Stanford CEHG 2014 Winter Symposium

JANUARY 13, 2014
SHERATON HOTEL
PALO ALTO, CA

Stanford University

About the Center for Computational, Evolutionary and Human Genomics

The Center for Computational, Evolutionary and Human Genomics (CEHG) was launched in 2012 by the School of Humanities and Sciences and the School of Medicine at Stanford University. Directed by Marcus Feldman, the Burnet C. and Mildred Finley Wohlford Professor in the School of Humanities and Sciences, and Carlos Bustamante, Professor of Genetics, the Center works at the forefront of the information age of genomics to improve human well-being.

Faculty and students from Stanford's seven schools collaborate on interdisciplinary research projects that support the computational analysis of genomic data. Researchers have access to vast amounts of information today but interpreting even the simplest genomes remains a daunting challenge. Ethical and legal questions also come into play. Addressing such issues will allow scientists to translate genomic data into scientific advances that can help promote global health, agriculture and biotechnology.

CEHG Executive Committee

Carlos **Bustamante**, Ph.D.
Marcus **Feldman**, Ph.D.
Hank **Greely**, J.D.
Dmitri **Petrov**, Ph.D.
Noah **Rosenberg**, Ph.D.
Chiara **Sabatti**, Ph.D.

Winter Symposium Planning Committee

Bridget **Algee-Hewitt**, Ph.D.
Jeremy **Hsu**
Rosario **Monge**
Pleuni **Pennings**, Ph.D.
Dmitri **Petrov**, Ph.D.
Cody Montana **Sam**

Stanford Center for Computational, Evolutionary and Human Genomics

Sheraton Palo Alto Hotel
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Palo Alto, CA 94301
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Logistics

The conference registration table will be outside the Cypress Room. All workshops and talks will take place in the Cypress Room. The poster session is in the Reception Room. Please refer to the Sheraton Hotel map on the back cover of this program. Parking is available at the hotel for $10 per vehicle. Stanford CEHG has purchased WiFi for all conference attendees.

CEHG WiFi Password:
serex7001

Morning Schedule

January 13, 2014
Cypress Room, Sheraton Palo Alto Hotel

10:00 - 10:45am	Computational Resources Workshop
10:00 - 10:45am	Career Panel
10:45 - 11:00am	Break
11:00 - 11:45am	GitHub Workshop
11:00 - 11:45am	NIH Career Awards
11:30 - 12:30pm	Lunch

Special Thanks

CEHG would like to sincerely thank the workshop presenters: Alexis Battle, Crystal Botham, Alex Chekholko, Stephanie Eberle, Julie Granka, Thomas Lee, Ruth Marinshaw, Jordan McCullough, Chris Pohalski, Sandeep Venkataram, Stanford School of Medicine Career Center

Afternoon Schedule

January 13, 2014
Cypress Room, Sheraton Palo Alto Hotel

	Session One: Chaired by Dmitri **Petrov**
12:30 - 12:40pm	Introduction by Carlos **Bustamante**
12:40 - 1:00pm	Richard **Klein**: Modern human origins
1:00 - 1:15pm	Sofia **Kyriaopoulou-Panagiotopoulou**: Computational models for studying condition-specific gene regulation
1:15 - 1:35pm	Noah **Rosenberg**: Bounds on population genetic statistics
1:35 - 1:55pm	Anne **Brunet**: Epigenetic regulation of aging
1:55 - 2:25pm	Break
	Session Two: Chaired by Hank **Greely**
2:25 - 2:45pm	Mildred **Cho**: Incidental findings of whole genome sequencing
2:45 - 3:00pm	Nicole **Creanza**: Worldwide linguistic and genetic variation
3:00 - 3:20pm	Jonathan **Pritchard**: Genetic load in human populations
3:20 - 4:00pm	Break
	Session Three: Chaired by Chiara **Sabatti**
4:00 - 4:20pm	Stephen **Quake**: Single cell genomics
4:20 - 4:35pm	Ethan **Jewett**: Theory and applications of a deterministic approximation to the coalescent model
4:35 - 4:55pm	Anshul **Kundaje**: The dynamic regulatory architecture of the human genome
4:55 - 5:05pm	Closing remarks by Marcus **Feldman**
5:05 - 6:00pm	Reception and poster session (Reception Room)

Speaker Biographies

Brunet
Anne Brunet is an Associate Professor in the Department of Genetics at Stanford University. Dr. Brunet obtained her B.Sc. from the Ecole Normale Supérieure in Paris, France and her Ph.D. from the University of Nice, France. She did her postdoctoral research training in Dr. Michael Greenberg's lab at Harvard Medical School. Dr. Brunet is interested in the molecular mechanisms of aging and longevity, with a particular emphasis on the nervous system. Her lab studies the molecular mechanism of action of known longevity genes, including FOXO transcription factors, in mammalian cells and organisms. She is particularly interested in the role of longevity genes in neural stem cells during aging. Another goal of the Brunet lab is to discover novel genes and processes regulating longevity using two model systems, the invertebrate C. elegans and an extremely short-lived vertebrate, the African killifish N. furzeri. Dr. Brunet has received several grants from the National Institute on Aging to study the importance of FOXO transcription factors in aging neural stem cells, the molecular mechanisms of dietary restriction, and to develop genetic tools for the short-lived fish *N. furzeri*.

Bustamante
Carlos Bustamante is a population geneticist whose research focuses on analyzing genome wide patterns of variation within and between species to address fundamental questions in biology, anthropology, and medicine. He received his B.A. in Biology (1997), M.S. in Statistics (2001), and Ph.D. in Biology (2001) from Harvard University. He was a Howard Hughes Medical Institute pre-doctoral fellow (1998-2001) and his Ph.D. thesis was advised by Profs. Dan Hartl, Richard Lewontin, and John Wakeley. Since 2010, he has been on the faculty in the Department of Genetics at the Stanford University School of Medicine. He has received multiple honors and awards including the Sloan Research Fellowship (2007) and a John D. and Catherine T. MacArthur Fellowship (2010). During his time as a faculty member at Cornell and Stanford, he has trained close to 50 post-doctoral fellows and graduate students as primary advisor. His group works on a variety of organisms and model systems ranging from humans and other primates to domesticated plants and animals. Much of their research is at the interface of computational biology, mathematical genetics, and evolutionary genomics.

Cho
Mildred Cho is Associate Director at the Stanford University Center for Biomedical Ethics and Associate Professor of Pediatrics (Genetics). She received her B.S. in Biology in 1984 from the Massachusetts Institute of Technology and her Ph.D. in 1992 from the Stanford University Department of Pharmacology. Her post-doctoral training was in Health Policy as a Pew Fellow at the Institute for Health Policy Studies at the University of California, San Francisco and at the Palo Alto VA Center for Health Care Evaluation. Before coming to Stanford, Dr. Cho was Assistant Professor of Bioethics in the Center for Bioethics and the Department of Molecular and Cellular Engineering at the University of Pennsylvania School of Medicine. She is a member of national advisory boards for the National Human Genome Research Institute and for the American Association for the Advancement of Science Public Policy Directorate.

Speaker Biographies

Creanza
Nicole Creanza is a postdoctoral fellow in the Department of Biology. She received her bachelor's degree from Harvard University and her PhD from the Rockefeller University. She works on computational and theoretical approaches to the comparison of cultural and genetic evolution in multiple systems: human language, viral evolution, and birdsong. Nicole received a NSF Graduate Research Fellowship for her doctoral work and a grant from the Stanford Center for Computational, Evolutionary and Human Genomics for her postdoctoral research.

Feldman
Marcus Feldman is the Burnet C. and Mildred Finley Wohlford Professor of Biological Sciences and director of the Morrison Institute for Population and Resource Studies at Stanford University. He uses applied mathematics and computer modeling to simulate and analyze the process of evolution. His specific areas of research include the evolution of complex genetic systems that can undergo both natural selection and recombination, and the evolution of learning as one interface between modern methods in artificial intelligence and models of biological processes, including communication. He also studies the evolution of modern humans using models for the dynamics of molecular polymorphisms, especially DNA variants. He helped develop the quantitative theory of cultural evolution, which he applies to issues in human behavior, and also the theory of niche construction, which has wide applications in ecology and evolutionary analysis.

Greely
Hank Greely is the Deane F. and Kate Edelman Johnson Professor of Law and Professor, by courtesy, of Genetics at Stanford University. He specializes in ethical, legal, and social issues arising from advances in the biosciences, particularly from genetics, neuroscience, and human stem cell research. He directs the Stanford Center for Law and the Biosciences, chairs the California Advisory Committee on Human Stem Cell Research, and serves on the Neuroscience Forum of the Institute of Medicine and the Advisory Council for the National Institute for General Medical Sciences of NIH. From 2007 to 2010 he was a co-director of the Law and Neuroscience Project. In 2006, he was elected a fellow of the American Association for Advancement of Science. Professor Greely graduated from Stanford in 1974 and from Yale Law School in 1977. He served as a law clerk for Judge John Minor Wisdom on the United States Court of Appeals and for Justice Potter Stewart of the United States Supreme Court. After working during the Carter Administration in the Departments of Defense and Energy, he entered private practice in Los Angeles in 1981 as a litigator with the law firm of Tuttle & Taylor, Inc. He began teaching at Stanford in 1985.

Jewett
Ethan Jewett is a PhD student in the Department of Biology. He received a bachelor's degree in physics from Reed College and a master's degree in applied mathematics from the University of Michigan. He has worked on methods for inferring species trees, coalescent models of genotype imputation, and basic approaches for reducing the computational complexity of evaluating coalescent formulas. Ethan also studies the relationship between genetic and cultural variation using empirical analyses of genetic and linguistic data.

Speaker Biographies

Klein

Richard G. Klein researches the archeological and fossil evidence for the evolution of human behavior. He has done fieldwork in Spain and especially in South Africa, where he has excavated ancient sites and analyzed the excavated materials since 1969. He has focused on the behavioral changes that allowed anatomically modern Africans to spread to Eurasia about 50,000 years ago, where they swamped or replaced the Neanderthals and other non-modern Eurasians. His book, The Human Career (3rd Edition, University of Chicago Press, 2009) summarizes his view of human evolution.

Kundaje

Anshul Kundaje is an Assistant Professor in the Genetics and Computer Science Depts. at Stanford University (since Sept 2013). Anshul obtained his PhD in Computer Science at Columbia University (2003-2008) in Christina Leslie's lab. Anshul's postdoctoral research (2008-2012), under Serafim Batzoglou and Arend Sidow at Stanford, focused on deciphering the regulatory architecture of the human genome as the lead computational analyst of the ENCODE (Encyclopedia of DNA Elements) consortium. Before joining the Stanford faculty in 2013, Anshul was a Research Scientist at MIT and The Broad Institute with Manolis Kellis. The Kundaje lab develops novel computational approaches for large-scale, integrative analysis of diverse functional genomic data to learn unified dynamic models of gene regulation and decipher the disruption and disregulation of regulatory pathways in disease contexts.

Kyriaopoulou

Sofia Kyriaopoulou-Panagiotopoulou is a PhD student in the Computer Science Department at Stanford. Her research focuses on developing machine learning algorithms to study gene regulation across different conditions. More broadly, Sofia is interested in integrating diverse genomic datasets to characterize and model the variation in gene expression and chromatin state across tissues, individuals, or species. Sofia has served as a teaching assistant for classes in machine learning, algorithms, and computational genomics. She received her B.Sc. in Computer Science from the Athens University of Economics and Business, where she did research on statistics and databases.

Petrov

Dmitri Petrov, Michelle and Kevin Douglas Professor of Biology, focuses on the genetics of adaptive evolutionary change in a range of organisms, from yeast, to flies, to humans. The work combines laboratory experiments with theory and computational analysis of data gathered by his and other research groups. Born in Russia, Professor Petrov received his M.Sc. in Physics and Molecular Biology in 1989 from Moscow Institute of Physics and Technology (MFTI), and his Ph.D. in Evolutionary Biology in 1997 from Harvard University with Daniel Hartl and Richard Lewontin. He was a Junior Fellow at the Harvard Society of Fellows and a Research Fellow in the Genetics Department at Harvard Medical School. Professor Petrov joined the Stanford faculty in 2000. At Stanford, Professor Petrov has been honored with several faculty awards, including the Terman Fellowship, the Hellman Faculty Award, and the Chambers Fellowship. Professor Petrov is a founding member of the Executive Committee for the new Stanford Center for Computational, Evolutionary and Human Genomics.

Speaker Biographies

Pritchard
Jonathan Pritchard is a Professor of Genetics and Biology at Stanford University and an Investigator at the Howard Hughes Medical Institute. He received his PhD in Biology from Stanford in 1998, where he worked with Marc Feldman. He subsequently moved to a postdoc in Statistics at Oxford with Peter Donnelly, and was a member of the faculty at the University of Chicago from 2001-2013. His work focuses on questions relating to genetic variation and evolution, including questions about population structure, population history and natural selection and the impact of genetic variation on phenotypic variation.

Quake
Stephen Quake studied physics (BS 1991) and mathematics (MS 1991) at Stanford University, after which he earned a doctorate in theoretical physics from Oxford University (1994) as a Marshall Scholar. He then returned to Stanford University, where he spent two years as a post- doc in Steven Chu's group. Quake joined the faculty of the California Institute of Technology in 1996, where he rose through the ranks and was ultimately appointed the Thomas and Doris Everhart Professor of Applied Physics and Physics. At Caltech, Quake received "Career" and "First" awards from the National Science Foundation and National Institutes of Health and was named a Packard Fellow. These awards supported a research program that began with single molecule biophysics and soon expanded to include the inventions of single molecule sequencing and microfluidic large scale integration, and their applications to biology and human health. He moved back to Stanford University in 2005 to help launch a new department in Bioengineering, where he is now the Lee Otterson Professor and an investigator of the Howard Hughes Medical Institute.

Rosenberg
Noah A. Rosenberg is Associate Professor in the Department of Biology at Stanford University. His research group studies problems in evolutionary biology and genetics through mathematical modeling, computer simulation, development of statistical methods, and inference from population-genetic data. Prof. Rosenberg's areas of interest include human evolutionary genetics, mathematical phylogenetics, theoretical population genetics, and the relationship of human evolution to the search for disease genes. Research from his laboratory has examined such topics as the connection between gene genealogies and species trees, the mathematical properties of statistics used in population genetics, and the inference of human evolutionary history from genetic markers. Prof. Rosenberg is the recipient of several awards for his work, including the Lancet Biomedical Research Paper of the Year award for his 2002 article "Genetic structure of human populations." He received his BA in mathematics from Rice University in 1997, his MS in mathematics from Stanford University in 1999, and his PhD in biology from Stanford University in 2001. Prof. Rosenberg previously served on the faculty of the University of Michigan.

Speaker Biographies

Sabatti Chiara Sabatti studied economics and statistics in Italy, at the Bocconi University in Milan. She earned a PhD in Statistics at Stanford, where she was also a post-doctoral fellow in the Genetics department. She has spent 9 happy years on the faculty at UCLA in the departments of Human Genetics and Statistics and has moved back to Stanford in 2009, where she is currently an Associate Professor of Biostatistics and Statistics. Chiara's research focuses on genetics and genomics: she develops models and algorithms for the analysis of high-throughput data with the broad goal of understanding how the cell selectively and dynamically uses the information coded in DNA and how this translates in phenotypes of medical relevance. She enjoys teaching, and finds that the history of statistics and genetics are full of "learning opportunities." She lives on campus with her family.

Upcoming Evolgenome Talks

Come to the Center's weekly presentations on evolutionary research.

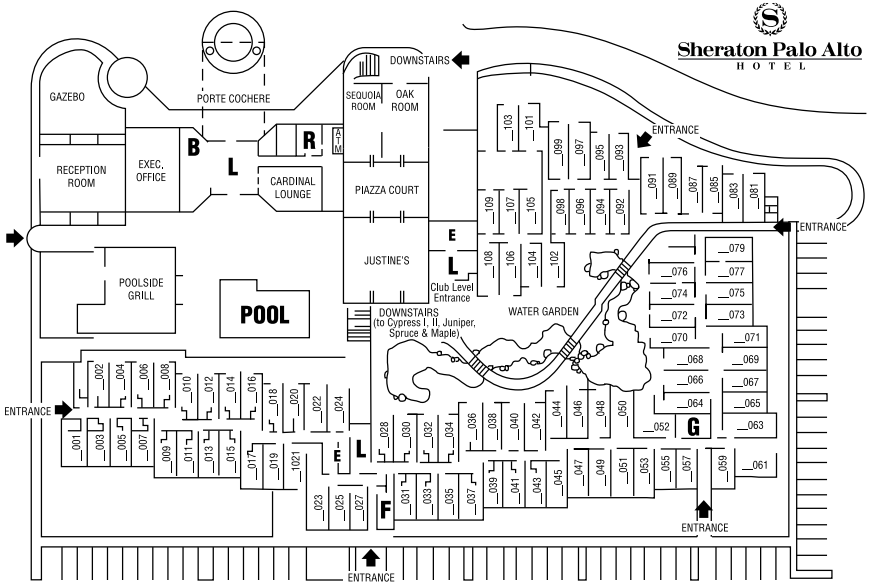|	
22 Jan 2014	Yang Li, Oxford University
27 Jan 2014	Roy Ronen, UCSD
5 Feb 2014	David Golan, Tel-Aviv University
12 Feb 2014	Dennis Wall
19 Feb 2014	Olga Sazonova, Montgomery/Quertermous Lab
26 Feb 2014	Eilon Sharon, Pritchard/Fraser Lab

Funding Oppportunities

The Stanford Center for Computational, Evolutionary and Human Genomics (CEHG) is now accepting applications for the 2014 Fellowship Program, Trainee Research Grants, and Faculty Small Grants. Please visit our website cehg.stanford.edu for more information.

Notes

Stanford Center for Computational, Evolutionary and Human Genomics

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Sheraton Palo Alto
H O T E L

GAZEBO

PORTE COCHERE

DOWNSTAIRS

SEQUOIA ROOM OAK ROOM

ENTRANCE

RECEPTION ROOM

EXEC. OFFICE

B

L

R

ATM

CARDINAL LOUNGE

PIAZZA COURT

103 101
099 097 095 093
091 089 087 085 083 081

JUSTINE'S

E

L

109 107 105 098 096 094 092
108 106 104 102
Club Level Entrance

POOLSIDE GRILL

POOL

DOWNSTAIRS
(to Cypress I, II, Juniper, Spruce & Maple)

WATER GARDEN

_079
_076 _077
_074 _075
_072 _073
_070 _071
_068 _069
_066 _067
_064 _065

ENTRANCE

ENTRANCE

002 004 006 008
010 012 014 016 018 020 022 024
001 003 005 007 009 011 013 015 017 019 021

E **L**
028 030 032 034 036 038 040 042 044 046 048 050 052 **G** _063
_059 _061

023 025 027 **F** 031 033 035 037 039 041 043 045 047 049 051 053 055 057

ENTRANCE

ENTRANCE

E = ELEVATOR **L** = LOBBY **G** = GUEST LAUNDRY **F** = FITNESS ROOM **R** = RESTROOM **B** = BUSINESS CTR/GIFT SHOP

Cover photo Linda Cicero / Stanford University News Service