat, M.-C. King, L. G. Shaffer and E. E. Eichler, 2010 A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. Nat Genet **42:** 203-209.
22. Bahlo M, Stankovich J, Danoy P, Hickey PF, Taylor BV, **Browning SR**; Australian and New Zealand Multiple Sclerosis Genetics Consortium (Anzgene), Brown MA, Rubio JP, 2010 Saliva-derived DNA performs well in large-scale, high-density single-nucleotide polymorphism microarray studies. Cancer Epidemiol Biomarkers Prev. **19**: 794-8.
23. Field, J; **Browning, SR**; Johnson, LJ; et al., 2010 A Polymorphism in the HLA-DPB1 Gene Is Associated with Susceptibility to Multiple Sclerosis. Plos One **5**: e13454.
24. **Browning, S. R.,** and B. S. Weir, 2010 Population Structure with Localized Haplotype Clusters. Genetics, 185: 1337-1344.
25. Browning, B.L. and **Browning, S.R.** §, 2011 A Fast, Powerful Method for Detecting Identity by Descent. American Journal of Human Genetics. **88**:173-182.
26. **Browning, S.R.** and Browning, B.L., 2011 Haplotype phasing: existing methods and new developments. Nature Reviews Genetics **12**: 703-714.
27. Li, L.; Li, Y.; **Browning, S. R.**; et al., 2011 Performance of genotype imputation for rare variants identified in exons and flanking regions of genes. PLoS One **6**: e24945
28. **Browning, S.R.** and Browning, B.L., 2011 Population Structure Can Inflate SNP-Based Heritability Estimates. American Journal of Human Genetics **89**: 191-193.
29. **Browning, S.R.** and Thompson, E.A., 2012 Detecting Rare Variant Associations by Identity-by-Descent Mapping in Case-Control Studies. Genetics, **190**: 1521-1531.
30. **Browning, S.R.** and Browning, B.L., 2012 Identity by Descent Between Distant Relatives: Detection and Applications. Annual Review of Genetics. 46: 617-633.
31. **Browning, S.R.** and Browning, B.L., 2013 Identity-by-descent-based heritability analysis in the Northern Finland Birth Cohort. Human Genetics. 132: 129-138.

32. Myles-Worsley, M.; Tiobech, J.; **Browning, S. R.**; et al., 2013 Deletion at the SLC1A1 glutamate transporter gene co-segregates with schizophrenia and bipolar schizoaffective disorder in a 5-generation family. American journal of medical genetics. Part B, Neuropsychiatric genetics. 162B: 87-95.
33. Browning B.L. and **Browning, S.R.**, 2013 Improving the Accuracy and Efficiency of Identity by Descent Detection in Population Data. Genetics, 194:459-471.
34. Nelson, S. C., et al. 2013 Imputation-based genomic coverage assessments of current human genotyping arrays." G3-Genes, Genomes and Genetics 3:1795-1807.
35. Browning, B. L. and **Browning, S.R.**§ 2013 Detecting identity by descent and estimating genotype error rates in sequence data. Am J Hum Genet 93:840-851.
36. *Qian, Y., Browning, B.L. and **Browning, S.R.** 2014 Efficient clustering of identity-by-descent between multiple individuals. Bioinformatics 30:915-922.
37. *Zhang, Q.S., Browning, B.L. and **Browning, S.R.** 2015 Genome-wide haplotypic testing in a Finnish cohort identifies a novel association with low-density lipoprotein cholesterol. Eur J Hum Genet. 23:672–677.
38. Lehnert, K ; Ward, H; Berry, SD; Ankersmit-Udy, A; Burrett, A; Beattie, EM; Thomas, NL; Harris, B; Ford, CA; **Browning, S.R.**; Rawson, P; Verkerk, GA ; van der Does, Y; Adams, LF; Davis, SR; Jordan, TW; MacGibbon, AKH; Spelman, RJ; Snell, RG. 2015 Phenotypic population screen identifies a new mutation in bovine DGAT1 responsible for unsaturated milk fat. Sci Rep. 5:8484.
39. **Browning, S.R.** and Browning B.L., 2015 Accurate Non-parametric Estimation of Recent Effective Population Size from Segments of Identity by Descent. Am J Hum Genet 97:404–418.
40. **The 1000 Genomes Project Consortium**, 2015 A global reference for human genetic variation. Nature 526:68–74.
41. Browning, B.L. and **Browning S.R.** 2016 Genotype imputation with millions of reference samples. Am J Hum Genet. 98:116-126.
42. Conomos, MP, CA Laurie, AM Stilp, SM Gogarten, CP McHugh, SC Nelson, T Sofer, L Fernández-Rhodes, AE Justice, M Graff, KL Young, AA Seyerle, CL Avery, KD Taylor, JI Rotter, GA Talavera, ML Daviglus, S Wassertheil-Smoller, N Schneiderman, G Heiss, RC Kaplan, N Franceschini, AP Reiner, JR Shaffer, RG Barr, KF Kerr, **SR Browning**, BL Browning, BS Weir, ML Avilés-Santa, GJ Papanicolaou, T Lumley, AA Szpiro, KE North, K Rice, TA Thornton, CC Laurie. 2016 Genetic Diversity and Association Studies in U.S. Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. Am J Hum Genet. 98:165–184.
43. Schick, UM, D Jain, CJ Hodonsky, JV Morrison, JP Davis, L Brown, T Sofer, MP Conomos, C Schurmann, CP McHugh, SC Nelson, S Vadlamudi, A Stilp, A Plantinga, L Baier, SA Bien, SM Gogarten, CA Laurie, KD Taylor, Y Liu, PL Auer, N Franceschini, A Szpiro, K Rice, KF Kerr, JI Rotter, RL Hanson, G Papanicolaou, SS Rich, RJF Loos, BL Browning, **SR Browning**, BS Weir, CC Laurie, KL Mohlke, KE North, TA Thornton, AP Reiner. 2016. Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. Am J Hum Genet 98: 229-242.
44. **Browning SR**, K Grinde, A Plantinga, SM Gogarten, AM Stilp, RC Kaplan, ML Aviles-Santa, BL Browning, CC Laurie. 2016. Local Ancestry Inference in a large US-Based Hispanic/Latino Study: Hispanic Community Health Study / Study of Latinos (HCHS/SOL). G3: Genes, Genomes, Genetics 6: 1525-1534.
45. *Zhang QS, Browning BL, **Browning SR**. 2016. ASAFE: Ancestry-Specific Allele Frequency Estimation. Bioinformatics 32:2227-2229.

46. Fu W, **Browning SR**, Browning BL, Akey JM. 2016. Robust Inference of Identity by Descent from Exome-Sequencing Data. Am J Hum Genet 99:1106-1116.
47. Jain D, Hodonsky CJ, Schick UM, …, **Browning SR**, et al. 2017. Genome-wide association of white blood cell counts in Hispanic/Latino Americans: the Hispanic Community Health Study/Study of Lations. Human Molecular Genetics, 26:1193-1204.
48. *Brown LA, Sofer T, Stilp AM, …, **Browning SR**, et al. 2017. Admixture Mapping Identifies An Amerindian Ancestry Locus Associated With Albuminuria in U.S. Hispanics: The Hispanic Community Health Study/Study of Latinos. Journal of the American Society of Nephrology, 28:2211-2220.
49. Sofer T, Baier LJ, **Browning SR**, Thornton TA, et al. 2017. Admixture mapping in the Hispanic Community Health Study/Study of Latinos reveals regions of genetic associations with blood pressure traits. PLoS One 12:e0188400.
50. Kerr KF, Avery CL, Lin HJ, … **Browning SR**, et al. 2017. Genome-wide Association Study of Heart Rate and Its Variability in Hispanic/Latino Cohorts. Heart Rhythm 14:1675-1684.
51. Hodonsky CJ, Jain D, Schick UM, … **Browning SR**, et al. 2017. Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. PLoS Genetics 13:e1006760
52. **Browning, S.R.**, Browning, B.L., Zhou, Y., Tucci, S. and Akey, J.M., 2018. Analysis of human sequence data reveals two pulses of archaic Denisovan admixture. Cell 173:53-61.
53. Browning, B.L., Zhou, Y. and **Browning, S.R.**, 2018. A One-Penny Imputed Genome from Next-Generation Reference Panels. The American Journal of Human Genetics 103:338-348.
54. **Browning, S.R.**, Browning, B.L., Daviglus, M.L., Durazo-Arvizu, R.A., Schneiderman, N., Kaplan, R.C. and Laurie, C.C., 2018. Ancestry-specific recent effective population size in the Americas. PLoS Genetics 14:e1007385.
55. Zhou, Y., Tian, X., Browning, B.L. and **Browning, S.R.**, 2018. POPdemog: visualizing population demographic history from simulation scripts. Bioinformatics, 34:2854-2855.
56. Wang, H., Cade, B.E., Sofer, T., Sands, S.A., Chen, H., **Browning, S.R.**, Stilp, A.M., Louie, T.L., Thornton, T.A., Craig Johnson, W. and Below, J.E., 2019. Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 28:675-687.
57. *Grinde, K.E., Brown, L.A., Reiner, A.P., Thornton, T.A. and **Browning, S.R.**, 2019. Genome-wide significance thresholds for admixture mapping studies. The American Journal of Human Genetics, 104:454-465.
58. *Tian, X., Browning, B.L. and **Browning, S.R.**, 2019. Estimating the Genome-wide Mutation Rate with Three-Way Identity by Descent. The American Journal of Human Genetics, 105:883-893.
59. Harris, D.N., Kessler, M.D., Shetty, A.C., Weeks, D.E., Minster, R.L., **Browning, S.**, Cochrane, E.E., Deka, R., Hawley, N.L., Reupena, M.A.S. Naseri, T., Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Population Genetics Working Group, McGarvey, S.T., and O'Connor, T.D. 2020. Evolutionary history of modern Samoans. Proceedings of the National Academy of Sciences, 117:9458-9465.
60. Kessler, M.D., Loesch, D.P., Perry, J.A., Heard-Costa, N.L., Taliun, D., Cade, B.E., Wang, H., Daya, M., Ziniti, J., Datta, S., Celedón, J.C., Soto-Quiros, M.E., Avila, L., Weiss, S.T., Barnes, K., Redline, S.S., Vasan, R.S., Johnson, A.D., Mathias, R.A., Hernandez, R., Wilson, J.G., Nickerson, D.A., Abecasis, G., **Browning, S.R.**, Zöllner, S., O'Connell, J.R., Mitchell, B.D., National Heart Lung and Blood Institute Trans-Omics

for Precision Medicine (TOPMed) Consortium, TOPMed Population Genetics Working Group, and O'Connor, T.D. 2020. De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. Proceedings of the National Academy of Sciences, 117:2560-2569.

61. Zhou, Y., **Browning, S.R.** and Browning, B.L., 2020. A fast and simple method for detecting identity by descent segments in large-scale data. The American Journal of Human Genetics, 106:426-437.
62. *Zhou, Y., Browning, B.L. and **Browning, S.R.**, 2020. Population-specific recombination maps from segments of identity by descent. The American Journal of Human Genetics, 107:137-148.
63. Zhou, Y., **Browning, S.R.** and Browning, B.L., 2020. IBDkin: fast estimation of kinship coefficients from identity by descent segments. Bioinformatics, 36:4519-4520.
64. **Browning, S.R.** and Browning, B.L., 2020. Probabilistic estimation of identity by descent segment endpoints and detection of recent selection. The American Journal of Human Genetics, 107:895-910.
65. §Lin, B.M., *§Grinde, K.E., Brody, J.A., Breeze, C.E., Raffield, L.M., Mychaleckyj, J.C., Thornton, T.A., …, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Kidney Working Group, Rich, S.S., Lin, D.Y., **Browning, S.R**., Franceschini, N., 2021. Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 63, 103157.
66. Taliun, D., Harris, D.N., Kessler, M.D., …, **Browning, S.R.**, …, Abecasis, G.R. 2021. Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 590:290-299.
67. Zhou, Y. and **Browning, S.R.**, 2021. Protocol for detecting introgressed archaic variants with SPrime. STAR protocols, 2:100550.
68. Browning, B.L., Tian, X., Zhou, Y. and **Browning, S.R.**, 2021. Fast two-stage phasing of large-scale sequence data. The American Journal of Human Genetics, 108:1880-1890.
69. Granot-Hershkovitz, E., Sun, Q., Argos, M., Zhou, H., Lin, X., **Browning, S.R.** and Sofer, T., 2022. AFA: Ancestry-specific allele frequency estimation in admixed populations: The Hispanic Community Health Study/Study of Latinos. Human Genetics and Genomics Advances, 3(2), p.100096.
70. Browning, B.L. and **Browning, S.R.**, 2022. Genotype error biases trio-based estimates of haplotype phase accuracy. The American Journal of Human Genetics, 109(6), pp.1016-1025.
71. Browning, B.L. and **Browning, S.R.**, 2022. Statistical phasing of 150,119 sequenced genomes in the UK Biobank. The American Journal of Human Genetics.
72. Acosta-Uribe, J., Aguillón, D., Cochran, J.N., Giraldo, M., Madrigal, L., Killingsworth, B.W., Singhal, R., Labib, S., Alzate, D., Velilla, L., Moreno, S., …, **Browning, S.R.**, Lopera, F. and Kosik, K.S. 2022. A neurodegenerative disease landscape of rare mutations in Colombia due to founder effects. Genome Medicine, 14(1), pp.1-22.
73. *Tian, X., Cai, R. and **Browning, S.R.**, 2022. Estimating the genome-wide mutation rate from thousands of unrelated individuals. The American Journal of Human Genetics, 109(12), pp.2178-2184.
74. **Browning, S.R.**, Waples, R.K. and Browning, B.L., 2023. Fast, accurate local ancestry inference with FLARE. American Journal of Human Genetics.

* First author is trainee whose primary supervisor for this work was Sharon Browning.
§ Joint first author.

9. Patents and Other Intellectual Property N/A

10. Funding History

10a. Funded Projects

2002 Research Starter Grant in Informatics awarded by PhRMA foundation. PI Sharon Browning

2006 University of Auckland Research Committee new staff research grant. PI Sharon Browning

2007 Subcontract to Bruce Weir University of Washington from NIH Theoretical Population Genetics grant. PI of subcontract Sharon Browning.

2007 Marsden FastStart award (Royal Society of New Zealand). PI Sharon Browning.

R01 HG005701 (S Browning) 8/25/2010 6/30/2025
NIH/NHGRI "Identity by descent in population data"
Role: PI.

R01 GM075091 (B Weir) 7/15/2011 4/30/2015
NIH/NIGMS "Theoretical Population Genetics"
Role: Investigator.

P01 GM099568 (B Weir) 6/5/2012 4/30/2018
NIH/NIGMS "Statistical and Population Genetics"
Role: PI of one component project.

R01 HG004960 (B Browning) 9/1/2012 6/30/2017
NIH/NHGRI "Improving genotype call accuracy"
Role: Investigator.

HHSN268201300005C (B Weir) 9/30/2013 12/8/2016
NIH/NHLBI "Omics in Latinos (Ola) - Genetic Analysis"
Role: Investigator

R01 GM110068 (J Akey, S Browning) 7/1/2014 3/31/2019
NIH/NIGMS "Fossil Free Sequencing of Archaic Genomes"
Role: PI

R01 HG008359 (B Browning, S Browning) 9/15/2015 5/31/2023
NIH/NHGRI "Improved modeling of genotype data"
Role: PI (2015-2019), Investigator (2019-2023)

R01 HG010869 (S Browning) 1/6/2020 12/31/2023
NIH/NHGRI "Local ancestry inference for complex admixtures"
Role: PI

10b. Pending Applications
N/A

11. Public Health Practice Activities N/A

12. Conferences and Symposiums

Conference organization:

2008 Session chair for New Zealand Statistical Association annual meeting (Session on Statistical Genetics).
2009 Chair of organizing committee, New Zealand Molecular Mapping annual meeting, Auckland, New Zealand, Dec 8.
2012 Organizer/moderator of invited session at American Society of Human Genetics annual meeting. Session Title: "Emerging applications of identity by descent segment detection". San Francisco, Nov 10.

Invited presentations:

2001 Australasian Biometrics and New Zealand Statistical Association Joint Conference, Christchurch, New Zealand, Dec 10-13.
2001 Joint Statistical Meetings.
2006 New Zealand Statistical Association annual meeting, Auckland, New Zealand.
2008 New Zealand Statistical Association annual meeting, Hamilton, New Zealand.
2009 Australian GeneMappers Conference, Katoomba, NSW, Australia, April 14-17.
2009 Women in Genome Sciences seminar, Genome Sciences, U. of Washington, Seattle, July 2.
2009 Australasian Conference on Statistical Methods for Genomic Data Analysis, Queensland University of Technology, Oct 5-6.
2010 BioInfo Summer, Walter and Eliza Hall Institute for Medical Research, Melbourne, Australia, December 1.
2011 Work-In-Progress seminar, CHRU, May 25.
2011 CHARGE LA / Redondo Beach Investigator meeting, Oct 28.
2011 Department of Human Genetics, Emory University, Atlanta, Nov 14.
2012 International Seminar Speaker Series of STAGE (Strategic Training for Advanced Genetic Epidemiology), Toronto, Canada, Oct 5.
2013 Quantitative Genetics & Genomics Gordon Research Conference, Galveston Island, Texas, Feb 17-22
2013 Joint Statistical Meetings. Montreal, Canada, Aug 3-8.
2013 Workshop in Biostatistics, Stanford, Nov 7.
2013 Impact of Large-Scale Genomic Data on Statistical and Quantitative Genetics (SQG) Conference, Seattle, Nov 24-26.
2014 Department of Epidemiology and Biostatistics, Case Western Reserve University, April 7.
2014 Biological Sequence Analysis and Probabilistic Models conference, Oxford, UK, July 16-19.
2015 ENAR (Eastern North America Region of the International Biometrics Society) Spring Meeting, Miami, Florida, March 15-18
2016 Special Topics in Genetics Seminar, University of Iowa, Feb 15.
2017 Department of Biostatistics, University of Florida, Jan 27.
2017 GeneMappers 2017 conference, Geelong, Victoria, Australia, April 26-28.
2018 Fisher meeting "100 years of quantitative genetics theory and its applications: celebrating the centenary of Fisher 1918". Edinburgh, UK, Oct 9.
2018 Department of Biostatistics, University of Washington, Dec 6.
2019 Program in Quantitative Genetics, Harvard, Feb 5.
2019 Division of Medical Genetics, Department of Medicine, University of Washington, April 1.
2019 Keynote address, RECOMB Satellite on Computational Methods in Genetics, Washington DC, May 4.
2019 Department of Computational Biology, Cornell, Sept 9.
2019 American Society of Human Genetics Annual Meeting, session on "Recent Progress on Identity-by-Descent". Houston, Texas, Oct 15-19.
2019 Vancouver Machine Learning: Genomics. Vancouver, Canada, Dec 16.
2020 University of Pennsylvania Institute for Biomedical Informatics, Feb 5.
2020 University of Southern California Center for Genetic Epidemiology (seminar by zoom), April 29.
2021 University of North Carolina, Chapel Hill, Department of Biostatistics (seminar by zoom), Jan 28.
2022 UC Berkeley Center for Theoretical and Evolutionary Genetics (seminar by zoom), Oct 28.

Contributed oral presentations:
2006 International Genetic Epidemiological Society Annual Meeting, Tampa Bay, Florida, Nov 16-17.
2007 American Society of Human Genetics Annual Meeting, San Diego, California, Oct 23-27.
2009 American Society of Human Genetics Annual Meeting, Honolulu, Hawaii, Oct 20-24.
2015 Joint Statistical Meeting, Seattle, Washington, August 8-13.
2016 Society for Molecular Biology and Evolution conference, Gold Coast, Australia, July 3-7.
2016 Probabilistic Modelling in Genomes Conference, Oxford, UK, Sept 12-14.
2016 American Society of Human Genetics Annual Meeting, Vancouver, Canada, Oct 18-22.

13. University Service (list entire history; Activity, Dates, [Role])
Member of working group for Early Career Academic Women's Network, U. of Auckland, 2007-2008.
Internal review panel for Health Research Council grant applications, University of Auckland, 2009.
Internal (Biostatistics department) review: Applications for CDF funding. 2012, 2018.
Search committee, 2013 Faculty Recruitment, Department of Biostatistics, University of Washington.
Computing committee, Department of Biostatistics, University of Washington. 2010-2019.
Graduate student admissions committee, Dept of Biostatistics, University of Washington, 2012-2021.
Member of promotion committees, Department of Biostatistics, University of Washington, 2014, 2016.
Chair of promotion committee, Department of Biostatistics, University of Washington, 2019.
Chair of emergency preparedness committee, Dept of Biostatistics, University of Washington, 2021-2022.

14. Professionally-Related Community Service (list entire history; Activity, Dates, [Role])
Grant review for Paykell Trust, New Zealand, 2009.
Masters thesis grading for Massey University, 2007, 2009.
Statistical consulting for ViaLactia, New Zealand, 2007-2010.
Reviewed application for Erwin Schrödinger-Fellowship for the Austrian Science Fund (FWF), 2012.

15. [Other Pertinent Information As Needed]

16. Teaching History

16a) Formal Courses, including Distance Learning
- 1999, 2000 Introductory statistics, Texas A&M, North Carolina State University. 100% responsibility, approximately 100 students.
- 2001 Population genetics, North Carolina State University. 100% responsibility, approximately 20 students.
- 2001, 2002 Statistics for bioinformatics, North Carolina State University. 100% responsibility, approximately 20 students.
- 2006, 2007, 2008, 2009 Undergraduate Bioinformatics, University of Auckland. 20% responsibility, approximately 5 students.
- 2006, 2007 Graduate Bioinformatics, University of Auckland. 50-100% responsibility, approximately 15 students.
- 2010 Professional skills for statisticians, University of Auckland. 60% responsibility, 30 students.
- 2011 Winter, Biost 582A, Student Seminar, University of Washington.
- 2011-2022 Biost 581, Statistical Genetics Seminar, University of Washington.
- 2012 Fall, Biost 600B, Identity by Descent working group, University of Washington.
- 2014-2020, Stat/Biostat 550, Statistical Genetics I: Mendelian Genetics, University of Washington.

16b) Other Teaching
- Instructor for Summer Institute in Statistical Genetics, North Carolina/Dublin/New Zealand/Seattle, 2001-2004, 2008-2009.

16c) Independent Study
Phillip Keung, Spring 2011-Fall 2012.
Rui Zhang, Fall 2011-Winter 2012.
Anna Plantinga, Fall 2014-Fall 2015.
Qian Zhang, Fall 2012-Spring 2015.
Kelsey Grinde, Fall 2015-Fall 2016.
Yalan Xing, Fall 2016.
Ruoyi Cai, Fall 2019-Fall 2022.
Seth Temple, Spring 2020-Fall 2022.
Nobuaki Masaki, Winter 2021-

17. Advising and Formal Mentoring

17a) PhD Dissertations, Chair
Lisa Brown, Biostatistics, University of Washington, co-chair, graduated 2016.
Xiaowen Tian, Biostatistics, University of Washington, graduated 2020.
Kelsey Grinde, Biostatistics, University of Washington, graduated 2019.
Ruoyi Cai, expected 2024
Seth Temple, expected 2024

17b) Masters Theses, Chair
Sandunie Dineika Chandrananda, University of Auckland, 2009.
Steven M. Foltz, University of Washington, co-chair, 2013.

17c) Mentored Scientists and Post-Docs
Nicoleen Cloete, 2009-2010.
Zheng Cai, 2012-2013.
Wenqing Fu, co-mentor on awarded K99 (with Joshua Akey), 2015-2017.
Ying Zhou, 2017-2020.
Ping-Hsun Hsieh, co-mentor on awarded K99 (with Evan Eichler), 2019-present.
Ryan Waples, 2020-present.

17d) MS and PhD Committees in Non-Chair Role
Debbie Leader, Statistics PhD examination committee, University of Auckland, 2009.
Xiuwen Zheng, Biostatistics PhD committee, reading committee, U. of Washington, 2011-2013.
Chris Glazner, Statistics PhD committee, reading committee, U. of Washington, 2012-2014.
Matt Conomos, Biostatistics PhD committee, reading committee, U. of Washington, 2013-2014.
Rebecca Harris, Biology PhD Graduate School Representative, U. Washington, 2013-2017.
Alison Fohner, Public Health Genetics PhD Graduate School Rep., U. Washington, 2013-2015.
Serge Sverdlov, Statistics PhD Graduate School Representative, University of Washington, 2014.
Fiona Grimson, Statistics PhD committee, University of Washington, 2015-2016.
Daniel Kim, Biostatistics MPH committee, University of Washington, 2015-2016.
Qian Zhang, Biostatistics PhD committee, University of Washington, 2015-2018.
Aaron Baraff. Statistics PhD committee, University of Washington, 2016-2022.
Michael Goldberg. Genome Sciences PhD Graduate School Rep., U. Washington, 2019-2021.
Michelle Noyes. Genome Sciences PhD Graduate School Rep., U. Washington, 2019-.
Sanne Aalbers. Public Health Genetics PhD, University of Washington, 2020-
Jacob Alfieri. Biostatistics MS committee, University of Washington, 2021.

17e) Other Mentoring
Audrey Feng, Summer project, 2006.
Jessica Thomas, Honors project, 2006.
Ting Chen, Summer project, 2007.
Bo Madsen, Visiting PhD student, 2007.
Ashley Yi Lu, Honors project, 2010.
Caitlin McHugh, Poster project mentoring, Summer 2011.
Phillip Keung, Research Assistant, Fall 2010-Fall 2012.
Steven Foltz, Research Assistant, Fall 2011-Summer 2013.

Elisa Sheng, Research Assistant, Winter 2012-Summer 2012.
Qian Zhang, MD/PhD rotation. Summer 2012. Research Assistant Fall 2012-Winter 2015.
Yu Qian, Visiting PhD student, 2013.
Jun Hwang, Research Assistant, Fall 2013-Summer 2014.
Anna Plantinga, Research Assistant, Fall 2013-Spring 2014.
David Whitney, Research Assistant, Fall 2013-Summer 2015.
Qianmin Cui, Undergraduate research, Winter 2013-Spring 2013.
Bridget Lin, Undergraduate research, Fall 2013-Spring 2015.
Kelsey Grinde, Research Assistant, Fall 2014-Summer 2015.
Xiaowen Tian, Undergraduate research, Winter 2013-Summer 2014, Research Assistant Fall 2014-Fall 2018
Tracy Dong, Research Assistant, Fall 2015-Summer 2017.
Lisa Brown, Research Assistant, Fall 2015-Summer 2016.
Kaleigh Ervin, Statistical Genetics Training Grant mentoring, Fall 2017-Spring 2018.
Alex Paynter, Summer research, 2018.
Jonah Joffe, Summer research, 2018.
Yiwei Zhang, Summer research, 2019.
Ruoyi Cai, Research Assistant, Fall 2019-
Seth Temple, Research Assistant, Spring-Summer 2021.
Nobuaki Masaki, Research Assistant, Fall 2021-
Robert Trujillo, Research Assistant, Fall 2022-

17f) Academic Advising

Caitlin McHugh. Fall 2010-Winter 2014.
Brenda Price. Fall 2012-Fall 2014.
Qian Zhang. Fall 2012-Winter 2015.
Jeremy Roth. Fall 2013-Fall 2015.
Yunqi Bu. Fall 2013-Summer 2016.
Yatong Li. Fall 2014-Summer 2016.
Yalan Xing. Fall 2016-Winter 2017.
Amarise Little. Fall 2016-Fall 2018.
Edward Zhao. Fall 2017-Fall 2019.
Si Cheng. Fall 2018-Fall 2020.
Jacob Alfieri. Fall 2019-Summer 2020.
Ruoyi Cai. Fall 2019-Fall 2022.
Angela Dahl. Fall 2020-
Nobuaki Masaki, Fall 2021-