



Reconstructing the Human Past - Using Ancient and Modern Genomics

-  [Download Poster PDF Poster](#)

[See all years](#)

2019 Symposia

- [Synthetic Morphogenesis](#)
- [Human Past](#)
 - [Speakers and Organisers](#)
 - [Programme](#)
 - [Registration and Abstract Submission](#)
 - [Childcare](#)
 - [Accommodation and Shuttles](#)
 - [Sponsors](#)
 - [Financial Assistance](#)
 - [Contact](#)
- [Probing Neural Dynamics](#)
- [Cell Types](#)

- [Mechanical Forces in Development](#)
- [Microbiology](#)
- [Multiomics](#)
- [Systems Genetics](#)
- [Seeing is Believing](#)
- [Non-Coding Genome](#)
- [Metabolism Meets Epigenetics](#)

Location & dates

EMBL Heidelberg, Germany 31 Mar - 3 Apr 2019

Deadlines

Registration closed Abstract submission closed



Programme

Got something to say? Tweet it! [#EESHuman](#)

or Download the poster [here](#).

Day 1 - Sunday 31 March 2019

Time	Speaker
11:30- 13:15	Registration and light refreshments
13:15- 13:30	Opening Remarks

Time	Speaker
13:30 - 14:30	Keynote Talk Of Neandertals and Denisovans Svante Pääbo - Max Planck Institute for Evolutionary Anthropology, Germany
14:30- 17:30	Session 1 - Archaic Human Genomics Chair: Johannes Krause
14:30- 15:00	Doing more with less: 25 years of technological advances in ancient DNA Beth Shapiro - University of California, Santa Cruz, USA
15:00- 15:30	The Importance of Outliers in Large Sample Size Ancient DNA Studies David Reich - Harvard Medical School, USA
15:30- 16:00	Coffee break
16:00- 16:30	Genomic tales of archaic hominin admixture Joshua Akey - Princeton University, USA
16:30- 16:45	Neandertal population histories from sediment nuclear DNA Benjamin Vernot - Max Planck Institute for Evolutionary Anthropology, Germany
16:45- 17:00	A third high-coverage Neandertal genome Fabrizio Mafessoni - Max Planck Institute for Evolutionary Anthropology, Germany
17:00- 17:15	Reconstructing ancient DNA fragments on a single- molecule level Matthias Meyer - Max Planck Institute for Evolutionary Anthropology, Germany

Time	Speaker
17:15- 17:30	80,000 years of Neandertal genetic continuity in Europe Stephane Peyregne - Max Planck Institute for Evolutionary Anthropology, Germany
17:30- 18:00	Flash Talk Session I Poster No: 49, 51, 53, 57, 61, 67, 73, 87, 101, 59
18:00- 19:00	Dinner in the EMBL Canteen
19:00- 23:00	Welcome reception and poster pinning with live music by Jazz Duo in the ATC Rooftop Lounge

Day 2 - Monday 1 April 2019

Time	Speaker
08:15- 09:00	Meet the Editors Session
09:00- 12:00	Session 2 - Human Evolution From Genome-Wide Data Chair: David Reich
09:00- 09:15	Reconstructing population separation history from whole genome sequences Ke Wang - Max Planck Institute for the Science of Human History, Germany
09:15- 09:30	Large-scale whole genome sequencing of the Estonian population reveals new insights into population history Mait Metspalu - University of Tartu, Estonia
09:30- 10:00	Using ancient DNA to understand the formation and evolution of the Icelandic gene pool Agnar Helgason - deCODE genetics, Iceland

Time	Speaker
10:00- 10:30	Detecting selection using ancient DNA Rasmus Nielsen - University of California, Berkley, USA
10:30- 11:00	Coffee break
11:00- 11:15	Strong selective sweeps before 45,000BP displaced archaic admixture across the human X chromosome Kasper Munch - Aarhus University, Denmark
11:15- 11:30	The demographic et adaptive history of central African hunter-gatherers and farmers Etienne Patin - Institut Pasteur / CNRS, France
11:30- 11:45	The limits of long-term selection against Neandertal introgression Martin Petr - Max Planck Institute for Evolutionary Anthropology, Germany
11:45- 12:00	Phylogeography and domestication of the aurochs: an ancient genome tale Thierry Grange - Institut Jacques Monod, France
12:00- 13:30	Lunch
12:45- 13:30	Meet the Speaker Session I
13:30- 16:30	Session 3 - Computational Population Genetics Applied to Human Data I Chair: Anna-Sapfo Malaspinas
13:30- 14:00	Using inference of human history to gain medically relevant insights Ida Moltke - University of Copenhagen, Denmark

Time	Speaker
14:00- 14:30	Probabilistic methods to estimate demography from whole genome sequences Richard Durbin - University of Cambridge, UK
14:30- 15:00	Investigating human history from modern and ancient genomes: New methods and insights Stephan Schiffels - Max Planck Institute for the Science of Human History, Germany
15:00- 15:30	Coffee break
15:30- 15:45	Ancient genomes from the Bavarian Lech Valley suggest stratified patrilocal households in the European Bronze Age Philipp Stockhammer - Ludwig Maximilians University Munich & Max Planck Institute for the Science of Human History, Germany
15:45- 16:00	The genomic history of the Iberian Peninsula over the past 8000 years Iñigo Olalde - Harvard Medical School, USA
16:00- 16:15	Ancient human genome-wide data from a 3000-year interval in the Caucasus corresponds with eco-geographic regions Wolfgang Haak - Max Planck Institute for the Science of Human History, Germany
16:15- 16:30	The Geometry of Admixture Benjamin Peter - Max Planck Institute for Evolutionary Anthropology, Germany
16:30- 17:00	Flash Talk Session II Poster No: 46, 48, 50, 54, 62, 91, 93, 95, 105, 109

Time	Speaker
17:00-19:00	Poster Session I (odd numbers)

from 19:00	Free evening
------------	---------------------

Day 3 - Tuesday 2 April 2019

Time	Speaker
08:15-09:00	Career Workshop Chair: Rachel Coulthard-Graf
09:00-12:00	Session 4 - Computational Population Genetics Applied to Human Data II Chair: David Reich
09:00-09:15	The paleogenetic reconstruction of the spread of the domestic cat reconstructs past human migrations, trading and warfaring routes Eva-Maria Geigl - Institut Jacques Monod, France
09:15-09:30	Genetic reconstruction of human dwelling environment in the Upper Palaeolithic South Caucasus Mariya Antonosyan - Russian-Armenian University, Armenia
09:30-10:00	Representing population structure with effective migration surfaces John Novembre - University of Chicago, USA
10:00-10:30	Tracing canids through the human past Pontus Skoglund - The Francis Crick Institute, UK
10:30-11:00	Coffee break
11:00-11:15	The Anglo-Saxon migration and formation of the early English gene pool Joscha Gretzinger - Max Planck Institute for the Science of Human History, Germany

Time	Speaker
11:15- 11:30	Reconstructing the human past of Eurasian migration: from molecules to history Michael McCormick - Harvard University, USA
11:30- 11:45	Ancient admixture from an extinct ape lineage into bonobos Martin Kuhlwilm - Institut de Biologia Evolutiva, CSIC-Universitat Pompeu Fabra, Spain
11:45- 12:00	Ancient Brazilian Genomics Diana Ivette Cruz Dávalos - University of Lausanne, Switzerland
12:00- 13:30	Lunch
12:45- 13:30	Meet the Speaker Session II
13:30- 16:30	Session 5 - Ancient Human population dynamics Chair: Anna-Sapfo Malaspinas
13:30- 14:00	Genetic history on the Tibetan Plateau in the last 5,200 years Qiaomei Fu - Chinese Academy of Sciences, China
14:00- 14:30	Inferring the evolution of early humans from complete genome sequences Mattias Jakobsson - Uppsala University, Sweden
14:30- 15:00	Paleogenomic insights into the peopling of the Americas Maanasa Raghavan - University of Chicago, USA
15:00- 15:30	Coffee break

Time	Speaker
15:30- 16:00	Integrating Written Sources, Archaeology, and Genomics: A cemetery-based Paleogenomic Approach to recent Human Population History Patrick J. Geary - Institute for Advanced Study, USA
16:00- 16:15	Population history of modern humans from the Early Upper Palaeolithic in Europe Mateja Hajdinjak - Max Planck Institute for Evolutionary Anthropology, Germany
16:15- 16:30	Early human dispersals within the Americas J. Víctor Moreno-Mayar - University of Lausanne, Switzerland
16:30- 17:00	Flash Talk Session III Poster No: 66, 70, 74, 80, 84, 88, 94, 100, 104, 108
17:00- 19:00	Poster Session I I (even numbers)
19:00- 20:30	Conference Dinner in the EMBL Canteen
20:30- 00:00	Conference Party with the "Who2ladies" in the ATC Foyer

Day 4 - Wednesday 3 April 2019

Time	Speaker
09:00- 12:45	Session 6 - Domestication & Microbial Evolution Chair: Johannes Krause
09:00- 09:30	Genomic reconstructions of ancient pathogens Kirsten Bos - Max Planck Institute for the Science of Human History, Germany

Time	Speaker
09:30-10:00	The archaeology of beneficial microbes: from the human microbiome to milk Christina Warinner - Max Planck Institute for the Science of Human History, Germany
10:00-10:30	Coffee break
10:30-11:00	Tracking six millenia of horse selection, admixture and management with complete genome time-series Ludovic Orlando - Toulouse University, France
11:00-11:30	Human gene expression evolution - a mammalian perspective Henrik Kaessmann - Center for Molecular Biology of Heidelberg University, Germany
11:30-11:45	6,500 year old Salmonella enterica genomes link human-host adaptation to animal domestication Felix M. Key - Massachusetts Institute of Technology, USA
11:45-12:00	5,000-year-old genome of Yersinia pestis sheds light on the emergence and rapid spread of plague during the Neolithic and Bronze Age Nicolas Rascovan - MIVEGEC Institute, France
12:00-12:15	Uncovering the genomic history of the second plague pandemic through analysis of historical Yersinia pestis genomes Maria Spyrou - Max Planck Institute for the Science of Human History, Germany
12:15-12:30	Poster Prize Award Ceremony and Closing Remarks
12:30	Packed Lunch