EMILIA HUERTA-SANCHEZ
emiliahs@stat.berkeley.edu

Department of Statistics
Center for Theoretical Evolutionary Genomics
347 Evans Hall, Berkeley, CA 94720
Office phone: (510) 643-0060

EDUCATION

Cornell University, Ithaca, NY

2008 Ph.D. in Applied Mathematics Thesis: Patterns of genetic variation under alternative population genetic models **Advisors:** Richard Durrett and Carlos Bustamante

2005 M.S. Applied Mathematics

Mills College, Oakland, CA

2002 B.A. Mathematics and B.A. French

APPOINTMENTS

UC Berkeley, Berkeley, CA

2009 - present NSF Minority Postdoctoral Research Fellow **Advisor:** Prof. Rasmus Nielsen

2008 - 2009 Visiting VIGRE Assistant Professor

Trinity College Dublin, Ireland

Spring 2008 GeneTime Fellow
Host: Prof. Dan Bradley

Research interests

Population genetics, human genetics, demographic inference, natural selection, analyses of genetic variants from next-generation sequencing data, high altitude adaptation.

TEACHING EXPERIENCE

Course Instructor

Fall 2010	Stat 98/198 (VIGRE seminar)
Fall 2009	Stat 98/198 (VIGRE seminar)
Spring 2009	Stat 134 (Introduction to Probability)
Fall 2008	Stat 20 (Introduction to statistics)
Fall 2008	Stat 98/198 (VIGRE seminar)

Teaching assistant

Fall 2006	Math 111 (Calculus I)
Fall 2005	Multivariate Calculus

PUBLICATIONS

B. Peter, **E. Huerta-Sanchez** and R. Nielsen. Distinguishing between selective sweeps from standing variation and from a de novo mutation. *Submitted to Plos Genetics*.

K. E. Lohmueller, A. Albrechtsen, Y. Li, S. Y. Kim, T. Korneliussen, N. Vinckenbosch, G. Tian, **E. Huerta-Sanchez** et al. Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. *PLoS Genetics*.

X. Yi*, Y. Liang*, **E. Huerta-Sanchez*,** X. Jin*, Z. X. P. Cuo*, J.E. Pool* et al. Archaelogy Augments Tibet's Genetic History—Response. *Science* 329(5998):1467-1468, 2010.

X. Yi*, Y. Liang*, **E. Huerta-Sanchez*,** X. Jin*, Z. X. P. Cuo*, J.E. Pool* et al. Sequencing of 50 human exomes reveals adaptation to high altitude. *Science* 329(5987):75-78, 2010. (Subject of a 'Perspectives' article in the same issue and media coverage)

Y. Li*, N. Vinckenbosch*, G. Tian*, **E. Huerta-Sanchez*,** T. Jiang* et al. Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. *Nature Genetics* 42, 969-972, 2010.

C. Murray*, **E. Huerta-Sanchez*,** F. Casey and D. Bradley. Cattle demographic history modelled from autosomal sequence variation. *Phil. Trans. R. Soc. B* 365:2531-2539, 2010.

* **Joint first author**

E. Huerta-Sanchez, R. Durrett, and C. D. Bustamante. Population genetics of polymorphism and divergence under fluctuating selection. *Genetics* 178:325-337, 2008.

E. Huerta-Sanchez and R. Durrett. Wagner's canalization model. *Theoretical Population Biology* 71(2):121-130, 2007.

B. Gonzales, **E. Huerta-Sanchez,** C. Kribs, A. Ortiz-Nieves and T. Vazquez-Alvarez. Am I Too Fat? Bulimia as an Epidemic. *Journal of Mathematical Psychology* 47(5-6): 515-526, 2003.

E. Huerta-Sanchez, A. Lopez, D. Uminsky. Iterations of Even-Odd Splitting Map Can Make Integration Easier *The Pi Mu Epsilon Journal*. Vol. 11, No. 5, 241-250, 2001.

E. Huerta-Sanchez, K. Rios-Soto, G. Jordan-Salivia. *The Effects of Mass Transportation During a Deliberate Release of Smallpox*. Technical report for the Mathematical and Theoretical Biology Institute(MTBI). Cornell University, Ithaca, NY Summer 2002.

Publications in preparation

Estimating the distribution of family sizes in the lambda coalescent (with Rick Durrett and Carlos Bustamante). One of the underlying assumptions of the Kingman's coalescent is that the offspring distribution is binomial, leading to a limiting process (as the population tends to infinity) which is the Kingman's coalescent model. We study here an alternative coalescent model called the Beta coalescent which is a better representation for some marine species which are characterized by very large family sizes.

Characterizing the genetic basis behind high altitude adaptation in Tibetans. To further characterize the genetic adaptation we identified, we are analyzing sequences of the candidate regions to estimate the timing and strength of selection.

Tibetan Demographic History. The timing of when Tibetans inhabited the Tibetan plateau is still an open question, with varying estimates from the archaeological record and genetic studies. In this project, we aim to reconcile both types of evidence by employing divergence estimates from the closely related Han Chinese population.

PRESENTATIONS

Characterizing the genetic signature of high altitude adaptation in Tibetans. 2011 Society of Molecular Biology and Evolution (SMBE), Kyoto, Japan.

Sequencing of 50 human exomes reveals adaptation to high altitude. 2010 American Society of Human Genetics, Washington D.C., U.S.A.

Sequencing of 50 human exomes reveals adaptation to high altitude. 2010 Society of Molecular Biology and Evolution (SMBE), Lyon, France.

Sequencing of 50 human exomes reveals adaptation to high altitude. 2010 Bay Area Population Genomics Conference, UC Berkeley, CA, USA.

Modeling large family size: Lambda coalescent. 2008 Young investigators in Population Genetics Workshop, Tuscon, Arizona, USA.

Wagner's Canalization Model. 2006 Cornell Probability Summer School, Ithaca, NY.

OUTREACH

Undergraduate mentor for the Society for Molecular Biology and Evolution (SMBE) conference, 2010-2011. Guided undergraduates through their first academic conference experience.

Co-organized VIGRE seminar 2009, 2010, designed to introduce a diverse group of undergraduate students to statistics, content covered both practical applications in industry and academic research, and small research projects.

Co-organized Cal Day 2009, an annual university open house for prospective students and community members to visit the campus to meet the faculty and students to explore research and other activities.

Participated in the founding of the Summer Math Institute (SMI) in Cornell University, targeting underrepresented minorities and first generation college students for pre-PhD research training, and helped run the program in 2006.

Was on co-organizing committee for the Expanding Your Horizons (EYH) program, a one day conference for middle school girls to experience the mathematical sciences in practical workshops, Cornell University, 2004-2007

2007

OTHER EXPERIENCE

Member of the NSF Evolutionary Genetics grant review panel for the Evolutionary Processes Cluster of the Division of Environmental Biology, October 19-21, 2010, Arlington, VA.