

### Postdoctoral Advisees

1. 1982-1983 Tom Meagher, Statistical Laboratory, University of Cambridge  
Current Position; Professor, Univ. of St. Andrews, UK
2. 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.
3. 1997-1999 Jochen Kumm, Department of Statistics, University of Washington  
Current Position; Director of Bioinformatics, Stanford Genome Technology  
Center
4. 1997-2000 E. Warwick Daw; Statistics and Medical Genetics, Univ. Washington  
Current Position: Research Statistiician, Division of Statistical Genomics  
Washington University, St. Louis
5. 2000-2002 Andrew George, Department of Statistics, University of Washington  
Current Position; University of Queensland, Australia
6. 2004-2006 Adele Mitchell, Department of Statistics and Genome Training Grant,  
University of Washington  
Current position; Merck, Boston, MA, USA.
7. 2004-2007 Liping Tong, Department of Statistics, University of Washington  
Current Position; Department of Public Health Sciences, Loyola University,  
Chicago.
8. 2010-2012 Chaozhi Zheng, Department of Statistics, University of Washington  
Current position, Research Scientist, Biometris, University of Wageningen
9. 2013-2015 Jesse Raffa, Department of Statistics, University of Washington  
Current position; Research Scientist, Laboratory for Computational  
Physiology, Massachusetts Institute of Technology
10. 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.

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

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 or more individuals in the presence of genotyping error
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

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

- 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

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