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## Education

### Graduate:

**University of Washington**, Seattle, WA  
Doctor of Philosophy in Statistics, August 2006 (emphasis: statistical genetics)  
*Selected Courses:* Advanced Applied Statistics, Advanced Statistical Theory, Applied Regression, Bayesian Statistics, Computational Genomics, Microarray Analysis, Population Genetics, Statistical Genetics, Stochastic Modeling

### 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

**Department of Statistics**, University of Oxford (2006 - present)

- Postdoctoral Research Assistant, 2006-present
  - Polygene Project: development and application of genomewide association methods and analyses (collaboration with deCODE Genetics, University of Aarhus BiRC, and Radboud University Nijmegen Medical Centre) (advisor: Prof Jotun Hein, Bioinformatics)
- Practical Instructor, 2007-present
  - Oxford Bioinformatics Programme: taught in three week-long tutorials on Statistical Data Mining (April-May 2007, February 2008)

- Oxford Bioinformatics Programme: taught one lecture and practical for Molecular Evolution Series (December 2007)

**Statistics Department**, University of Washington (2001 - 2006)

- Research Assistant, 2003 - 2006
  - thesis: *Exploring Rates and Patterns of Variability in Gene Conversion and Crossover in the Human Genome* (advisor: Dr. Matthew Stephens, Statistics)
- Teaching Assistant, 2001 - 2003
  - developed lectures and taught weekly courses to undergraduate and graduate level students, including computer coding (R, S-Plus, SAS) and demonstrative labs

**Affymax Research Institute**, Santa Clara, CA (Summer 2000)

- Laboratory Technician (internship)
  - participated in the synthesis of chemical libraries and presented weekly progress reports

## Activities

Graduate Student Senator, University of Washington, 2002 - 2003

## Prizes

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

Postdoctoral Research Travel Award, SMBE Annual Meeting, June 2008

## Selected Posters and Presentations

**SMBE 2008 Annual Meeting**, Barcelona, Spain (06/06/08)

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

**Mathematical Biology Seminar**, University of Oxford, United Kingdom (05/06/08)

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

**ASHG 57<sup>th</sup> Annual Meeting**, San Deigo, California (10/27/07)

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

**Polygene Group Workshop**, deCODE Genetics, Iceland (06/04/07)

- Presentation – *Testing SNPs Imputed with HapMap Data*

**Mathematical Biology Seminar**, University of Oxford, United Kingdom  
(01/16/07)

- Seminar Presentation – *Exploring Rates and Patterns of Variability in Gene Conversion and Crossover in the Human Genome* (work with M. Stephens)

**ASHG 56<sup>th</sup> Annual Meeting**, New Orleans, Louisiana (10/09/06)

- Poster Presentation – *msHOT: Simulating Crossover and Gene Conversion Hotspots with the ms Simulator* (work with M. Stephens)

**Evolution and Population Genetics Seminar**, University of Washington, Seattle (01/31/06, 02/02/06)

- Seminar Presentation – *Estimating crossover recombination and gene conversion rates from the human genome* (work with M. Stephens)

**ASHG 55<sup>th</sup> Annual Meeting**, Salt Lake City, Utah (10/28/05)

- Poster Presentation – *Genome-wide Variation in Rates of Gene Conversion and Crossover* (work with M. Stephens)

**WNAR/IMS Annual Meeting**, University of Fairbanks, Alaska  
(06/23/05)

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

## Publications

Hellenthal, G; Auton, A.; and Stephens, 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.; & Stephens, M (2006) The Effects of Genotype-Dependent Recombination, and Transmission Asymmetry, on Linkage Disequilibrium, *Genetics* **172**: 2001-2005.

Crawford, D.C.; T. Bhangale, T.; Li, N.; Hellenthal, G.; Reidner, M.J.; Nickerson, D.A.; & Stephens, M (2004) Evidence for Substantial Fine-Scale Variation in Recombination Rates Across the Human Genome, *Nature Genetics* **36**:700-706.

## References

(available upon request)