



## SPEAKER BIOGRAPHICAL SKETCHES

Ancient DNA and Human Evolution

Friday, April 29, 2016

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**Sriram Sankararaman** is an Assistant Professor of Computer Science and Human Genetics at UCLA. His research interests lie at the interface of computer science, statistics and biology. He is interested in developing statistical machine learning algorithms to understand evolutionary processes and the genetics of complex phenotypes.



**Christina Warinner** is a Presidential Research Professor and Assistant Professor of Anthropology at the University of Oklahoma, where she is pioneering the study of the ancestral human microbiome. Her findings were named among the top 100 scientific discoveries of 2014 by *Discover Magazine*, and her research has been featured in more than 75 news articles and multiple documentaries. She is a 2014 Kavli Fellow and a 2012 TED Fellow, and her TED Talks on ancient dental calculus and the evolution of the human diet have been viewed more than 1.5 million times.



**Matthias Meyer** is a biochemist and Group Leader of the Advanced DNA Sequencing Techniques Group at the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany. He has developed many methods that improve the scope of DNA sequencing in evolutionary studies, a work that has led to the generation of the first high-quality genome sequences from archaic humans as well as the recovery of the oldest DNA sequences known to date from fossils discovered outside the permafrost.



**Kay Prüfer** is a Group Leader at the Max Planck Institute for Evolutionary Anthropology. His group's main research focus lies on the development and application of computational methods for the evolutionary analysis of genome sequences. He has contributed to the analysis of the chimpanzee, rhesus macaque and Neandertal genome sequences. More recently, he has led the consortia to analyze the bonobo and Altai Neandertal genome sequences.



**Brenna Henn** is an Assistant Professor in the Department of Ecology and Evolution at Stony Brook University, SUNY. She received her Ph.D. in anthropology and evolutionary genetics from Stanford University where she studied the deep population structure and complex migration patterns of African hunter-gatherer groups. Henn led several African genomic projects aimed at understanding the origins of modern humans and dispersals Out-of-Africa during a postdoctoral appointment in Dr. Carlos Bustamante's lab (2010) in the Dept. of Genetics, Stanford University School of Medicine. She also worked at 23andMe, Inc. working on their ancestry team and doing research development with Dr. Joanna Mountain.



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**Joshua M. Akey** is a Professor in the Department of Genome Sciences at the University of Washington. He received a B.S. degree in Molecular Biology from the University of Pittsburgh and a Ph.D. in Human Genetics from the University of Texas-Houston. His research focuses on understanding the evolutionary forces that have shaped patterns of human genomic diversity and the genetic architecture of complex phenotypes.



**Tony Capra** is an Assistant Professor in the Department of Biological Sciences at Vanderbilt University with appointments in the Vanderbilt Genetics Institute, Center for Structural Biology, and the Department of Biomedical Informatics. He uses the tools of computer science and statistics to address problems in genetics, evolution, and biomedicine. Current research in his group is focused on studying the processes that have driven recent human evolution and integrating diverse biological data to generate testable hypotheses about the functions of genetic variants, with a particular focus on gene regulation. His Ph.D. is in Computer Science, from Princeton University, and his postdoc training was in comparative human genomics.



**Johannes Krause** is Director of the Archaeogenetics Department at the Max Planck Institute for the Science of Human History in Jena, Germany. Despite his strong focus on evolutionary genetics and ancient DNA research, Krause's work includes a large variety of topics ranging from method development in high-throughput DNA sequencing and innovative targeted DNA enrichment strategies, to phylogenetics of Pleistocene megafauna such as woolly mammoth and cave bear, and complete genome-wide studies of ancient and archaic human populations. His team recently demonstrated the application of DNA capture techniques to reconstruct complete ancient pathogen genomes such as *Yersinia pestis* isolated from victims of the Black Death.



**María C. Ávila-Arcos** was born in Mexico City and attended college at the National Autonomous University of Mexico (UNAM) where she received her B.Sc. in genome sciences. Her Ph.D. is in paleogenomics from the Centre for GeoGenetics, University of Copenhagen. After completing her Ph.D., Ávila-Arcos focused her research on the genetic characterization of past and present populations of Latin America. She began this research as a postdoc in Copenhagen and continued it during a second postdoc at Stanford University. In November 2015, she joined the International Laboratory for Human Genome research at UNAM as junior faculty where she continues to study the genetics of underrepresented populations.

### Upcoming CARTA Symposia

October 14, 2016 **Implications of Anthropogeny for Medicine and Public Health**

Winter 2017 **Awareness of Death and Personal Mortality: Implications for Anthropogeny**

Spring 2017 **Extraordinary Variations of the Human Mind: Lessons for Anthropogeny**

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