Postdoctoral Advisees (*: with independent support)

1. 1982-1983*   Tom Meagher, Fullbright Fellow
   Statistical Laboratory, University of Cambridge
   Current Position; Professor, Univ. of St. Andrews, UK
2. 1986-1987*   Alun Thomas, Acting Assistant Professor
   Department of Statistics, University of Washington
   Current Position; Professor of Medical Genetics, University of Utah
3. 1988-1989*   Paul Joyce, Acting Assistant Professor
   Department of Statistics, University of Washington
   Final Position; Dean of Sciences, University of Idaho
4. 1995-1997   Simon Heath, Department of Statistics, University of Washington
   Current Position; Statistical Genomics and Bioinformatics Development
   Group Leader, National Center for Genomic Analysis, Barcelona, Spain.
5. 1997-1999   Jochen Kumm, Department of Statistics, University of Washington
   Current Position; Director of Bioinformatics, Stanford Genome Technology
   Center
6. 1997-2000   E. Warwick Daw; Statistics and Medical Genetics, Univ. Washington
   Current Position: Research Statistiician, Division of Statistical Genomics
   Washington University, St. Louis
7. 2002*   David Henderson, Visiting Assistant Professor
   Department of Statistics, University of Washington
   Current Position; Independent Genomics Research Consultant, Seattle.
8. 2000-2002   Andrew George, Department of Statistics, University of Washington
   Current Position; University of Queensland, Australia
9. 2001-2004*   Oliver Will, NSF VIGRE Postdoctoral Fellow
   Department of Statistics, University of Washington
   Current Position; Biotechnology Research Scientist, Philadelphia.
10. 2004-2006   Adele Mitchell, Department of Statistics and Genome Training Grant,
    University of Washington
    Current position; Merck, Boston, MA, USA.
11. 2004-2007   Liping Tong, Department of Statistics, University of Washington
    Current Position; Department of Public Health Sciences, Loyola University,
    Chicago.
12. 2010-2012   Chaozhi Zheng, Department of Statistics, University of Washington
    Current position, Research Scientist, Biometris, University of Wageningen
13. 2013-2015   Jesse Raffa, Department of Statistics, University of Washington
    Current position; Research Scientist, Laboratory for Computational
    Physiology, Massachusetts Institute of Technology
14. 2014-2015   John Ranola, Department of Statistics and Genome Training Grant,
    University of Washington
    Current position; Research Statistical Geneticist, Department of Laboratory
    Medicine, University of Washington

Graduate Students; Ph.D. Students

1. Fall 1981;   Kevin Donnelly; Ph. D., Cambridge University
           a.k.a Caoimhin adrai O'Donnail
           Genetic linkage, detectable relationships and other topics.

2. Dec. 1985;   Alun Thomas, Ph.D., Cambridge University.
           Data structures, methods of approximation and optimal computation for pedigrees

3. March 1988;   Gary Churchill, Ph.D. Biostatistics, University of Washington.
           Stochastic models for DNA sequence data

4. June 1990;   Charles Geyer ; Ph.D., Statistics, University of Washington.
           Likelihood and exponential families

5. Aug. 1990;   Nuala Sheehan; Ph.D., Statistics, University of Washington.
           Genetic restoration on complex pedigrees.

6. Dec. 1990;   Mariza de Andrade; Ph.D., Biostatistics, University of Washington.
           Estimation of genotypic parameters under non-normal models.

7. Dec. 1991;   Sun Wei Guo; Ph.D., Biostatistics, University of Washington.
           Monte Carlo methods in quantitative genetics

8. June 1993;   Shili Lin; Ph.D., Statistics, University of Washington.
           Markov chain Monte Carlo estimates of probabilities on complex structures.

9. Aug. 1993;   Heike Blossey (Bickeboeller); Ph.D., Statistics, University of Washington.
           The Poisson clumping heuristic and survival of a genome continuum.

10. Aug. 1995;   Hongzhe Li; Ph.D., Statistics, University of Washington.
           Semiparametric estimation of major gene and random environmental effects for age of onset.

11. June 1996;   Ian Painter; Ph.D., Statistics, University of Washington.
           Inference in a discrete parameter space.

12. Aug. 1998;   Jinko Graham; Ph.D. Biostatistics, University of Washington.
           Disequilibrium fine-mapping of a rare allele via coalescent models of gene ancestry.

13. July 1999;   Sharon Browning; Ph.D., Statistics, University of Washington
           Monte Carlo likelihood calculation for identity by descent data.

14. Aug, 2000;   Mary Beatrix Jones; Ph.D., Statistics, University of Washington
           Likelihood inference for parametric models of dispersal

15. June 2001;   Nicola Chapman; Ph.D., Biostatistics, University of Washington.
           Genome descent in isolated populations

16. Aug. 2001;   Eric Anderson; Ph.D., Quantitative Ecology and Resource Management, University of Washington.
           Monte Carlo methods for inference in population genetic models

17. Aug. 2003   Amy Anderson; Ph.D., Statistics, University of Washington.
           The genetic structure of related recombinant inbred lines

18. Aug. 2003   Na (Michael) Li; Ph.D., Biostatistics, University of Washington.
           Modeling and inference for linkage disequilibrium and recombination (Co-adviser with Matthew Stephens)

19. Aug. 2003   Solveig (Solly) Sieberts; Ph.D., Statistics, University of Washington.
           Joint relationship inference from three of more individuals in the presence of genotyping error

Graduate Students; Ph.D. . Thesis advisees (contd.)

20. Dec. 2003   Anne-Louise Leutenegger; Ph.D. Biostatistics, Univ. of Washington.
Estimation of random genome sharing: Consequences for linkage detection
(Co-adviser with Francoise Clerget-Darpoux for Univ. Paris XI)

21. Aug. 2005   Saonli Basu; Ph.D., Statistics, University of Washington.
Allele-sharing methods for linkage detection using extended pedigrees

22. Nov. 2005   William Stewart; Ph.D., Statistics, University of Washington.
Alternative models for estimating genetic maps from pedigree data

23. Aug. 2006   Arindam RoyChoudhury; Ph.D., Statistics, University of Washington.
Likelihood inference for population structure, using the coalescent

24. June 2009   Yanming Di; Ph.D., Statistics, University of Washington.
Conditional tests for localizing trait genes

25. March 2013   Ming Su; Ph.D., Electrical Engineering, University of Washington.
Probabilistic inference in modern genetic linkage analysis
(Co-adviser with Richard Shi (EE))

26. June 2014   Christopher Glazner; Ph.D., Statistics, University of Washington.
Monte Carlo estimation of identity by descent in populations

27. June 2014   Serge Sverdlov; Ph.D., Statistics, University of Washington.
Functional quantitative genetics and the missing heritability problem

28. March 2017   Fiona Grimson; Ph.D., Statistics, University of Washington.
Scalable methods of inference of identity by descent

29. August 2019   Bowen Wang; Ph.D., Statistics, University of Washington.
Realized genome sharing in random effects models for quantitative genetic traits

30. December 2022   Aaron Baraff; Ph.D., Statistics, University of Washington.
Likelihood-based haplotype frequency modeling using variable-order Markov chains

Diploma and M.S. Thesis advisees

June 1981; Patty Solomon; Dip Stat, Cambridge University
The inheritance of height; An analysis of a Finnish population on the basis of simple genetic models.

June 1982; Alun Thomas; Dip. Stat., Cambridge University
Marriage patterns and gene extinction on Tristan da Cunha.

June 1984; Daniel Goodman; Dip. Stat., Cambridge University
Linkage analysis in a Newfoundland genealogy.

June 1985; Christine Hackett; Dip.Stat., Cambridge University
An analysis of Faroese marriage data; the patterns of migration and the consequent genetic variation.

June 1988; Ellen Walters ; M.S., Biostatistics, University of Washington.
Comparison of linkage analysis designs based on individuals affected with recessive diseases

Aug. 1994; Colin C. Wilson; M.S.; Quantitative Ecology and Resource Management, University of Washington.
Bayesian estimation of genealogical structure in small populations.

Aug. 1997; Beatrix Jones; M.S., Statistics, University of Washington.
Phylogeny inference via conditional independence modelling

June 2001; Solveig Sieberts; M.S., Statistics, University of Washington.
Recessive lethals: a possible explanation for excess sharing in sibs

June 2005 Ting-Yuan Liu; M.S., Statistics, University of Washington.
Analysis of haplotype structure: Application to the DARC gene region

Mar. 2006 Sinjian Grace Gé; Ph.Cand., Biostatistics, University of Washington.
Genetic analysis of longitudinal data on a time-varying quantitative trait.

Aug 2009 Zheng Cai; Visiting student, Statistics, University of Washington.
Simulaton of descent of chromosome segments in structured populations.
(Project during visit year from University of Utah.)

Aug 2011 Marshall Brown; M.S., Statistics, University of Washington.
The effect of linkage disequilibrium on inferring coancestry in populations.

Aug 2013 Chensheng Kuang; M.S., Statistics, University of Washington.
The size distribution of IBD groups under ESF and the coalescent
(M.S. project for Statistical Genetics special emphasis)