

## Personal Information

Address: Max Planck Institute for Evolutionary Anthropology  
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Languages: German (native)  
English (fluent)  
French (advanced)

Nationality: Switzerland

## Education & Employment

11. 2017 - **Group Leader**, Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany;
10. 2014 - 9. 2017 **Postdoctoral scholar** with John Novembre, Department of Human Genetics, University of Chicago, USA;
8. 2010 - 8.2014 **Ph.D.** in Integrative Biology with a designated emphasis in Computational Biology and Genomics, University of California, Berkeley, USA  
Advisors: Rasmus Nielsen and Montgomery Slatkin  
Title: *Inference from Two Non-Equilibrium Models in Population Genetics.*
8. 2008 - 2. 2010 **MSc** in Ecology and Evolution, University of Bern, Switzerland  
Advisor: Laurent Excoffier  
Title: *Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure.*
6. 2008 - 7. 2008 **Internship** on Lichen phylogenetics, Swiss Federal Research Institute WSL.  
Advisor: Christoph Scheidegger
10. 2005 - 8. 2008 **BSc** in Biology (with special qualification in Plant Sciences), University of Bern, Switzerland

## Publications

- submitted Key FM, Muslihudeen AA, Mundry R, Peter BM, D'Amato M, Dennis MY, Schmidt JM and Andrés, AM (submitted): Human local adaptation of the TRPM8 cold receptor along a latitudinal cline  
Peter, BM, Petkova D , Novembre J (submitted): Genetic landscapes reveal how human genetic diversity aligns with geography
- 2017 Jeong C, Peter BM, Basnyat B, Neupane M, Beall CM, Childs G, Craig SR, Novembre J and Di Rienzo A (2017): A longitudinal cline characterizes the genetic structure of human populations in the Tibetan plateau. **PLoS One** 12(4): e0175885. doi: [10.1371/journal.pone.0175885](https://doi.org/10.1371/journal.pone.0175885)
- 2016 Marc de Manuel M, Kuhlwilm M, Frandsen P, et al. [and 34 others, including Peter BM] (2016): Chimpanzee genomic diversity reveals ancient admixture with bonobos. **Science** Oct;354(6311):477–481. doi: [10.1126/science.aag2602](https://doi.org/10.1126/science.aag2602)  
 Novembre J, and Peter BM (2016) : Recent advances in the study of fine-scale population structure in humans. **Curr. Opin. Genet. Dev.** 41,98-105 doi: [10.1016/j.gde.2016.08.007](https://doi.org/10.1016/j.gde.2016.08.007)  
Peter BM (2016): Admixture, Population Structure, and F-Statistics. **Genetics** 202:1485-1501; doi: [10.1534/genetics.115.183913](https://doi.org/10.1534/genetics.115.183913)  
 Potter S, Bragg J, Peter, BM, Bi K, Moritz C (2016): Phylogenomics at the tips: inferring lineages and their demographic history in a tropical lizard, *Carlia amax*. **Molecular Ecology** 25, 1367–1380 doi: [10.1111/mec.13546](https://doi.org/10.1111/mec.13546)
- 2015 Nakagome S, Alkorta-Aranburu G, Amato R, Howie B, Peter BM, Hudson RR and Di Rienzo A (2015): Estimating the ages of selection signals from different epochs in human history. **Molecular Biology and Evolution** 33 (3): 657-669. doi: [10.1093/molbev/msv256](https://doi.org/10.1093/molbev/msv256)  
Peter BM and Slatkin M (2015): The effective founder effect in a spatially expanding population. **Evolution**, 69: 721-734. doi: [10.1111/evo.12609](https://doi.org/10.1111/evo.12609)
- 2014 Huerta-Sánchez E, Jin X, Bianba Z, Peter BM et al. (2014): Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. **Nature** 512 (7513), 194-197. doi: [10.1038/nature13408](https://doi.org/10.1038/nature13408)  
 Key FM, Peter B, Dennis M, et al. (2014): Selection on a Variant Associated with Improved Viral Clearance Drives Local Adaptive Pseudogenization of Interferon Lambda 4 (IFNL4). **PloS Genetics**, doi: [10.1371/journal.pgen.1004681](https://doi.org/10.1371/journal.pgen.1004681)  
 Clemente FJ, Cardona A, Inchley C, Peter BM et al. (2014): A Selective Sweep on a Deleterious Mutation in CPT1A in Arctic Populations. **American Journal of Human Genetics** 95 (5),584-589. doi: [10.1016/j.ajhg.2014.09.016](https://doi.org/10.1016/j.ajhg.2014.09.016)  
 Reppell M, Koch E, Peter BM, and Novembre J (2014): Surfing waves of data in San Diego: sophisticated analyses provide a broad view of human genetic diversity. **Genome Biology**, 15 (12) 562 doi: [10.1186/s13059-014-0562-4](https://doi.org/10.1186/s13059-014-0562-4)
- 2013 Peter BM and Slatkin M (2013): Detecting Range Expansions from Genetic Data. **Evolution**, 67:3274-3289. doi: [10.1111/evo.12202](https://doi.org/10.1111/evo.12202)

- 2012 [Peter BM](#), Huerta-Sánchez E, and Nielsen, R (2012): Distinguishing selection from standing variation from selection on a de novo mutation. **PLoS Genetics**, 8(10): e1003011. doi: [10.1371/journal.pgen.1003011](https://doi.org/10.1371/journal.pgen.1003011)
- 2010 [Peter BM](#), Wegmann D, and Excoffier L (2010): Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure. **Molecular Ecology**, 19: 4648-4660. doi: [10.1111/j.1365-294X.2010.04783.x](https://doi.org/10.1111/j.1365-294X.2010.04783.x)

## Awards

- 2016 Best Poster by a Postdoc, 3rd Midwest Popgen Meeting
- 2013 Runner-up for Best Talk, Computational Biology Retreat, UC Berkeley.
- 2012 Finalist for Walter Fitch Award, Society for Molecular Biology and Evolution
- 2010 Volz-Award for best M.Sc. Thesis at the Institute of Ecology and Evolution, University of Bern
- Fakultätspreis (Faculty award) for the best M.Sc. Thesis in Biology at the University of Bern

## Fellowship

- 2014-2016 Swiss National Science Foundation Early Postdoc Mobility fellowship (18 months, 76,000 USD)

## Teaching Experience

- August 2017 Guest Faculty at Environmental Genomics course at Mount Desert Island Biological Lab (1 week)
- March 2017 Instructor at Environmental Genomics course, University of Birmingham, UK (1 week)
- August 2016 Guest Faculty at Environmental Genomics course at Mount Desert Island Biological Lab (1 week)
- Fall 2013 Graduate Student Instructor for Human Genetics and Genomics class at UC Berkeley (4hr/week). Instructors: Rasmus Nielsen and Montgomery Slatkin
- Spring 2013 Graduate Student Instructor for Population and Evolutionary Genetics class at UC Berkeley (4hr/week). Instructors: Doris Bachtrog and Rasmus Nielsen
- Summer 2012 Graduate Student Instructor for Python-bootcamp at UC Berkeley (2 weeks)

## Professional Service

Membership:	European Society for Evolutionary Biology (ESEB) Society for Molecular Biology and Evolution (SMBE) Society for Systematic Biologists (SSB) American Society of Human Genetics (ASHG)
Reviewing for:	Nature Genetics, Annals of Applied Statistics, PLoS Genetics, Genetics, Molecular Biology and Evolution, Molecular Phylogenetics and Evolution, Theoretical Population Biology, Molecular Ecology, Molecular Ecology Resources, European Journal of Human Genetics, Methods in Ecology and Evolution
Symposia organized:	ESEB 2017: Spatial Population Genetics (with Flora Jay, Marjo Saastamoinen and Emanuel Fronhofer) SMBE 2017: Population genomics of ancient DNA (with Joshua Schraiber)
Other:	Student representative on UC Berkeley Department of Integrative Biology Graduate Student Admission Committee (2012)

## Outreach

2008-2012	Swiss Biology Olympiad: Leading and preparing lectures, labs and exams for talented Swiss high school students in a wide variety of biological subjects (Ecology, Evolution, Ethology, Biochemistry, Statistical Analysis).
2013	Berkeley High School: Teaching First-year high school students about genetics, evolution and Ancient DNA

## Talks and posters

2017	Poster, ESEB <sup>1</sup> 2017, Groningen, Netherlands: “Impact of Selection on ABBA-BABA statistics” Poster, SMBE <sup>2</sup> , Austin TX, USA: “Landscapes of human migration rates” Lightning Talk, SSB <sup>3</sup> Standalone Meeting, Baton Rouge LA, USA: “F-statistics for phylogenetics”
2016	Invited Talk, Department of Biology, University of Fribourg, Switzerland: “Fine-scale population structure in humans” Invited Talk, INRA Montpellier, France: “Fine-scale population structure in humans” Poster, Estimating Effective Migration Maps in Humans. ASHG <sup>4</sup> , Vancouver, Canada Poster, 3rd Midwest Popgen Meeting: “Trees, Population structure, what the F...!”
2015	Talk, Dermitzakis Lab, University of Geneva, Switzerland, “A global perspective on fine-scale population structure in Europe”

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<sup>1</sup>European Society for Evolutionary Biology

<sup>2</sup>Society for Molecular Biology and Evolution

<sup>3</sup>Society for Systematic Biology

<sup>4</sup>American Society for Human Genetics

- Poster, “Probabilistic Modelling in Genomics” in Cold Spring Harbor NY, USA: “Trees, Population structure, what the F...!”
- Talk, ESEB<sup>1</sup> 2015 in Lausanne, Switzerland: “A worldwide perspective on isolation-by-distance patterns in humans”
- Talk, SBE<sup>2</sup> 2015 in Vienna, Austria: “Inferring selection from a spatially explicit demographic model based on a large number of human populations”
- 2014 Poster, ASHG<sup>4</sup> 2014 in San Diego, CA, USA: “The effective founder effect in a spatially expanding population.”
- Invited talk, Australian National University in Canberra, Australia, Moritz Lab, “Inferring the origin of a range expansion”
- Talk, SBE<sup>2</sup> 2014 in San Juan, Puerto Rico: “The effective founder effect in an spatially expanding population.”
- 2013 Invited talk: University of Chicago, Chicago IL: “Inferring the origin of a range expansion” Novembre/Stephens labs
- Invited talk at the Max Planck Institut für Evolutionäre Anthropologie, Leipzig, Germany: “Which way did they go: Inferring the origin of a range expansion”
- Talk, SBE<sup>2</sup> 2013 in Chicago, IL, USA: “Inferring the origin of a range expansion from genetic data.”
- Talk, Evolution<sup>5</sup> 2013 in Snowbird UT, USA “Inferring the origin of a range expansion from genetic data.”
- 2012 Talk, SBE<sup>2</sup> 2012 (Fitch symposium) in Dublin, Ireland: “Which way did they go? Detecting asymmetric migration from genetic data.”
- Talk, BAPG<sup>6</sup> in Davis, CA, USA: “Which way did they go? Detecting asymmetric migration from genetic data.”
- 2011 Talk, SBE<sup>2</sup> 2011 in Kyoto, Japan: “A method to distinguish selection on standing variation from selection on a new mutation.”
- 2010 Talk, Biology 2010<sup>7</sup> in Neuchatel, Switzerland: “Distinguishing between population bottleneck and population subdivision by a Bayesian model choice procedure.”
- 2009 Talk, Evolution in Metapopulations workshop in La Fouly, Switzerland: “Influence of population structure on population size change estimation procedures.”

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<sup>5</sup>annual meeting of the Society for the Study of Evolution

<sup>6</sup>San Francisco Bay Area Population Genetics

<sup>7</sup>annual meeting of the Swiss Zoological, Botanical and Mycological Societies