

John Novembre

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Education

BA, Biochemistry, The Colorado College

Advisor: Ralph Bertrand-Garcia 1996-2000

PhD, University of California-Berkeley

Integrative Biology with Designated emphasis in Computational Biology/Genomics

Dissertation: *Statistical methods for neutral and adaptive genetic variation in continuous isolation-by-distance models*

Advisor: Montgomery Slatkin 2000-2006

Postdoctoral training, University of Chicago

Department of Human Genetics

Advisor: Matthew Stephens 2006-2008

Academic Appointments

University of California–Los Angeles

Department of Ecology & Evolution

Assistant Professor 2008-2013

Associate Professor 2012-2013

University of Chicago

Department of Human Genetics (primary), Department of Ecology & Evolution (secondary)

Associate Professor 2013-2017

Professor 2017-

Honors

Boettcher Scholar 1996-2000

Stanford University Summer Research Fellowship (lab of R. Baldwin) 1998

Alberts Summer Research Prize (to visit lab of L. Excoffier, Univ. of Geneva) 1999

Outstanding Research Presentation, West Coast Biological Sciences Undergraduate Conference 1999

Rhodes Scholar Finalist 1999

American Institute of Chemists Award in Biochemistry, Phi Beta Kappa 2000

J. Juan Reid Award for extracurricular and scholastic achievement, 2000

Howard Hughes Medical Institute Predoctoral Fellow 2001-2006

NSF-EAPSI Japanese Society for the Promotion of Science Summer Fellow 2005

National Science Foundation Postdoctoral Fellow in Bioinformatics 2006-2008

Searle Scholar 2009-2012

Distinguished Faculty Teaching Award, Dept of Ecology and Evolutionary Biology, UCLA 2011

Alfred P. Sloan Research Fellow 2012-2014

NAS-Kavli Frontiers of Science Fellow	2016
Honorary doctoral degree, The Colorado College	2016
New York Times “18 Memorable People We Met Across the Country in 2018”	2018
MacArthur Fellow	2015-2020

Publications

Notation: * indicates authors contributed equally
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Research papers

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. 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.
10. Alexander DH, Novembre J, Lange K. (2009) Fast model-based estimation of ancestry in unrelated individuals. *Genome Research* 19:1655-1664.
11. Coop G, Pickrell JK, Novembre J, Kudaravalli 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.
12. 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.
13. Pickrell JK, Coop G, Novembre J, Kudaravalli 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.
14. 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.

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. 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, Elkahoulou 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.
17. 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]
18. vonHoldt BM, 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.
19. 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, Chissole 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.
20. 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.
21. 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.
22. 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.
23. 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.
24. 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.
25. Kessner D, Novembre J. (2014). forqs: forward-in-time simulation of recombination, quantitative traits and selection. *Bioinformatics* 30:576-7.
26. Freedman AH, Gronau I, Schweizer RM, Ortega-Del Vecchyo 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, Tadiogola 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
27. 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.
28. 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.

29. Rañola JM, Novembre J, Lange K. (2014). Fast spatial ancestry via flexible allele frequency surfaces. *Bioinformatics* 30 (20), 2915-2922
30. 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
31. Han E, Sisheimer J, Novembre J (2015). Fast and accurate Site Frequency Spectrum Estimation from Low Coverage Sequence Data. *Bioinformatics* 31:720-7.
32. Kessner D, Novembre J. (2015) Power analysis of artificial selection experiments using efficient whole genome simulation of quantitative traits. *Genetics* 199:991-1005.
33. 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, Tarrrier 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.
34. 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]
35. Petkova D, Novembre J, Stephens M. (2016) Visualizing spatial population structure with estimated effective migration surfaces. *Nature Genetics* 48:94-100.
36. 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.
37. 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.
38. 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.
39. 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.
40. 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, Anedakin S, Arandjelovic M, Boesch C, Köhl H, Vigilant L, Langergraber K, Novembre J, Gut M, Gut I, Navarro A, Carlsen F, Andrés AM, Siegmund HR, Scally A, Excoffier L, Tyler-Smith C, Castellano S, Xue Y, Hvilson C, Marques-Bonet T. (2016). Chimpanzee genomic diversity reveals ancient admixture with bonobos. *Science* 354:477-481.
41. Marcus JH, Novembre J (2017) Visualizing the Geography of Genetic Variants. *Bioinformatics* 33(4):594-595.
42. Koch E, Novembre J (2017) A Temporal Perspective on the Interplay of Demography and Selection on Deleterious Variation in Humans. *G3* 7(3):1027-1037.

43. Steri M, Orrù V, Idda ML, Pitzalis M, Pala M, Zara I, Sidore C, Faà V, Floris M, Deiana M, Asunis I, Porcu E, Mulas A, Piras MG, Lobina M, Lai S, Marongiu M, Serra V, Marongiu M, Sole G, Busonero F, Maschio A, Cusano R, Cuccuru G, Deidda F, Poddie F, Farina G, Dei M, Virdis F, Olla S, Satta MA, Pani M, Delitala A, Cocco E, Frau J, Coghe G, Loreface L, Fenu G, Ferrigno P, Ban M, Barizzone N, Leone M, Guerini FR, Piga M, Firinu D, Kockum I, Lima Bomfim I, Olsson T, Alfredsson L, Suarez A, Carreira PE, Castillo-Palma MJ, Marcus JH, Congia M, Angius A, Melis M, Gonzalez A, Alarcón Riquelme ME, da Silva BM, Marchini M, Danieli MG, Del Giacco S, Mathieu A, Pani A, Montgomery SB, Rosati G, Hillert J, Sawcer S, D'Alfonso S, Todd JA, Novembre J, Abecasis GR, Whalen MB, Marrosu MG, Meloni A, Sanna S, Gorospe M, Schlessinger D, Fiorillo E, Zoledziwska M, Cucca F. (2017) Overexpression of the Cytokine BAFF and Autoimmunity Risk. *New England Journal of Medicine* 376(17):1615-1626.
44. Jeong C, Peter BM, Basnyat B, Neupane M, Beall CM, Childs G, Craig SR, Novembre J, Di Rienzo A. (2017) A longitudinal cline characterizes the genetic structure of human populations in the Tibetan plateau. *PLoS One* 12(4):e0175885.
45. Smith J, Coop G, Stephens M, Novembre J. (2018) Estimating Time to the Common Ancestor for a Beneficial Allele. *Mol Biol Evol.* 35(4):1003-1017.
46. Reppell M, Novembre J. (2018) Using pseudoalignment and base quality to accurately quantify microbial community composition. *PLoS Comput Biol.* 14(4):e1006096.
47. Chiang CWK, Marcus JH, Sidore C, Biddanda A, Al-Asadi H, Zoledziwska M, Pitzalis M, Busonero F, Maschio A, Pistis G, Steri M, Angius A, Lohmueller KE, Abecasis GR, Schlessinger D, Cucca F, Novembre J. (2018) Genomic history of the Sardinian population. *Nature Genetics* 50:1426-1434
48. Schweizer RM, Durvasula A, Smith J, Vohr SH, Stahler DR, Galaverni M, Thalmann O, Smith DW, Randi E, Ostrander EA, Green RE, Lohmueller KE, Novembre J, Wayne RK. (2018) Natural Selection and Origin of a Melanistic Allele in North American Gray Wolves. *Mol Biol Evol.* 5(5):1190-1209.
49. de Barros Damgaard P, Martiniano R, Kamm J, Moreno-Mayar JV, Kroonen G, Peyrot M, Barjamovic G, Rasmussen S, Zacho C, Baimukhanov N, Zaibert V, Merz V, Biddanda A, Merz I, Loman V, Evdokimov V, Usmanova E, Hemphill B, Seguin-Orlando A, Yediay FE, Ullah I, Sjögren KG, Iversen KH, Choin J, de la Fuente C, Ilardo M, Schroeder H, Moiseyev V, Gromov A, Polyakov A, Omura S, Senyurt SY, Ahmad H, McKenzie C, Margaryan A, Hameed A, Samad A, Gul N, Khokhar MH, Goriunova OI, Bazaliiskii VI, Novembre J, Weber AW, Orlando L, Allentoft ME, Nielsen R, Kristiansen K, Sikora M, Outram AK, Durbin R, Willerslev E. (2018) The first horse herders and the impact of early Bronze Age steppe expansions into Asia. *Science.* 2018 360(6396).
50. Jeong C, Witonsky DB, Basnyat B, Neupane M, Beall CM, Childs G, Craig SR, Novembre J, Di Rienzo A. (2018) Detecting past and ongoing natural selection among ethnically Tibetan women at high altitude in Nepal. *PLoS Genet.* 14(9):e1007650.
51. Lindo J, Haas R, Hofman C, Apata M, Moraga M, Verdugo RA, Watson JT, Viviano Llave C, Witonsky D, Beall C, Warinner C, Novembre J, Aldenderfer M, Di Rienzo A. (2018) The genetic prehistory of the Andean highlands 7000 years BP though European contact. *Sci Adv.* 4(11):4921
52. Al-Asadi H, Petkova D, Stephens M, Novembre J. (2019) Estimating recent migration and population-size surfaces. *PLoS Genet.* 15(1):e1007908
53. Al-Asadi H, Dey KK, Novembre J, Stephens M. (2019) Inference and visualization of DNA damage patterns using a grade of membership model. *Bioinformatics* 35:1292-1298
54. Koch E*, Schweizer RM*, Schweizer TM, Stahler DR, Smith DW, Wayne RK, Novembre J. (2019) De novo mutation rate estimation in wolves of known pedigree. *Mol Biol Evol.* 36:2536-2547
55. Dickson BG, Albano CM, Anantharaman R, Beier P, Fargione J, Graves TA, Gray ME, Hall KR, Lawler JJ, Leonard PB, Littlefield CE, McClure ML, Novembre J, Schloss CA, Schumaker NH, Shah VB, Theobald DM. (2019) Circuit-theory applications to connectivity science and conservation. *Conserv Biol.* 2019 Apr;33(2):239-249.

56. Marcus JH*, Posth C*, Ringbauer H*, Lai L, Skeates R, Sidore C, Beckett J, Furtwängler A, Olivieri A, Chiang CWK, Al-Asadi H, Dey K, Joseph TA, Liu CC, Der Sarkissian C, Radzevičiūtė R, Michel M, Gradoli MG, Marongiu P, Rubino S, Mazzarello V, Rovina D, La Fragola A, Serra RM, Bandiera P, Bianucci R, Pompianu E, Murgia C, Guirguis M, Orquin RP, Tuross N, van Dommelen P, Haak W, Reich D, Schlessinger D, Cucca F, Krause J, Novembre J. (2020) Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. *Nat Commun.* Feb 24;11(1):939. doi: 10.1038/s41467-020-14523-6.
57. Peter BM, Petkova D, Novembre J. (2020) Genetic landscapes reveal how human genetic diversity aligns with geography. *Mol Biol Evol.* 37:943-951
58. Biddanda A, Rice DP, Novembre J. (2020). A variant-centric perspective on geographic patterns of human allele frequency variation. *eLife.* 9:e60107
59. Marcus J, Ha W, Barber RF, Novembre J. (2021). Fast and flexible estimation of effective migration surfaces. *eLife.* 10:e61927.
60. Ringbauer H, Novembre J, Steinrücken M. (2021). Parental relatedness through time revealed by runs of homozygosity in ancient DNA. *Nature Communications.* 12(1), 1-11.
61. Zhang S, Johnson RA, Novembre J, Freeland E, Conley D. (2021). Public attitudes toward genetic risk scoring in medicine and beyond. *Social Science & Medicine.* 274, 113796.
62. Spangenberg L, Fariello MI, Arce D, Illanes G, Greif G, Shin JY, Yoo SK, Seo JS, Robello C, Kim C, Novembre J, Sans M, Naya H. (2021) Indigenous Ancestry and Admixture in the Uruguayan Population. *Front Genet.* 12:733195
63. Ortega-Del Vecchyo D, Lohmueller KE, Novembre J. (2022) Haplotype-based inference of the distribution of fitness effects. *Genetics*, 220:iyac002.
64. Biddanda, A, Steinrücken, M, & Novembre, J. (2022). Properties of 2-locus genealogies and linkage disequilibrium in temporally structured samples. *Genetics*, 221(1).
65. Liu CC, Witonsky D, Gosling A, Lee JH, Ringbauer H, Hagan R, Patel N, Stahl R, Novembre J, Aldenderfer M, Warriner C, Di Rienzo A, Jeong C. (2022). Ancient genomes from the Himalayas illuminate the genetic history of Tibetans and their Tibeto-Burman speaking neighbors. *Nature Communications*, 13(1), 1-14.
66. Muktopavela RA, Petr M, Ségurel L, Korneliussen T, Novembre J, & Racimo F. (2022). Modeling the spatiotemporal spread of beneficial alleles using ancient genomes. *Elife*, 11, e73767.
67. Skeen HR, Willard DE, Jones AW, Winger BM, Gyllenhaal EF, Tsuru BR, Hackett SJ, and Novembre J. (2023). Intestinal microbiota of Nearctic-Neotropical migratory birds vary more over seasons and years than between host species. *Molecular Ecology*, 32:3290-3307.
68. Cotter DJ, Hofgard EF, Novembre J, Szpiech ZA, & Rosenberg NA. (2023). A rarefaction approach for measuring population differences in rare and common variation. *Genetics*, 224(2), iyad070.
69. Sohail M, Palma-Martínez MJ, Chong AY, Quinto-Cortés CD, Barberena-Jonas C, Medina-Muñoz S G, ..., Novembre J, Garcia-García L & Moreno-Estrada A. (2023). Mexican Biobank advances population and medical genomics of diverse ancestries. *Nature*, 622(7984), 775-783.

Perspectives and Literature reviews:

70. Novembre J, Di Rienzo A. (2009) Spatial patterns of variation due to natural selection in humans. *Nature Reviews Genetics* 10:745-755.
71. 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.
72. 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.
73. Novembre J. (2012) Commentary on Sokal, Oden, and Thomson's "a problem with synthetic maps (1999)". *Hum Biol* 84:623-6.

74. Veeramah KR, Novembre J. (2014). Demographic Events and Evolutionary Forces Shaping European Genetic Diversity. In: Chakravarti, 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).
75. Novembre J (2014). Variations on a Common STRUCTURE: New Algorithms for a Valuable Model. *Genetics* 197(3):809-811.
76. Novembre J (2015). Human Evolution: ancient DNA steps into the language debate. *Nature (New and Views)* 11:164-165.
77. Novembre J. (2016) Pritchard, Stephens, and Donnelly on Population Structure. *Genetics* 204(2):391-393.
78. 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.
79. Novembre J, Barton NH. (2018) Tread Lightly Interpreting Polygenic Tests of Selection. *Genetics*. 2018 Apr;208(4):1351-1355.
80. Novembre J, Beier P, Fargione J, Lawler J, Selkoe K. (2018) Scientific obituary: Brad McRae (1966-2017). *Mol Ecol. Aug;27(15):3035-3036*.
81. Liu CC, Shringarpure S, Lange K, Novembre J. (2020) Exploring Population Structure with Admixture Models and Principal Component Analysis. *Methods Mol Biol.* 2090:67-86
82. Lewis AC, Molina SJ, Appelbaum PS, Dauda B, Di Rienzo A, Fuentes A, Fullerton SM, Garrison NA, Ghosh N, Hammonds EM, Jones DS. (2022) Getting genetic ancestry right for science and society. *Science.* 376(6590):250-2.
83. Novembre, J. (2022). The background and legacy of Lewontin's apportionment of human genetic diversity. *Philosophical Transactions of the Royal Society B*, 377(1852), 20200406.
84. Novembre, J., Stein, C., Asgari, S., Gonzaga-Jauregui, C., Landstrom, A., Lemke, A., ... & Tishkoff, S. (2022). Addressing the challenges of polygenic scores in human genetic research. *The American Journal of Human Genetics*, 109(12), 2095-2100.
85. Steiner, M. C., & Novembre, J. (2022). Population genetic models for the spatial spread of adaptive variants: A review in light of SARS-CoV-2 evolution. *PLoS Genetics*, 18(9), e1010391.
86. Gloss, A. D., Steiner, M. C., Novembre, J., & Bergelson, J. (2023). The design of mapping populations: Impacts of geographic scale on genetic architecture and mapping efficacy for defense and immunity. *Current Opinion in Plant Biology*, 74, 102399.

Other:

87. 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>.
88. National Academies of Science, Engineering, and Medicine Report (2023) Use of Race, Ethnicity, and Ancestry as Population Descriptors in Genomics Research. <https://www.nationalacademies.org/our-work/use-of-race-ethnicity-and-ancestry-as-population-descriptors-in-genomics-research>

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Ongoing Support:

NIH/NIGMS R35 GM149521(PI: Novembre)

2023-2028

Theory, Methods, and Resources for Understanding and Leveraging Spatial Variation in Population Genetic Data

Role: Principal Investigator

NIH/NIGMS R01 GM132383(PI: Novembre) 2019-2024
Extending tools for visualization of geographic structure in population genomic data
Role: Principal Investigator

NIH / NHGRI R01 HG010773 (PI: He, MPI: Novembre) 2020-2024
Refining mutation rates and measures of purifying selection with an application to understanding the impact of non-coding variation on neuropsychiatric diseases
Role: MPI - Principal Investigator

NIH / NIGMS T32 GM139782 (PI: Thornton) 2021-2026
Genetic Mechanisms and Evolution Graduate Training Program
Role: Co-director of T32 program

Completed Support (last 3 years):

NIH/NCI U01 CA198933 (PI: Novembre) 2015-2019
Tools for visualization of geographic structure in population genomic data
Role: Principal Investigator

NIH/NIGMS R01 GM108805 (PI: Novembre) 2014-2019
Population genetic consequences of recent explosive population growth in humans
Role: Principal Investigator

NIH/NHGRI R01 HG007089 (PI: Novembre) 2013-2019
Haplotype-based analysis methods for population genomics
Role: Principal Investigator

NIH/ NHLBI R01 HL119577 (PI: Di Rienzo) 2014-2019
Genetic adaptations to high altitude
Role: Co-Investigator

Service: Extramural

Invited, Elected, Appointed

Advisory Boards

Advisory Board for Justice, Diversity, Equity, Inclusion, NIH ClinGen Project 2022-
Advisory Board for Beyond the Medical NIH research project 2022-
Scientific Advisory Board, Embark 2022-
National Academy of Sciences Committee on Use of Race, Ethnicity, and Ancestry as
Population Descriptors in Genomics Research 2022-2023
Co-chair, Polygenic Risk Scores Guidance Writing Committee, ASHG 2021-2022
Professional Practices and Social Implications Committee, ASHG 2019-2022
Scientific Advisory Board, Ancestry.com 2012-2018
Scientific Advisory Board, CartaGENE Study 2014-2012
Member, American Society of Human Genetics Task Force on Ancestry Testing 2011-2008
Advisor, one-day summit meeting for National Bone Marrow Donor Transplant Program 2010

Editorial work

Associate Editor, Genetics 2016-

Associate Editor, Molecular Biology and Evolution 2010-2018
 Guest editor, PLoS Genetics (4 submissions) 2014, 2009
 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, PLoS One, Proceedings of the Royal Society B, Statistical Applications in Genetics and Molecular Biology, Trends in Genetics.

External examiner/grant reviewer

External Examiner, Cambridge University PhD Defense, William Barrie 2023
 NIH Review Panel F08 Fellowship panel: Genes, Genomes, and Genetics 2021
 External examiner, Trinity College Dublin PhD Defense, Ross Bryne 2020
 NIH Review Panel GVE panel, ad hoc panel member, June 2019
 NIH Review Panel NIGMS MIRA R35, November 2017
 External examiner, Copenhagen University PhD Defense, Jose Victor Moreno Mayar, May 2017
 NIH Review Panel NIGMS MIRA R35, March 2017
 NIH Review Panel ZRG1 BST-T (03) Study Section, November 2016
 Fellowship Application Reviewer, NSF Graduate Research Fellowships 2016
 Opponent, Public defense of Pontus Skoglund’s doctoral thesis, Uppsalla Univeristy 2013
 External examiner, viva examination of D Phil thesis by Anjali Hinch, Oxford University 2013
 Grant Proposal Reviewer for: NIH EIA panel, UK Biotechnology and Biological Sciences Research Council, National Geographic, FWF Austria, Israeli Science Foundation, Royal Society of New Zealand

Other

Co-organizer, Computational Genomics Summer Institute, UCLA. 2016
 Consultant, Army Corps of Engineers on Reassessment of Ancestry of the Kennewick sample 2015-2016
 Co-chair Session on “Population Genomics” at CSHL Biology of Genomes meeting 2012
 Special Topics Editor, Molecular Ecology 2010-2009

Additional:

Organizer, Invited Session on Protections against Genetic Discrimination, American Society of Human Genetics Meeting, Virtual. 2020
 Co-founder and 3x lead organizer, Midwest Population Genetics Meeting, Chicago. 2019,16,14
 Co-organizer, MontyFest: A symposium in honor of Monty Slatkin 2015
 Co-organizer, Midwest Population Genetics Meeting, Ann Arbor, Michigan. 2015
 Co-organizer, Symposium on “Theory and Inference in Spatial Population Genetics” at the Society for Molecular Biology and Evolution Meeting 2015, 2008

Service: Intramural

University of Chicago

Leadership:

Co-chair, HG/GSSB DEI Committee 2022-
 Co-director, Genetics Mechanisms & Evolution T32 graduate training program 2021-
 Co-director, Biological Sciences Division Quantitative Biology Bootcamp 2020-
 Chair, Search Committee for population geneticist, Dept of Ecology & Evolution 2016
 Co-chair, Search Committee for computational biologist, Dept of Human Genetics 2014-2013

Co-organizer, Mitchell Symposium on Ancient DNA studies 2014

Committee membership:

BSD Computing Activities and Services Committee 2021-
Steering Committee, Genetics, Genomics and Systems Biology Committee 2016-
Search Committee for BSD Dean of Graduate Affairs 2021
BSD Faculty Hiring Diversity Working Group 2020-2022
BSD Information Systems and Informatics Committee 2019-2021
Admissions Committee, Dept of Human Genetics 2014-2020
University Data Science Special Report Committee 2017-2018
Faculty Advisory Council to the Dean of Biological Sciences Division 2016-2018
Search Committee for Strategic Hire Evolutionary Cell Biologist 2016
Committee on Appointments and Promotions (ad hoc service, 2 cases) 2014-2013

Other:

Lecture, New York City UChicago Alumni Group 2020
Co-organizer, Darwin's Weekly Seminar, Dept of Ecology and Evolutionary Biology 2015-2016
Organizer, Departmental Seminar, Dept of Human Genetics 2013-2017

University of California–Los Angeles

Leadership:

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

Committee membership:

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

Teaching/Training/Outreach

Inter-departmental Program Training Appointments

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

Undergraduate courses

BIOS 20235: Biological Systems (w/I. Rebay) 2024-
EEB 135/235: Evolutionary genetics (taught jointly with EEB235) 2012-2010
LS1: Evolution, Ecology, and Biodiversity. (w/ M Alfaro, J Lloyd-Smith) 2012-2011

Graduate courses (Ph.D.)

HG 47500: Genetic Mechanisms from Variation to Evolution. (w/F. Spitz)	2021-
BSDG 30900: Biological Sciences Division Quantitative Bootcamp 17,19-	2015-
HG 48600: Fundamentals of Computational Biology: Models and Inference. (w/M Stephens)	2016-
HG 46900: Human Genetic Variation and Disease. (w/A. Di Rienzo)	2015-2021
HG 47100: Introduction to Statistical Genetics. (w/ Nancy Cox, Lin Chen and Brandon Pierce)	2014-2015
MGCB 32100, "Senior Graduate Student Ethics": Lecture on Genetics, Race, and Discrimination.	2017, 2019, 2021
EEB 135/235: Evolutionary genetics	2012-2010
EEB 200A: Evolution. Co-instructors: M. Alfaro and R. Wayne	2012-2008
EEB 263: Seminar in Population genetics	2011,2009
Bootcamp on Quantitative Skills for Ecology and Evolution. (w/M Alfaro, J Lloyd-Smith)	2012-2010
Guest lectures, HG210 (3x), HC70A (3x), MCDB 172 (2x), Soc Gen 102 (2x), CS/SysBio M184 (1x), CS/SysBio M185 (2x), Geography Grad Seminar (1x)	2012-2008

Short courses and guest lectures

Graduate PopGen short course, University of Copenhagen. Guest lecturer	2021
Population genomics workshop, FAS Informatics Group at Harvard University	2019
Computational Genomics Summer Institute, UCLA, Steering Committee and Lecturer	2019-2016
Instructor, Genomic Analysis of Complex Traits Sardinian Summer School (5x)	2019-2012
City University of New York BIO 31234, Guest Lecture	2018
The Jackson Laboratory. 54th Annual Short Course on Medical and Experimental Mammalian Genetics. Invited guest lecture	2014
Mount Desert Island Biological Laboratory, Environmental Genomics Short Course (3x) Invited guest lecture. Organizers: J Colbourne, J Shaw, B King	2010-2014
Summer Institute in Statistical Genetics. MCMC for Genetics. Co-instructor with EA Anderson	2012
Instructor, Coalescent Theory and Methods short course. University of Berne, Switzerland Co-instructors: L Excoffier, M Foll, M Blum	2011
Watson School of Biological Science. Topics in Biology: Evolution Student Instructor for N. Patel, N. Shubin, C. Bergman	2005
Evolutionary Genetics. Student Instructor for M. Slatkin. University of California-Berkeley	2001-2002

Research trainees:

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

Rose Putler, UCLA. Presently: Researcher at University of Michigan	2009-2010
Joe Marcus, University of Washington. Presently: Grail Biosciences	2013-2014
Chris Porras, University of Chicago. Presently: Mt Sinai MD/PhD program	2017-2020
Achu Menon, University of Chicago.	2020-2021
Axel Norman-Zagal, UNAM	2023

Graduate (Ph. D)

Margaret Steiner, Human Genetics PhD student, NSF GRFP Fellow	2021-
Xinyi Li, Human Genetics PhD student	2020-
Arjun Biddanda, Human Genetics PhD student (postdoctoral fellow at Hopkins)	2015-2020
Joseph Marcus, Human Genetics, NSF GRFP Fellow PhD student (Grail)	2015-2020
Hussein Al-asadi, Committee on Evolutionary Biology, NSF GRFP Fellow PhD student (joint with M Stephens; Adaptive Biotechnologies)	2013-2018

Evan Koch, Ecology & Evolution, NSF GRFP Fellow PhD student (postdoctoral fellow Harvard University / Broad Institute)	2013-2018
Joel Smith, Ecology & Evolution, NSF GRFP Fellow PhD student (Zymeworks)	2013-2018
Diego Vicente Ortega del Vecchyo, Bioinformatics IDP, UC-MEXUS fellow PhD student (group leader LIIGH)	2010-2016
Colin Rundel, co-advised Statistics PhD student (assistant teaching professor at Duke University)	2010-2011
Darren Kessner, Bioinformatics IDP PhD Student (faculty at the Marlborough School)	2009-2014
Eunjung Han, T32 fellow PhD student (research scientist at Amazon Alexa Machine Learning)	2009-2014

Postdoctoral

Luke Anderson-Trocmé, NSERC Fellow	2023-
Hao Shen	2022-
Hannah Moots, Neubauer Collegium Fellow	2021-2024
Mashaal Sohail, Chicago Fellow (Assistant Professor, UNAM)	2019-2021
Daniel Rice, Chicago Fellow (NCBI)	2017-2020
Harald Ringbauer (group leader, Max Planck Institute for Evolutionary Anthropology)	2018-2019
Mark Reppell (research scientist at Abbvie pharmaceuticals)	2014-2017
Ben Peter, Swiss NSF Ambizione Postdoctoral fellow (group leader at Max Planck Institute for Evolutionary Anthropology)	2014-2017
Charleston Chiang, NIH-NSRA fellow Postdoctoral fellow (Assistant professor at University of Southern California)	2011-2015
Alex Platt (Research professor at Temple University)	2011-2013
Daniel Wegmann, (professor at University of Fribourg)	2009-2011
Adam Freedman, NSF Bioinformatics Postdoctoral fellow (data scientist at Harvard University)	2009-2012
Krishna Veeramah, Mellon Foundation fellow (Assoc. Prof at Stony Brook University)	2009-2010

Sabbatical Host

Enrique Lessa, Professor, Universidad de la Republica, Uruguay.	2014
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Genetics, Race, and Discrimination Curriculum Outreach/Development

MGCB 32100, “Senior Graduate Student Ethics”: Guest Lecture (3x) <i>Initiated a guest lecture within the student ethics course to help train students in understanding and addressing issues of Genetics, Race, and Discrimination in the classroom and research fields.</i>	2017-2021
Interviewed by Amy Harmon for piece on genetics and race in the New York Times, <i>Discussed how genetics is abused by racist individuals and how geneticists need to confront this more directly.</i>	2018
Faculty advisor, Reading group on Race and Genetics, Department of Human Genetics <i>A reading group that covered the history of race concepts in human genetics. Material shared via a website: https://voices.uchicago.edu/geneticists-against-hate/</i>	2020
Invited speaker for online workshop, “How and Why to Include Eugenics History in in Genetics Classes.” Genetics Society of America TAGC meeting, May. <i>Spoke on the practices we have developed at University of Chicago and lessons learned for running effective sessions discussing eugenics, race, and discrimination.</i>	2020

Inclusive mentoring activities:

Co-Chair, DEI committee for Human Genetics Department / GGSB program	2022-
Member, BSD Faculty Hiring Diversity Working Group	2020-2022
Co-founder and 3x lead organizer, Midwest Population Genetics Meeting, Chicago.	2014-2019

Initiated a regional meeting that is heavily student focused – all talks are by students or faculty new to the region apart from a keynote talk by a senior professor.

Mentor, ASHG Trainee-Mentor Luncheon	2017, 2019
Undergrad diversity mentor, Society for Molecular Biology meeting	2011, 2008
Role modeling how scientific interactions can foster community and time with family abroad: <i>Lecturer in 1st, 3rd, and 6th Latin American School of Evolution for graduate students. Montevideo, Uruguay and Buenos Aires, Argentina.</i>	2019,13,09
<i>Instructor for 4 days of a Human Genomics course, Institut Pasteur, Montevideo, Uruguay.</i>	2016
<i>Advisor, UruGenoma project, director: Hugo Naya</i>	2015-
<i>Two-week research visit to Enrique Lessa, the Universidad de la Republica, Uruguay.</i>	2003

Outreach

Public/non-academic venue lectures

Public Lecture for Iowa City Darwin Day, Iowa City, IA.	2020
Public Lecture for Pint of Science Series, Baderbauer Brewery, Chicago, IL.	2018
Public Lecture for Chicago Science & Technology Society, The Pint, Chicago, IL.	2018
Lecture, Elective Studies Supper Club, Illinois Humanities, Chicago, IL.	2017
Keynote speaker, Opening Convocation, Colorado College.	2016
Panel conversation with Tara Zahra at the Economic Club of Chicago.	2016
Lecture at MacArthur Fellows Retreat at the Johnson Foundation.	2016
Public Lecture for Pint of Science Series, Blue Moon Pub, Chicago, IL.	2015

Selected Outreach / Online products

<u>Online interview</u> : Reddit Science Ask Me Anything Series	2015
<u>Radio interview</u> : WBEZ Chicago Morning Shift	2015
“University of Chicago computational biologist receives MacArthur Genius Grant	
<u>Video interview</u> “Computational Biologist John Novembre, 2015 MacArthur Fellow”	2015
<u>Radio interview</u> : NPR Morning Edition “Genome Maps May Spot Disease In African-Americans”	2011
<u>Video interview</u> : Science Central News “Gene-ography” video for distribution on ABC networks	2008
<u>Video</u> by American Musum of Natural History	2008
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).	

Additional Outreach:

PBSNews, What scientists are thankful for this Thanksgiving	2016
Media surrounding announcement of MacArthur Fellowship	2015
- 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.	
Media surrounding dog domestication research:	2013
- Freedman et al research 18th out of top 25 science stories of 2013 in Science News Magazine	
Outreach from ancestry-based recombination map estimation research:	2011
- Covered by media outlets: 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	
Outreach from dog domestication research:	2010

- Covered by world media outlets: 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
- Outreach from “Genes mirror geography in Europe” research: 2008
- Covered by world media outlets: 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: New Scientist, Technology Review, Discover Magazine, Popular Science, Tech Herald, Science Daily
- Covered by science journals: Nature Reviews Genetics, Nature Podcast, ScienceNOW
- Source for background on population genetics by science journalists at: Discover Magazine, 2008-
Nature, New Scientist, New York Times, Los Angeles Times, Huffington Post

Invited Speaking

Departmental Seminars

- Department of Computational Biology, University of Southern California 2023
- Department of Computational Biology, Cornell University 2023
- Department of Genetics, Cambridge University 2023
- Genome Sciences Training Program, University of Michigan 2022
- Institute for Ecology and Evolution, University of Oregon 2022
- Department of Science, Technology, & Mathematics, Galludet University, April. 2021
- Lewontin 1972 Seminar Series, Stanford University, September. 2021
- Department of Biology, University of Iowa, February. 2020
- Department of Biology, University of Illinois-Chicago, February. 2020
- Population Genetics Groups Seminar, Arizona State University, January. 2020
- Human Genetics Seminar Series, University of Utah, May. 2019
- Department of Systems Biology, Columbia University, April. 2019
- A. Watson Armour Seminar Series, The Field Museum, February. 2018
- University of Maryland School of Medicine, Institute for Genome Sciences, May. 2018
- Genome Science Seminar Series (GS3) at University of Virginia sponsored by the Center for Public Health Genomics (CPHG), April. 2018
- Broad Institute, Medical and Population Genetics Program, March. 2018
- University of California - San Diego, Genetics, Bioinformatics and Systems Biology Colloquium, February. 2018
- Duke University Program in Genetics and Genomics Distinguished Lecturer Series, Nov. 2017
- bioCaddie Seminar Series, March. 2017
- McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, February. 2017
- 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

- 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
- 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, Jan. 2014
- 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, UCSF, June. 2013
- 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, UCSB, February. 2012
- 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
- Department of Basic Sciences, The Commonwealth Medical College, November. 2010
- Department of Biological Sciences, University of Idaho, November. 2010
- Dept. of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, June. 2010
- Department of Human Genetics, University of Michigan, May. 2010
- 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, Nov. 2008
- Department of Biological Sciences, Humboldt State University, October. 2008
- Dept. of Molecular and Computational Biology, University of Southern California, Sept. 2008
- 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

- Gordon Conference for Human Genetics and Genomics 2023
- Global Genomics & Health Equity and Institute for Biomedical Informatics Symposium 2023

on “*Human Genomic Diversity and Medicine: Challenges and Solutions to Reduce Health Disparities*” University of Pennsylvania

- Keynote, MexPopGen meeting, December. 2020
- Online workshop, “Raising a Woke Generation of Geneticists: How and Why to Include Eugenics History in Genetics Classes.” Genetics Society of America TAGC meeting, May. 2020
- Plenary speaker. Advances in Genome Biology and Technology. San Marcos, Florida, Feb. 2020
- Reconstructing the Human Past – Using Ancient and Modern Genomics. EMBO Heidelberg, March. 2019
- Workshop on the Polygenic Turn, Edmond J Safra Center for Ethics, Oct. 2018
- Gene Flow detection session. SMBE Annual Meeting, Japan, July. 2018
- Keynote, Mathematical Computational Evolutionary Biology Meeting, Montpellier, France, June. 2018
- Keynote for Great Lakes Bioinformatics Consortium Conference, May. 2017
- Plenary for Gordon Research Conference on Quantitative Genetics and Genomics, Feb. 2017
- National Academy of Sciences/ Kavli Frontiers of Science meeting, November. 2016
- CSHL Banbury Meeting “Ancient DNA and Archaeology”, May (discussant) 2016
- Center for Computational, Evolutionary and Human Genomics Annual Symposium, Stanford University, February. 2016
- “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) 2015
- 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
- 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
- 1000 Genomes Community Meeting, University of Michigan, July. 2012
- Mathematical Biosciences Institute workshop “Spatial Models of Micro and Macro Systems,” April. 2012
- Royal Society Discussion meeting on Human evolution, migration and history revealed by genetics, immunity and infection, June. 2011
- NSF MIGRATE workshop, Max Planck Institute for Ornithology, Germany, June. 2010
- American Association for Anthropological Genetics symposium at the AAPA meeting. April. 2010

- 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, Oct. 2009
- Darwin 200 South American Celebration Conference, Uruguay, September. 2009
- Gordon Conference on Ecological and Evolutionary Functional Genomics, July. 2009
- Kavli Institute for Theoretical Physics, Population Genetics Program, December. 2008
- Third International Symposium on Conservation Genetics, American Museum of Natural History, September. 2007