Curriculum Vitae of Garrett Hellenthal

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UCL Genetics Institute (UGI)
Department of Genetics, Evolution and Environment
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Education

Graduate:

University of Washington, Seattle, WA

Doctor of Philosophy in Statistics, August 2006 (emphasis: statistical genetics)

thesis title: "Exploring Rates and Patterns of Variability in Gene Conversion and Crossover in the Human Genome" (advisor: Dr. Matthew Stephens, Statistics)

selected courses: Advanced Applied Statistics, Advanced Statistical Theory, Applied Regression, Bayesian Statistics, Computational Genomics, Microarray Analysis, Population Genetics, Statistical Genetics, Stochastic Modelling

programming languages: C, perl, R, SAS, S-Plus, SPSS

Undergraduate:

Santa Clara University, Santa Clara, CA

Bachelor of Science in Mathematics, June 2001

Major: Mathematics (emphasis in Applied Math)
Minor: Chemistry
Honors and Awards: Dean's List 1997-1998

Institute for European Studies (IES), Vienna, Austria
Studies Abroad Program (Santa Clara University), Fall Quarter 1999

Experience

UCL Genetics Institute, University College London, London, United Kingdom (2012 - present)

- Sir Henry Dale Research Fellow, Department of Genetics, Evolution and Environment, 2012-present

Wellcome Trust Centre for Human Genetics, Oxford, United Kingdom (2009 - 2012)

- Postdoctoral Research Assistant, Wellcome Trust Case Control Consortium 2 (advisor: Prof Peter Donnelly, Statistical Genetics), 2009-present
  - chief analyst for multiple sclerosis genome-wide association study; collaboration with International Multiple Sclerosis Genetics Consortium (IMSGC)
  - chief analyst for People of the British Isles (POBI) project categorizing population structure across United Kingdom

Department of Statistics, University of Oxford, Oxford, United Kingdom (2006 - 2009)

- Postdoctoral Research Assistant, Polygene Project (advisor: Prof Jotun Hein, Bioinformatics), 2006-2009
  - development and application of genome-wide association study methods; collaboration with deCODE Genetics, University of Aarhus, and Radboud University Nijmegen Medical Centre
- Instructor, Oxford Bioinformatics Programme, Doctoral Training Centre, 2007-2009
  - lectures and practicals on "Statistical Data Mining", "Molecular Evolution", and "Introduction to Biological Systems"

Statistics Department, University of Washington, Seattle, United States (2001 - 2006)

- Research Assistant, Dr. Matthew Stephens, 2003 - 2006
  - development of novel statistical methods to explore genome-wide recombination rates in humans
- Teaching Assistant, Statistics Department, 2001 - 2003
  - lectures and practicals to undergraduate and graduate level students, including computer coding (R, S-Plus, SAS) and statistical methodology

Affymax Research Institute, Santa Clara, United States (Summer 2000)

- Laboratory Technician (internship)
  - synthesis of chemical libraries

Activities

Graduate Student Senator, University of Washington, 2002 - 2003

Prizes

Imperial College Junior Research Fellowship, 2009 (declined to attend Wellcome Trust Centre for Human Genetics)

Postdoctoral Research Travel Award, SMBE Annual Meeting, June 2008

Student Oral Competition Award, WNAR/IMS Annual Meeting, June 2005

NIH/NHGRI Genome Training Grant Awardee, University of Washington, 2004-2006

Selected Presentations

University of Leicester, Leicester, United Kingdom (April 2, 2014)

- EMBO: Human evolution in the genomic era conference – *Making inferences from genome diversity* (work with S. Myers, D. Falush, W.Bodmer, P. Donnelly, G. Band, G. Busby, C. Capelli, D. Lawson, S. Leslie, J. Wilson, B. Winney)

London School Hygiene and Tropical Medicine, London, United Kingdom (March 12, 2013)

- Bloomsbury Centre for Genetic Epidemiology and Statistics Seminar – *Identifying and dating historical admixture events in humans using DNA* (work with S. Myers, D. Falush, D. Lawson, J. Wilson, C. Capelli, G. Busby)

University of Warwick, Warwick, United Kingdom (October 15, 2012)

- MiR@W - Models and Inference in Population Genetics – *Inferring Human Admixture History and Relatedness Using DNA* (work with S. Myers, D. Falush, D. Lawson)

University College London, London, United Kingdom (August 23, 2011)

- UCL Genetics Institute Seminar – *New Haplotype-Based Methods for Inference of Population Structure and Admixture Events* (work with S. Myers, D. Falush, D. Lawon, C. Capelli, G. Busby)

Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany (December 7, 2010)

- Department of Human Evolution Seminar – *Identifying and Dating Population Admixture Events Using SNP Data* (work with S. Myers, D. Falush)

Genomics of Common Diseases $4^{\mathbf{th}}$ **Annual Meeting**, Houston, United States (October 8, 2010)

- Platform Presentation – *The genetics of multiple sclerosis susceptibility* (on behalf of WTCCC2, IMSGC)

Greek Stochastics β **Annual Meeting**, Lefkada, Greece (August 26, 2010)

- Platform Presentation – *Identifying and Dating Population Admixture Events Using Dense Genetic Variation Data* (work with S. Myers, D. Falush)

International Multiple Sclerosis Genetics Consortium Annual Meeting, Toronto, Canada (April 11, 2010)

- Presentation – *Genome-wide Association Analysis of Multiple Sclerosis* (on behalf of WTCCC2)

Imperial College London, London, United Kingdom (October 24, 2008)

- Centre for Biostatistics Seminar – *Estimating Human Admixture History Using a Copying Model* (work with D. Falush, S. Myers)

Society for Molecular Biology and Evolution $16^{\mathbf{th}}$ **Annual Meeting**, Barcelona, Spain (June 6, 2008)

- Contributed Presentation – *Inferring Human Colonization History Using a Copying Model* (work with D. Falush, S. Myers)

American Society of Human Genetics $57^{\mathbf{th}}$ **Annual Meeting**, San Diego, United States (October 27, 2007)

- Platform Presentation – *Inference of the Peopling of the World Under Sequential Bottlenecks with Admixture* (work with D. Falush, A.Auton)

deCODE Genetics, Reykjavik, Iceland (June 4, 2007)

- Presentation – *Testing SNPs Imputed with HapMap Data*

WNAR/IMS Annual Meeting, University of Fairbanks, Fairbanks, United States (June 23, 2005)

- Student Paper Talk – *A New Method for Estimating Rates of Gene Conversion from Population Data* (work with M. Stephens)

Publications

Hellenthal, G.; Busby, G.B.; Band, G.; Wilson, J.F.; Capelli, C.; Falush, D.; and Myers S. (2014) A genetic atlas of human admixture history, *Science* **343**:747-51.

International Multiple Sclerosis Genomics Consortium (IMSGC), Wellcome Trust Case Control Consortium 2 (WTCCC2) et al (2013) Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis, *Nature Genetics* **45(11)**:1353-60.

Lawson, D.; Hellenthal, G.; Myers, S.; and Falush, D (2012) Inference of population structure using dense haplotype data, *PLoS Genetics* **8(1)**:e1002453.

Bowden, R.; MacFie, T.; Myers, S.; Hellenthal, G.; Nerrienet, E.; Bontrop, R.; Freeman, C.; Donnelly, P.; and Mundy, N (2012) Genomic tools for evolution and conservation in the chimpanzee: Pan troglodytes ellioti is a genetically distinct population, *PLoS Genetics* **8(3)**:e1002504.

Sawcer, S*; Hellenthal, G*; Pirinen, M*, Spencer, CA*; International Multiple Sclerosis Genetics Consortium (IMSGC) and the Wellcome Trust Case Control Consortium (WTCCC2) (2011) Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis, *Nature* **476**:214-219.

International Parkinson's Disease Genomics Consortium (IPDGC) and the Wellcome Trust Case Control Consortium 2 (WTCCC2) (2011) A two-stage meta-analysis identifies several new loci for Parkinson's disease, *PLoS Genetics* **7(6)**:e1002142.

Sawcer, S; and Hellenthal, G (2011) The major histocompatibility complex and multiple sclerosis: a smoking gun?, *Brain* **134(3)**:638-640.

Hellenthal, G; Auton, A; and Falush, D (2008) Inferring Human Colonization History Using a Copying Model, *PLoS Genetics* **4(5)**:e1000078.

Hellenthal, G and Stephens, M (2007) msHOT: modifying Hudson's ms simulator to incorporate crossover and gene conversion hotspots, *Bioinformatics* **23(4)**:520-521.

Hellenthal, G and Stephens, M (2006) Insights into recombination from population genetic variation, *Current Opinion in Genetics & Development* **16**:565-572.

Hellenthal, G; Pritchard, J.K.; and Stephens, M (2006) The effects of genotype-dependent recombination, and transmission asymmetry, on linkage disequilibrium, *Genetics* **172**:2001-2005.

Crawford, D.C.; Bhangale, T.; Li, N.; Hellenthal, G.; Reider, M.J.; Nickerson, D.A.; and Stephens, M (2004) Evidence for substantial fine-scale variation in recombination rates across the human genome, *Nature Genetics* **36:**700-706.

* denotes joint first authors

Brief Biographical Sketch

I am currently a Sir Henry Dale Fellow working at the UCL Genetics Institute (UGI) at University College London (since Sept 2012), jointly funded by the Wellcome Trust and the Royal Society. My primary work involves developing and applying statistical methodology to genome-wide DNA in order to learn about human demography, collaborating with colleagues at the University of Oxford, Max Planck Institute for Evolutionary Anthropology, and University of Bristol. One project involves characterizing genetic structure across the United Kingdom in the Peopling of the British Isles (POBI) dataset (http://www.peopleofthebritishisles.org/). Other current research interests include studying genetic differentiation among different strains of yeast and identifying genetic regions under selection.

I received my undergraduate degree, Bachelor of Science in Mathematics, at Santa Clara University in 2001. I received my Doctor of Philosophy in Statistics at the University of Washington (with an emphasis in statistical genetics) under the supervision of Dr. Matthew Stephens in 2006. My thesis work was on the development of a new statistical model for estimating rates of gene conversion using Single-Nucleotide-Polymorphism (SNP) data. I subsequently worked as a postdoctoral researcher at the Unversity of Oxford and the Wellcome Trust Centre for Human Genetics, identifying regions of the genome associated with multiple sclerosis susceptibility using a sample of

>10,000 case subjects and healthy controls as part of the Wellcome Trust Case Control Consortium 2 (WTCCC2) project.

References

(available upon request)