

JOHN NOVEMBRE, PhD

The University of Chicago
Department of Human Genetics
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Curriculum Vitae Formatted to Guidelines for UChicago Biological Sciences Division

ACADEMIC APPOINTMENTS

- 2017- **Professor, University of Chicago**, Department of Human Genetics, Department of Ecology and Evolutionary Biology (secondary appointment)
- 2013-2017 **Associate Professor, University of Chicago**, Department of Human Genetics, Department of Ecology and Evolutionary Biology (secondary appointment)
- 2012-2013 **Associate Professor, University of California–Los Angeles**, Department of Ecology and Evolutionary Biology, Interdepartmental Program in Bioinformatics
- 2008-2012 **Assistant Professor, University of California–Los Angeles**, Department of Ecology and Evolutionary Biology, Interdepartmental Program in Bioinformatics

Ph.D.-Granting Committee, Program, Institute, and Center Appointments

- 2013- Committee on Evolutionary Biology, University of Chicago
- 2013- Committee on Genetics, Genomics, and Systems Biology, University of Chicago
- 2008-2013 Interdepartmental Program in Bioinformatics, UCLA
- 2012-2009 Center for Society and Genetics, UCLA

ACADEMIC TRAINING

- 2006-2008 **Postdoctoral training**, Department of Human Genetics
University of Chicago, Chicago, IL. Advisor: Matthew Stephens
- 2006 **PhD**, Integrative Biology, designated emphasis in Computational Biology/Genomics
University of California-Berkeley, Berkeley, CA. Advisor: Montgomery Slatkin
Dissertation title: *Statistical methods for neutral and adaptive genetic variation in continuous isolation-by-distance models*
- 2000 **BA**, Biochemistry *cum laude*
The Colorado College, Colorado Springs, CO. Advisor: Ralph Bertrand-Garcia

SCHOLARSHIP

Notation: * indicates authors contributed equally, **bold** indicates lab members

ORCID: 0000-0001-5345-0214

(a) Peer-reviewed publications in the primary literature, exclusive of abstracts:

1. Excoffier L, **Novembre J**, Schneider, S. (2000) SIMCOAL: a general coalescent program for simulation of molecular data in interconnected populations with arbitrary demography. *Journal of Heredity* 91:506-509.
2. **Novembre J**. (2002) Accounting for background nucleotide composition when measuring codon usage bias. *Molecular Biology and Evolution* 19(8):1390-1394.
3. Anderson EC, **Novembre J**. (2003) Finding haplotype block boundaries using the minimum description length principle. *American Journal of Human Genetics* 73(2):336-354.
4. Galvani AP, **Novembre J**. (2005) The evolutionary history of the CCR5-Delta32 HIV-resistance mutation. *Microbes and Infection* 7:302-309.
5. **Novembre J**, Galvani, AP, Slatkin, M. (2005) The geographic spread of the CCR5-Delta32 HIV-resistance mutation. *PLoS Biology* 3(11):e397.
6. Rosenblum EB, **Novembre J**. (2007) Ascertainment bias in spatially structured populations: a case study in the eastern fence lizard. *Heredity* 98:331-336.
7. **Novembre J**, Stephens M. (2008) Interpreting principal components analyses of spatial population genetic variation. *Nature Genetics* 40:646-649 [recommended by Faculty of 1000, featured in News & Views].
8. **Novembre J**, Johnson T, Bryc K, Kutalik Z, Boyko AR, Auton A, Indap A, King KS, Bergman S, Nelson MR, Stephens M, Bustamante CD. (2008) Genes mirror geography within Europe. *Nature* 456: 98-101.
9. Coop G, Pickrell JK, **Novembre J**, Kudravalli S, Li J, Absher D, Myers RM, Cavalli-Sforza LL, Feldman MW, Pritchard JK. (2009) The role of geography in human adaptation. *PLoS Genetics* 5:e1000500.
10. Auton A, Bryc K, Boyko AR, Lohmueller KE, **Novembre J**, Reynolds A, Indap A, Wright MH, Degenhardt JD, Gutenkunst RN, King KS, Nelson MR, Bustamante CD. (2009) Global distribution of genomic diversity underscores rich complex history of continental human populations. *Genome Research* 19:795-803.
11. Pickrell JK, Coop G, **Novembre J**, Kudravalli S, Li JZ, Absher D, Srinivasan BS, Barsh GS, Myers RM, Feldman MW, Pritchard JK. (2009) Signals of recent positive selection in a worldwide sample of human populations. *Genome Research* 19:826-837.
12. **Novembre J**, Slatkin M. (2009) Likelihood-based inference in isolation-by-distance models using the spatial distribution of low-frequency alleles. *Evolution* 63:2914-2925.

13. Alexander DH, **Novembre J**, Lange K. (2009) Fast model-based estimation of ancestry in unrelated individuals. *Genome Research* 19:1655-1664.
14. **Novembre J**, Di Rienzo A. (2009) Spatial patterns of variation due to natural selection in humans. *Nature Reviews Genetics* 10:745-755
15. Francois O, Currat M, Ray, N, **Han E**, Excoffier L, **Novembre J**. (2010). Principal component analysis under population genetic models of range expansion and admixture. *Molecular Biology and Evolution* 27:1257-1268.
16. Royal CD, **Novembre J**, Fullerton SM, Goldstein DB, Long JC, Bamshad MJ, Clark AG. (2010). Inferring Genetic Ancestry: Opportunities, Challenges, and Implications. *American Journal of Human Genetics* 14:661-673.
17. vonHoldt B, Lohmueller K, **Han E**, Pollinger J, Parker HG, Quignon P, Degenhardt JD, Boyko AR, Earl DE, Auton A, Reynolds A, Bryc K, Brisin A, Knowles J, Mosher DS, Spady TC, Elkahlon A, Geffen E, Pilot M, Jdrzejewski W, Greco C, Randi E, Bannasch D, Wilton A, Shearman J, Cargill M, Jones PG, Qian Z, Huang W, Ding Z, Zhang Y, Bustamante CD, Ostrander EA, **Novembre J**, Wayne RK. (2010). Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. *Nature* 464:898-902.
18. **Wegmann D**, **Kessner D**, **Veeramah KR**, Mathias RA, Nicolae DL, Yanek LR, Sun YV, Torgerson DG, Rafaels N, Mosely T, Becker LC, Ruczinski I, Beaty TH, Kardia SLR, Meyers D, Barnes KC, Becker DM, Freimer N, **Novembre J**. (2011). Recombination rates in admixed individuals revealed by ancestry-based inference. *Nature Genetics* 43:847-853. [featured in News & Views]
19. vonHoldt BM1, Pollinger JP, **Earl DA**, Knowles JC, Boyko AR, Parker H, Geffen E, Pilot M, Jdrzejewski W, Jdrzejewska B, Sidorovich V, Greco C, Randi E, Musiani M, Kays R, Bustamante CD, Ostrander EA, **Novembre J**, Wayne RK. (2011) A genome-wide perspective on the evolutionary history of enigmatic wolf-like canids. *Genome Research* 21:1294-12305.
20. **Novembre J***, Ramachandran S*. (2011) Perspectives on Human Population Structure at the Cusp of the Sequencing Era. *Annual Review of Genomics and Human Genetics* 12:245-274.
21. Nelson MR*, **Wegmann D***, Ehm MG, **Kessner D**, St. Jean P, Verzili C, Shen J, Tang Z, Bacanu SA, Fraser D, Warren L, Aponte J, Zawistowski M, Liu X, Zhang H, Zhang Y, Li J, Li Y, Li L, Woolard P, Topp S, Hall MD, Nangle K, Wang J, Abecasis G, Zöllner S, Cardon LR, Whittaker JC, Chissoe SL, **Novembre J***, Mooser V* (2012). An abundance of rare variants in 202 drug target genes sequenced in 14,002 people. *Science* 337:100-104.
22. Yang W, **Novembre J**, Eskin E, Halperin E. (2012) A model-based approach for analysis of spatial structure in genetic data. *Nature Genetics* 44:725-731.
23. **Novembre J**, **E Han**. (2012) Human population structure and the adaptive response to pathogen-induced selection pressures. *Philos Trans R Soc Lond B Biol Sci.* 367(1590):878-86.

24. **Novembre J.** (2012) Commentary on Sokal, Oden, and Thomson's "a problem with synthetic maps (1999)". *Hum Biol* 84:623-6.
25. **Kessner D**, Turner TL, **Novembre J.** (2013). Maximum Likelihood Estimation of Frequencies of Known Haplotypes from Pooled Sequence Data. *Molecular Biology and Evolution* 30:1145-1158.
26. **Rundel C**, Wunder M, Alvarado A, Ruegg K, Harrigan R, Schuh A, Kelly J, Siegel R, DeSante D, Smith TB, **Novembre J.** (2013). Novel statistical methods for integrating genetic and stable isotopic data to infer individual-level migratory connectivity. *Molecular Ecology* 22:4163-4176.
27. Schaibley VM, Zawistowski M, Wegmann D, Ehm MG, Nelson MR, St Jean PL, Abecasis GR, **Novembre J**, Zöllner S, Li JZ. (2013). The influence of genomic context on mutation patterns in the human genome inferred from rare variants. *Genome Research* 23(12):1974-84.
28. **Han E**, Sinsheimer JS, **Novembre J.** (2013). Characterizing bias in population genetic inferences from low coverage sequencing data. *Molecular Biology and Evolution.* 31:723-735.
29. **Kessner D**, **Novembre J.** (2014). forqs: forward-in-time simulation of recombination, quantitative traits and selection. *Bioinformatics* 30:576-7.
30. Zawistowski M, Reppell M, **Wegmann D**, St Jean PL, Ehm MG, Nelson MR, **Novembre J**, Zöllner S. (2014). Analysis of rare variant population structure in Europeans explains differential stratification of gene-based tests. *Eur J Hum Genet* 22:1137-44.
31. **Freedman AH**, Gronau I, Schweizer RM, **Ortega-Del Vecchio D**, **Han E**, Silva PM, Galaverni M, Fan Z, Marx P, Lorente-Galdos B, Beale H, Ramirez O, Hormozdiari F, Alkan C, Vilà C, Squire K, Geffen E, Kusak J, Boyko AR, Parker HG, Lee C, Tadisotla V, Siepel A, Bustamante CD, Harkins TT, Nelson SF, Ostrander EA, Marques-Bonet T, Wayne RK, **Novembre J.** (2014) Genome sequencing highlights the dynamic early history of dogs. *PLoS Genet* 10(1):e1004016
32. Olalde I, Allentoft ME, Sánchez-Quinto F, Santpere G, **Chiang CWK**, Degiorgio M, Prado-Martinez J, Rodríguez JA, Rasmussen S, Quilez J, Ramírez O, Marigorta UM, Fernández-Callejo M, Prada ME, Encinas JM, Nielsen R, Netea MG, **Novembre J**, Sturm RA, Sabeti P, Marquès-Bonet T, Navarro A, Willerslev E, Lalueza-Fox C. (2014). Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. *Nature* 13:225-8.
33. Rañola JM, **Novembre J**, Lange K. (2014). Fast spatial ancestry via flexible allele frequency surfaces. *Bioinformatics* 30 (20), 2915-2922
34. Yang, WY, **Platt A**, **Chiang CWK**, Eskin E, **Novembre J**, Pasaniuc B (2014). Spatial Localization of Recent Ancestors for Admixed Individuals. *G3* 4:2505-18.
35. **Han E**, Sinsheimer J, **Novembre J** (2015). Fast and accurate Site Frequency Spectrum Estimation from Low Coverage Sequence Data. *Bioinformatics* 31:720-7.

36. **Kessner D, Novembre J.** (2015) Power analysis of artificial selection experiments using efficient whole genome simulation of quantitative traits. *Genetics* 199:991-1005.
37. Zoledziewska M*, Sidore C*, **Chiang CWK***, Sanna S, Mulas A, Steri M, Busonero F, **Marcus JH**, Marongiu M, Maschio A, **Ortega Del Vecchio D**, Floris M, Meloni A, Delitala A, Concas MP, Murgia F, Biino G, Vaccargiu S, Nagaraja R, Lohmueller KE, UK10K consortium, Timpson NJ, Soranzo N, Tachmazidou I, Dedoussis G, Zeggini E, The Understanding Society Scientific Group, Uzzau S, Jones C, Lyons R, Angius A, Abecasis GR*, **Novembre J***, Schlessinger D*, Cucca F*. (2015) Height-reducing variants and selection for short stature on the island of Sardinia. *Nature Genetics* 47:1352-6. [with Sidore et al, featured in News & Views]
38. Sidore C, Busonero F, Maschio A, Porcu E, Naitza S, Zoledziewska M, Mulas A, Pistis G, Steri M, Danjou F, Kwong A, **Ortega Del Vecchio D**, **Chiang CW**, Bragg-Gresham J, Pitzalis M, Nagaraja R, TARRIER B, Brennan C, Uzzau S, Fuchsberger C, Atzeni R, Reinier F, Berutti R, Huang J, Timpson NJ, Toniolo D, Gasparini P, Malerba G, Dedoussis G, Zeggini E, Soranzo N, Jones C, Lyons R, Angius A, Kang HM, **Novembre J**, Sanna S, Schlessinger D, Cucca F, Abecasis GR. (2015) Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. *Nature Genetics* 47:1272-81.
39. Schweizer RM, vonHoldt BM, Harrigan R, Knowles JC, Musiani M, Coltman D, **Novembre J**, Wayne RK. (2016) Genetic subdivision and candidate genes under selection in North American grey wolves. *Molecular Ecology* 25:380-402.
40. Schweizer RM, Robinson J, Harrigan R, Silva P, Galaverni M, Musiani M, Green RE, **Novembre J**, Wayne RK (2016). Targeted capture and resequencing of 1040 genes reveal environmentally driven functional variation in gray wolves. *Molecular Ecology* 25:357-379.
41. Petkova D, **Novembre J**, Stephens M. (2016) Visualizing spatial population structure with estimated effective migration surfaces. *Nature Genetics* 48:94-100.
42. **Chiang CWK**, Ralph P, **Novembre J.** (2016) Conflations of short IBD blocks can bias inferred length of IBD. *G3* doi: 10.1534/g3.116.027581.
43. **Freedman AH**, Schweizer RM, **Ortega-Del Vecchio D**, **Han E**, Davis BW, Gronau I, Silva PM, Galaverni M, Fan Z, Marx P, Lorente-Galdos B, Ramirez O, Hormozdiari F, Alkan C, Vilà C, Squire K, Geffen E, Kusak J, Boyko AR, Parker HG, Lee C, Tadisotla V, Siepel A, Bustamante CD, Harkins TT, Nelson SF, Marques-Bonet T, Ostrander EA, Wayne RK, **Novembre J.** (2016) Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. *PLoS Genetics* 12:e1005851.
44. **Novembre J, Peter B** (2016). Recent advances in the study of fine-scale population structure in humans. *Current Opinion in Genetics and Development* 41:98-105.
45. de Manuel M, Kuhlwilm M, Frandsen P, Sousa VC, Desai T, Prado-Martinez J, Hernandez-Rodriguez J, Dupanloup I, Lao O, Hallast P, Schmidt JM, Heredia-Genestar JM, Benazzo A, Barbujani G, **Peter BM**, Kuderna LF, Casals F, Angedakin S, Arandjelovic M, Boesch C, Kühl H, Vigilant L, Langergraber

K, **Novembre J**, Gut M, Gut I, Navarro A, Carlsen F, Andrés AM, Siegismund HR, Scally A, Excoffier L, Tyler-Smith C, Castellano S, Xue Y, Hvilsom C, Marques-Bonet T. (2016). Chimpanzee genomic diversity reveals ancient admixture with bonobos. *Science* 354:477-481.

(b) Peer-reviewed works in 'non-traditional' outlets:

N/A

(c) Peer-reviewed works accepted or in press

1. **Marcus JH, Novembre J.** (2016) Visualizing the Geography of Genetic Variants. *Bioinformatics*.

(d) Non-peer-reviewed original articles:

1. **Novembre J**, Witonsky D, Di Rienzo A. (2016) Technical Report: Assessment of the genetic analysis of Rasmussen et al. (2015). Report provided to the U.S. Army Corps of Engineers, St. Louis District and available from: <http://cdm16021.contentdm.oclc.org/cdm/ref/collection/p16021coll11/id/950>.

(e) Books:

N/A

(f) Book chapters: and Peer-reviewed Perspective Articles / Literature Reviews:

1. Veeramah KR, **Novembre J.** (2014). Demographic Events and Evolutionary Forces Shaping European Genetic Diversity. In: Chakravarati, A (2014) Human Variation: A Genetic Perspective on Diversity, Race, and Medicine. Cold Spring Harbor Press. Also published in: Cold Spring Harb Perspect Biol. 6(9).

(g) Other works that are publically available:

1. Video interview: *Science Central News* (2008) "Gene-ography" video for distribution on ABC networks (<http://www.sciencentral.com/video/2008/09/22/genetic-geography/>)
2. Video by American Musum of Natural History (2008): ([http://www.amnh.org/explore/science-bulletins/\(watch\)/human/news/genes-and-geography-they-go-together](http://www.amnh.org/explore/science-bulletins/(watch)/human/news/genes-and-geography-they-go-together)) Shown in the Hall of Human Origins at the American Museum of Natural History (NYC, NY), the Frank H. McClung Museum (Knoxville, TN), the Great Lakes Science Center (Cleveland, OH), and Science World (Vancouver, BC).
3. Radio interview: NPR Morning Edition (2011) "Genome Maps May Spot Disease In African-Americans" (<http://www.npr.org/2011/07/21/138548043/genome-maps-may-spot-disease-in-african-americans>)
4. Commentary: **Novembre J** (2014). Variations on a Common STRUCTURE: New Algorithms for a Valuable Model. *Genetics* 197(3):809-811.

5. News & Views: **Novembre J** (2015). Human Evolution: ancient DNA steps into the language debate. *Nature* (New and Views) 11:164-165.
6. Online interview: Reddit Science Ask Me Anything Series (2015) (https://www.reddit.com/r/science/comments/3tf9a1/science_ama_series_im_john_novembre_and_i_study/)
7. Video interview (2015) “Computational Biologist John Novembre, 2015 MacArthur Fellow” (<https://www.youtube.com/watch?v=czVNYdtAaB8>)
8. Radio interview: WBEZ Chicago Morning Shift (2015) “University of Chicago computational biologist receives MacArthur Genius Grant” (<https://www.wbez.org/shows/morning-shift/university-of-chicago-computational-biologist-receives-macarthur-genius-grant/c2665358-4a97-4e80-b470-6834d4d2444a>)
9. Commentary: **Novembre J.** (2016) Pritchard, Stephens, and Donnelly on Population Structure. *Genetics* 204(2):391-393.

(i) Works in review, in preparation, etc, not yet publically available

1. **Koch E, Novembre J.** (in review) A temporal perspective on the interplay of demography and selection on deleterious variation in humans.
2. **Smith J, Coop G, Stephens M, Novembre J.** (in review) Estimating Time to the Common Ancestor for a Beneficial Allele. *bioRxiv* doi: <http://dx.doi.org/10.1101/071241>
3. Pala M, Zappala Z, Marongiu M, Li X, Davis JR, Cusano R, Crobu F, Kukurba KR, Reiner F, Berutti R, Piras MG, Mulas A, Zoledziewska M, Marongiu M, Busonero F, Maschio A, Steri M, Sidore C, Sanna S, Fiorillo E, Battle A, **Novembre J**, Jones C, Angius A, Abecasis GR, Schlessinger D, Cucca F, Montgomery SB. (submitted) Population and individual effects of non-coding variants inform genetic risk factors. *bioRxiv*. <http://dx.doi.org/10.1101/065144>

FUNDING

(a) Past:

09-SSP-246 (PI: J Novembre) 07/01/2009–06/30/2012
 Searle Foundation
 Methods for Spatial Population Genetics: Ancestry Inference and Population Stratification
 Role: Principal Investigator

DBI-0933731 (PI: J Novembre) 09/01/2009–08/31/2012
 NSF

Research Starter Grant: Joint genetic and isotopic assignment methods to empower studies of avian migration

Role: Principal Investigator

Alfred P. Sloan Research Fellowship (PI: J Novembre) 09/15/2012–09/15/2014

Sloan Foundation

Alfred P. Sloan Research Fellowship in Computational Evolutionary Biology

Role: Principal Investigator

EF-1021397 (PI: R Wayne)

07/01/2010–6/30/2013

NSF

The genomic and ecological context of a major gene under selection in natural populations

Role: Co-PI

EF-0733033 (PI: R Wayne)

09/01/2007–8/31/2011

NSF / Office of Polar Programs

IPY: Genomic-scale SNP genotyping of the Arctic wolf: ecology and adaptation over space and time

Role: Co-PI

EF-0928690 (PI: Lloyd-Smith)

09/01/2009–08/31/2012

NSF

Collaborative Proposal: Evolutionary dynamics of invasion and escape in hierarchical systems

Role: Co-PI

(b) Current:

1U01 CA198933 (PI: Novembre)

06/01/15–05/31/18

NIH/NCI

Tools for Visualization of Geographic Structure in Population Genomic Data

Role: Principal Investigator

7R01 HG007089 (PI: Novembre)

03/01/13–12/31/17

NIH

Haplotype-based analysis methods for population genomics

Role: Principal Investigator

1R01 GM108805 (PI: Clark)

09/01/13–08/31/17

NIH/NIGMS

Population genetic consequences of recent explosive population growth in humans

Role: Co-Investigator

9R01 MH100027 (PI: Geschwind)

06/02/14–02/28/18

NIH

Autism Genetics, Phase II: Increasing Representation of Human Diversity.

Role: Co-Investigator

1P50 DA037844 (PI: Palmer)

07/01/14–06/30/19

NIH/NIDA

Integrated GWAS of complex behavioral and gene expression traits in outbred rats

Role: Co-Investigator

NSF 561K971 (PI: Payseur)

08/1/14–07/31/17

NSF

Identifying Genetic Determinants of Speciation from Genomic Maps of Ancestry in Hybrid Mice

Role: Co-Investigator

1R01 HL119577 (PI: Di Rienzo)

04/01/14–03/31/18

NIH/ NHLBI

Genetic adaptations to high altitude

Role: Co-Investigator

HONORS, PRIZES, AWARDS

2016	Kavli Frontiers of Science Fellow
2016	Honorary doctoral degree recipient, The Colorado College
2015-2020	MacArthur Fellow
2012-2014	Alfred P. Sloan Research Fellow
2011	Distinguished Faculty Teaching Award, Dept of Ecology and Evolutionary Biology, UCLA
2009-2012	Searle Scholar
2006-2008	National Science Foundation Postdoctoral Fellow in Bioinformatics
2005	Japanese Society for the Promotion of Science Summer Fellow
2001-2006	Howard Hughes Medical Institute Predoctoral Fellow
2001	National Science Foundation Graduate Fellowship (declined)
2000	J. Juan Reid Award for extracurricular and scholastic achievement, American Institute of Chemists Award in Biochemistry, Phi Beta Kappa
1999	Rhodes Scholar Finalist, Outstanding Research Presentation at the West Coast Biological Sciences Undergraduate Research Conference, Alberts Summer Research Prize
1998	Stanford University Summer Research Fellowship (lab of R. Baldwin)
1996-2000	Boettcher Scholar (full-expense merit-based fellowship for Colorado residents to attend a Colorado university)

INVITED SPEAKING

Departmental Seminars

(Summary: >40 total departmental invites, including >10 which are international and 1 postdoc-invited speaker.)

2017

- McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, February 2017 (scheduled).

2016

- Distinguished Speaker Series, **Max Planck Institute for Developmental Biology and the Friedrich Miescher Laboratory**, June 2016.
- Program in Genetics, **North Carolina State University**, April 2016.
- Biology Week, **Chicago State University**, April 2016.
- Biodiversity Research Seminar Series, **University of British Columbia**, March 2016.

2015

- Department Seminar, **International Laboratory for Human Genome Research of the Universidad Nacional Autonoma de Mexico (UNAM)**, November 2015.
- Biology Colloquium, **University of Wisconsin-Milwaukee**, November 2015.
- Department of Ecology and Evolution, **Stony Brook University**, October 2015.
- Department of Evolution, Ecology and Organismal Biology, **Ohio State University**, April 2015.
- Department of Biological Sciences, **Florida State University**, April 2015.
- Computational Biology Seminar Series (student-run), **UC-Berkeley**, February 2015.

2014

- Molecular Biology Seminar Series, **Genentech**, June 2014.
- **National Center for Biological Sciences**, Bangalore, India, February 2014.
- Postdoc-invited speaker, Department of Genome Sciences, **University of Washington**, January 2014

2013

- Seminars of the **Barcelona Biomedical Research Park**, Barcelona, September 2013.
- **The Jackson Laboratory**, September 2013.
- **Wellcome Trust Center for Human Genetics**, April 2013.
- Genetics Interdisciplinary Program, **University of Arizona**, April 2013.
- Genomics Seminar Series, **University of Wisconsin – Madison**, January 2013.
- Pharmaceutical/Pharmacogenomics Seminar Series, **University of California – San Francisco**, June 2013.

2012

- Department of Genome Sciences, **University of North Carolina**, December 2012.
- Evolutionary Genomics Group, **University of California – Berkeley**, August 2012.
- Department of Ecology and Evolution, **University of California-Davis**, June 2012.
- School of Public Health, **Harvard University**, March 2012
- Dept of Ecology, Evolution, and Marine Biology, **University of California-Santa Barbara**, February 2012.

2011

- **Center for Investigation in Biodiversity and Genetic Resources, Portugal**, March 2011.
- Licenciatura en Ciencias Genomicas, **Universidad Nacional Autonoma de Mexico**, February 2011.
- Center for Computational Science, **Tulane University**, February 2011.

2010-2009

- Department of Basic Sciences, **The Commonwealth Medical College**, November 2010.

- Department of Biological Sciences, **University of Idaho**, November 2010.
- Department of Evolutionary Genetics, **Max Planck Institute for Evolutionary Anthropology**, June 2010.
- Department of Human Genetics, **University of Michigan**, May 2010.

2009-2008

- Institute of Ecology and Evolution, **University of Berne**, January 2009.
- Department of Biostatistics, **University of Southern California**, December 2008.
- Department of Ecology and Evolutionary Biology, **University of California-Irvine**, November 2008
- Department of Biological Sciences, **Humboldt State University**, October 2008.
- Department of Molecular and Computational Biology, **University of Southern California**, September 2008.

2007 and earlier

- Department of Biology, **The Colorado College**, April 2007.
- Department of Human Genetics, **University of Michigan**, March 2007
- Department of Ecology and Evolution, **University of California-Los Angeles**, November 2005.
- Hayama Seminar, **Graduate University for Advanced Studies (Sokendai)**, Japan, August 2005.
- Department of Biology, **The Colorado College**, March 2004.
- Facultad de Ciencias, **Universidad de la Republica, Uruguay**, March 2003

Conference Presentations

(Summary: >30 total invited conference presentations, including 10 which were at international venues and 5 which were keynote or plenary talks.)

2017

- Plenary for **Gordon Research Conference on Quantitative Genetics and Genomics** (scheduled)
- Keynote for **Great Lakes Bioinformatics Consortium Conference** (scheduled)

2016

- **National Academy of Sciences/ Kavli Frontiers of Science meeting**, November 2016
- **Computational Genomics Summer Institute, University of California-Los Angeles**, July 2016.
- **CSHL Banbury Meeting “Ancient DNA and Archaeology”**, May 2016 (discusant)
- **Center for Computational, Evolutionary and Human Genomics Annual Symposium, Stanford University**, February 2016.

2015

- **“Sequencing the Human Past” Symposium, University of California-Los Angeles**, October 2015.
- **SardiNIA Symposium at the National Institute of Aging**, October 2015.
- **9th ISABS Conference in Forensic, Anthropological and Medical Genetics and Mayo Clinic Lectures on Translational Medicine**, Bol, Island of Brac, Croatia June 2015.
- **SMBE Symposium on Adaptive Evolution**, Montpellier, France, May 2015.
- **American Society of Human Genetics (ASHG) Genetic Ancestry Inference Roundtable II** (invited participant)

2014

- **NESCent Simbank Workgroup meeting**, November 2014.
- Keynote Speaker, **Pharmacogenomics Research Network Meeting**, Sept 2014.
- **Cell Symposium: Evolution of Modern Humans – From Bones to Genomes**, Sitges, Spain, March 2014.
- Grad-student invited keynote **Biomedical Computation at Stanford Conference, Stanford University**, January 2014.

2013

- **4th Biological Evolution Workshop**, Porto Alegre, Brazil. November 2013.
- Plenary Session, **Genomics: From Population to Personal, ASHI**, November 2013.
- **Coalescent Theory: New Developments and Applications Meeting**, Montreal, October 2013.
- Invited Session, **Insights from Large Scale Sequencing, ASHG**, October 2013.
- **NGx Dynamics of Microbiome in Health and Disease Conference**, August 2013
- **Biodiversity Genomics Conference and Workshop, Australia National University**, April 2013.

2012

- **1000 Genomes Community Meeting, University of Michigan**, July 2012.
- **Mathematical Biosciences Institute** workshop “Spatial Models of Micro and Macro Systems,” April 2012.

2011

- **Royal Society Discussion meeting** on Human evolution, migration and history revealed by genetics, immunity and infection, June 2011.

2010

- **NSF MIGRATE workshop**, Max Planck Institute for Ornithology, Germany, June 2010.
- **American Association for Anthropological Genetics symposium** at the AAPA meeting. April 2010.

2009

- Keynote, “Peopling of Europe” session, **4th Congress on DNA polymorphisms in human populations**, Rome, Italy, December 2009.
- **American Society for Human Genetics Genetic Anthropology at Fine Scales Workshop**, October 2009.
- **Darwin 200 South American Celebration Conference**, Uruguay, September 2009.
- **Gordon Conference on Ecological and Evolutionary Functional Genomics**, July 2009.

2008

- **Kavli Institute for Theoretical Physics, Population Genetics Program**, December 2008.

2007 and earlier

- **Third International Symposium on Conservation Genetics**, American Museum of Natural History, September 2007.

Community / Other

2017

- Lecture, Elective Studies Supper Club, **Illinois Humanities** (invited February 2017).

2016

- Keynote speaker, **Opening Convocation, Colorado College**.
- Panel conversation with Tara Zahra at the **Economic Club of Chicago**.
- Lecture at **MacArthur Fellows Retreat** at the Johnson Foundation.

2015

- Public Lecture for **Pint of Science Series**, Blue Moon Pub, Chicago, IL.

EDUCATION / TEACHING

Graduate courses (Ph.D.) at the University of Chicago:

- 2016 **HG48600: Fundamentals of Computational Biology: Models and Inference.** Co-instructor: Matthew Stephens.
- 2015-2016 **HG46900: Human Genetic Variation and Disease.** Co-instructor: Anna Di Rienzo
- 2014-2015 **HG47100: Introduction to Statistical Genetics.** Co-instructor: Nancy Cox (2014), Lin Chen and Brandon Pierce (2015)

Undergraduate courses at University of California–Los Angeles

- 2012-2010 **EEB 135: Evolutionary genetics (taught jointly with EEB235)**
- 2012-2011 **LS1: Evolution, Ecology, and Biodiversity.** Co-instructors: M Alfaro, J Lloyd-Smith

Graduate courses (Ph.D) at the University of California–Los Angeles

- 2012-2010 **EEB 235: Evolutionary genetics (taught jointly with EEB 135).**
- 2012-2008 **EEB 200A: Evolution.** Co-instructors: M. Alfaro and R. Wayne
- 2011,2009 **EEB 263: Seminar in Population genetics.**

Other (Short courses and miscellaneous)

- 2016-2015 **Biological Sciences Division Quantitative Bootcamp.** Afternoon Workshop Instructor. University of Chicago.
- 2014 **54th Annual Short Course on Medical and Experimental Mammalian Genetics.** Invited guest lecture. The Jackson Laboratory.
- 2014,2010-11 **Environmental Genomics Short Course.** Invited guest lecture. Organizers: J Colbourne, J Shaw, B King. Mount Desert Island Biological Laboratory.
- 2012 **MCMC for Genetics.** Co-instructor with EA Anderson. Summer Institute in Statistical Genetics.
- 2012-2010 **Two-day Bootcamp on Quantitative Skills for Ecology and Evolution.** Co-instructor with M Alfaro, J Lloyd-Smith. UCLA.
- 2012-2008 **Invited guest lectures, UCLA courses:** *HG210 (3x), HC70A (3x), MCDB 172 (2x), Soc Gen 102 (2x), CS/SysBio M184 (1x), CS/SysBio M185 (2x), Geography Grad Seminar (1x)*
- 2005 **Topics in Biology: Evolution.** Student Instructor for N. Patel, N. Shubin, C. Bergman. Waston School of Biological Sciences, Cold Spring Harbor, NY

2001-2002 **Evolutionary Genetics.** Student Instructor for M. Slatkin. University of California-Berkeley.

Other (International):

2016 Instructor for 4 days of a **Human Genomics course, Institut Pasteur, Montevideo, Uruguay.** Organizer: Hugo Naya.

2016-15,13-12 Guest lecture and workshop instructor, **Genomic Analysis of Complex and Monogenic Disorders, Sardinian Summer School.** Organizers: F Cucca, D Schlessinger.

2014 Guest lecture, **Population Genetics and Evolution School and Discussion Meeting. International Centre for Theoretical Sciences, Bangalore, India.** Organizer: D Agashe

2013 Opponent, Public defense of Pontus Skoglund's doctoral thesis, **Uppsala University**

2013 External examiner, viva examination of D Phil thesis by Anjali Hinch, **Oxford University**

2013, 2009 Lecturer in **1st and 3rd Latin American School of Evolution** for graduate students. Montevideo, Uruguay and Buenos Aires, Argentina.

2011 Instructor, **Coalescent Theory and Methods short course. University of Berne, Switzerland.** Co-instructors: L Excoffier, M Foll, M Blum

Research trainees:

(a) High school students and teachers

None

(b) Undergraduate (B.A., B.S.)

2009-2010 Rose Putler, UCLA. Presently: Researcher at University of Michigan

2013-2014 Joe Marcus, University of Washington. Presently: PhD student University of Chicago

(c) Medical (M.D.)

None

(d) Graduate (Ph. D)

2016- Arjun Biddanda, Human Genetics PhD student

2016- Joseph Marcus, Human Genetics, PhD student

2013- Hussein Al-asadi, Committee on Evolutionary Biology PhD student (joint with M Stephens; NSF GRFP Fellow)

2013- Evan Koch, Ecology & Evolution PhD student (NSF GRFP Fellow)

2013- Joel Smith, Ecology & Evolution student (NSF GRFP Fellow)

2010-2016 Diego Vicente Ortega del Vecchyo, Bioinformatics IDP PhD student (UC-MEXUS fellow with Novembre, starting postdoc at UC-Berkeley)

2010-2011 Colin Rundel, co-advised Statistics PhD student (currently assistant teaching professor at Duke University)

2009-2014 Darren Kessner, Bioinformatics IDP PhD Student (currently faculty at the Marlborough School)

2009-2014 Eunjung Han, co-advised PhD student (currently computational biologist Ancestry.com)

(e) Postdoctoral

2014- Mark Reppell, Postdoctoral fellow

2014- Ben Peter, Postdoctoral fellow (Swiss NSF Ambizione Fellow)
 2011-2015 Charleston Chiang, Postdoctoral fellow (NIH-NSRA fellow with Novembre, currently postdoc at UCLA)
 2011-2013 Alex Platt, Postdoctoral fellow (currently research professor at Temple University)
 2009-2011 Daniel Wegmann, Postdoctoral fellow (currently professor at University of Fribourg)
 2009-2012 Adam Freedman, Postdoctoral fellow (NSF Bioinformatics fellow with Novembre, currently data scientist at Harvard University)
 2009-2010 Krishna Veeramah, Postdoctoral fellow (currently a professor at Stony Brook University)

(f) Other

2014 Enrique Lessa, Professor, Universidad de la Republica, Uruguay. Sabbatical visitor.
 2013- University of Chicago PhD Committee member for: John Blischack, Choongwon Jeong, Michael Turchin, Silvia Kariuki, Alex Gileta, Katelyn Mika, Erin Fry, Ittai Eres, Roberto Marquez, Natalia Piland, Ayse Tenger-Trolander
 2008-2013 UCLA PhD Committee member for: Forrest Wren (Biomath), Pencheng Li (Bioinformatics Masters), John Michael Ranola (Biomath), David Alexander (Biomath), Bridget von Holdt (EEB), Jennifer Tom (Biomath), Wen-Yun Yang (Bioinformatics), Rena Schweizer (EEB), Stephanie Steele (EEB), Sergio Nigenda Morales (EEB), Sammi Ali (EEB Masters), Chris Chabot (EEB), Colin Rundel (Statistics)

INVITED, ELECTED, OR APPOINTED EXTRAMURAL SERVICE

2016- **Associate Editor**, *Genetics*
 2012- **Scientific Advisory Board**, Ancestry.com
 2010- **Associate Editor**, *Molecular Biology and Evolution*
 2016 **Fellowship Application Reviewer**, NSF Graduate Research Fellowships
 2016 **Co-organizer**, Computational Genomics Summer Institute, UCLA.
 2015-2016 **Consultant**, Army Corps of Engineers on Reassessment of Ancestry of the Kennewick sample
 2014-2012 **Scientific Advisory Board**, CartaGENE Study
 2014, 2009 **Guest editor**, *PLoS Genetics* (4 submissions)
 2012 **Co-chair** Session on "Population Genomics" at CSHL Biology of Genomes meeting
 2011-2008 **Member**, American Society of Human Genetics Task Force on Ancestry Testing
 2010 **Advisor** on genetic ancestry, one-day summit meeting for National Bone Marrow Donor Transplant Program
 2010-2009 **Special Topics Editor**, *Molecular Ecology*
 Various **Grant Proposal Reviewer** for: NIH BST panel, NIH EIA panel, UK Biotechnology and Biological Sciences Research Council, National Geographic, FWF Austria, Israeli Science Foundation, Royal Society of New Zealand
 Various **Manuscript Reviewer** for: *Nature*, *Science*, *PNAS*, *Nature Genetics*, *PLoS Genetics*, *Genetics*, *American Journal of Human Genetics*, *Annals of Human Genetics*, *Bioinformatics*, *BMC Bioinformatics*, *Conservation Genetics*, *Current Anthropology*, *European Journal of Human Genetics*, *Genetic Epidemiology*, *Genetical Research*, *Genes and Immunity*, *Genome Research*, *Human Biology*, *Human Heredity*, *ISMB*, *Journal of Molecular Evolution*, *Molecular Biology and Evolution*, *Molecular Ecology*,

ADDITIONAL SERVICE

University of Chicago

Committee membership:

2016-	Faculty Advisory Council to the Dean of Biological Sciences Division
2016-	Steering Committee, Genetics, Genomics and Systems Biology Committee
2014-	Admissions Committee, Dept of Human Genetics
2016	Search Committee for Strategic Hire Evolutionary Cell Biologist
2014-2013	Committee on Appointments and Promotions (ad hoc service, 2 cases)

Leadership:

2016	Chair , Search Committee for population geneticist, Dept of Ecology & Evolution
2014-2013	Co-chair , Search Committee for computational biologist, Dept of Human Genetics
2014	Co-organizer , Mitchell Symposium on Ancient DNA studies

Other:

2016-2015	Co-organizer , Darwin's Weekly Seminar, Dept of Ecology and Evolutionary Biology
2013-	Organizer , Departmental Seminar, Dept of Human Genetics
2016	Speaker, Computation in Science Series , March.
2015	Speaker, EvMorph Seminar Series , February.

University of California–Los Angeles

Committee membership:

2012	Search Committee for director of UCLA Computational Biology Initiative
2012-2011	<i>ad hoc</i> Committee to redesign life sciences math requirements
2012-2011	Executive Committee, Bioinformatics PhD IDP program
2011-2010	Curriculum committee, EEB Department
2011-2010	Graduate awards committee, EEB Department
2010-2009	EEB Seminar committee
2009	Search Committee for Director, Center for Society and Genetics
2008	Committee to design a core course for Human Biology and Society major
2008	EEB Ad hoc committee on graduate student support packages

Leadership:

2012-2009	Graduate advisor , Bioinformatics PhD IDP program
2012-2008	Organizer , EcoEvo Theory Group
2012-2010	Chair , EEB Department Website Redesign Committee

Other:

2011	Speaker , Department of Human Genetics Seminar Series, March.
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- 2009 **Speaker**, Behavior, Evolution, Culture Speaker Series (November), Department of Biomathematics (November), Center for Society and Genetics Indian Population History panel event (November)
- 2008 **Speaker**, DNA and History Faculty Seminar Series (October), Center for Society and Genetics Colloquium speaker (November).

Extramural (not indicated above)

Leadership:

- 2016, 2014 **Co-founder and lead organizer**, Midwest Population Genetics Meeting, Chicago.
- 2015 **Co-organizer**, MontyFest: A symposium in honor of Monty Slatkin.
- 2015 **Co-organizer**, Midwest Population Genetics Meeting, Ann Arbor, Michigan.
- 2015, 2008 **Co-organizer**, Symposium on “Theory and Inference in Spatial Population Genetics” at the Society for Molecular Biology and Evolution Meeting

Other

- 2015 Informal advisor, **UruGenomes project**, director: Hugo Naya
- 2011, 2008 Undergrad **diversity mentor**, **Society for Molecular Biology meeting**

International exchange:

- 2005 NSF-EAPSI/JSPS summer fellow in lab of Yoko Satta, **Sokendai, Hayama, Japan**.
- 2003 Two-week research visit to Enrique Lessa, the **Universidad de la Republica, Uruguay**.
- 1999 Summer research internship with Laurent Excoffier, **University of Geneva, Switzerland**.

Outreach via Press (not listed above):

- 2008- **Source for background on population genetics** by science journalists at: Discover Magazine, Nature, New Scientist, New York Times, Los Angeles Times, Huffington Post
- 2016 PBSNews, What scientists are thankful for this Thanksgiving
<http://www.pbs.org/newshour/rundown/scientists-give-thanks-thanksgiving/>
- 2015 Media surrounding announcement of **MacArthur Fellowship**
-Interviews with: *Chicago Tribune, Chicago Sun Times, WBEZ Morning Shift, PBS NewsHour, Fast Company, Colorado Springs Gazette*
-Announcement and summary of research featured in multiple additional venues.
- 2013 Media surrounding **dog domestication research**:
-Freedman et al research 18th out of top 25 science stories of 2013 in *Science News Magazine*
- 2011 Outreach from **ancestry-based recombination map estimation research**:
-Covered by media outlets including: *National Public Radio “Morning Edition”, Boston Globe, LA Times, Science News, Genome Web News, ScienceDaily, BET, EurekAlert, Bio-Medicine, Jerusalem Post, GPB News, Atlanta Pos, Medical Xpress, News-Medical.net, RedOrbit*
-Covered by science journals: *Nature Genetics News and Views*
- 2010 Outreach from **dog domestication research**:
-Covered by world media outlets including: *New York Times, Washington Post, San Francisco Chronicle, Toronto Star, Jerusalem Post, Reuters UK, India, and Africa, Malaysia Sun, Argentina Star, The Hindu Business Line, People’s Daily (China), Voice of America*
-Focus of a comedic news item on Colbert Report

2008

Outreach from “**Genes mirror geography in Europe**” research:

- Covered by world media outlets including: *New York Times*, *International Herald Tribune*, *Spiegel (Germany)*, *La Stampa (Italy)*, *Folha (Brazil)*, *World Journal (China)*, *Malaysia Sun*, *New Kerala (India)*.
- Covered by various science media outlets including: *New Scientist*, *Technology Review*, *Discover Magazine*, *Popular Science*, *Tech Herald*, *Science Daily*
- Covered by science journals: *Nature Reviews Genetics*, *Nature Podcast*, *ScienceNOW*