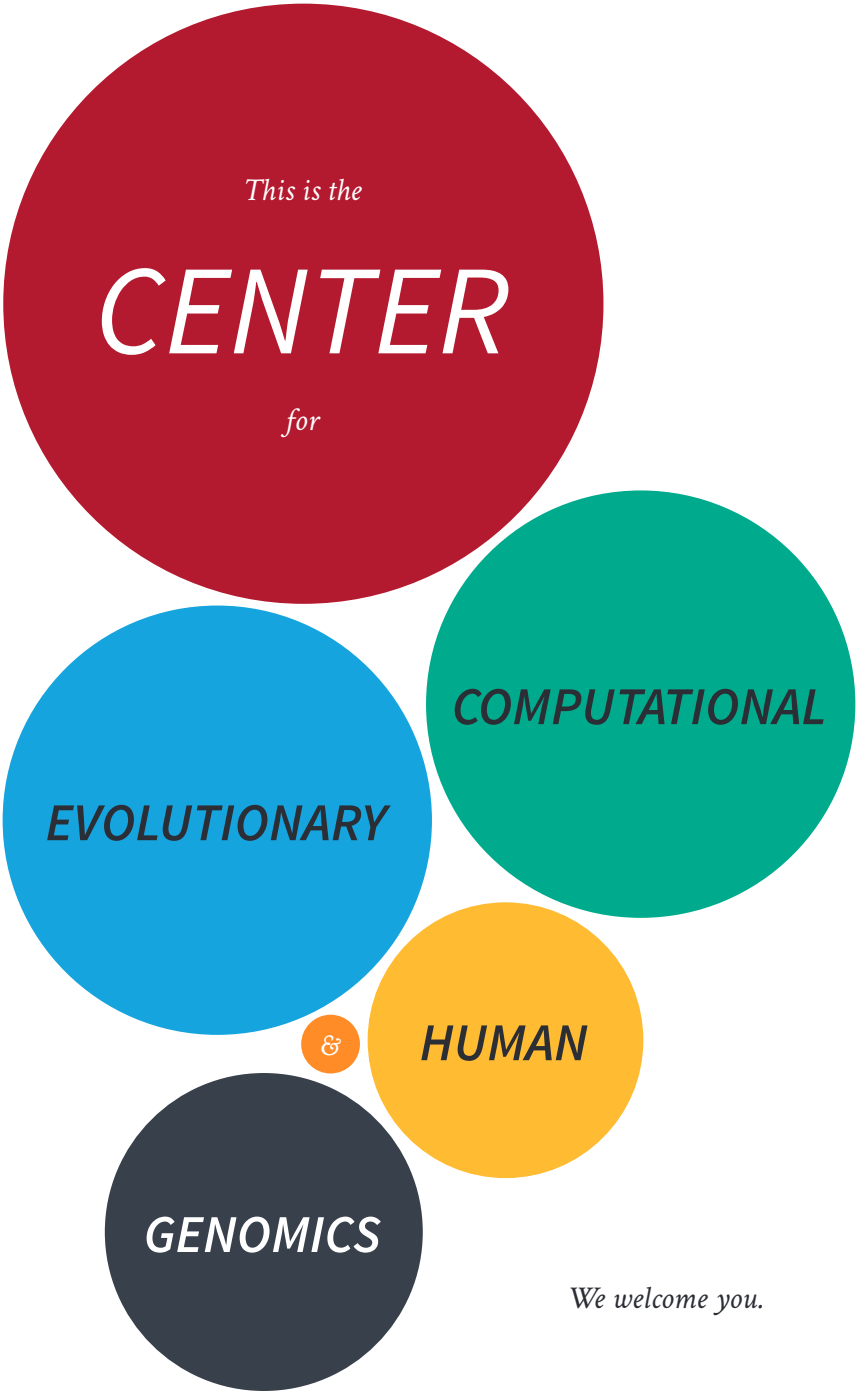
CEHG *Symposium*

Stanford Center for Computational Evolutionary and Human Genomics

presents

Genetics & Society Symposium 2015

Paul Brest Hall
April 13-14, 2015



We welcome you.

#gss15

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ABOUT THE CENTER

Stanford's Center for Computational, Evolutionary and Human Genomics (CEHG) is an interdisciplinary research program that is the intellectual home of 35 professors and over 200 postdoctoral scholars and graduate students. CEHG provides fellowships to researchers as they transition from graduate to postdoctoral studies and offers grants to trainees whose interests extend beyond their lab's domain. The Center also has research projects of its own: the largest focuses on the insights that the Y-chromosome offers into the origins of modern populations. Finally, CEHG sponsors renowned conferences, including Why We Can't Wait (WWCW), which aims to eliminate health disparities in genomic medicine.

ABOUT THE EVENT

The Center is proud to present the Genetics and Society Symposium 2015 (GSS15). The symposium aims to highlight current research from CEHG-affiliated Stanford labs and enable interactions between the CEHG community and the scientific genetics community at large. The first day, Monday, April 13th, will include presentations from guest speakers and CEHG faculty, a poster session, and an evening reception. The second event day, Tuesday, April 14th, will feature morning workshops as well as additional presentations from guest speakers and CEHG affiliates.

LOGISTICS

Registration is in the Paul Brest Hall foyer, talks are in Paul Brest Hall, workshops are in Jacobson Sorenson Hall, and the poster session/reception is in Rehnquist Courtyard. All are located in the Munger Housing Complex, with the following address: 555 Salvatierra Way, Stanford, CA 94305.

Parking Structure 6 (PS6) offers visitor pay and permit parking close to Munger Complex. PS6 is located at 560 Wilbur Drive, Stanford, CA 94305.

Please note that workshops are restricted to people who registered ahead of time on Eventbrite. The statistical genetics workshop will take place in room 123 of Jacob Sorensen Hall. The science writing workshop will take place in room 142 of Jacobson Sorenson Hall.

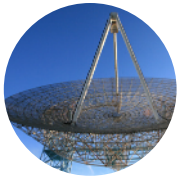
Tweet with us! Want to share your experience at the symposium with your friends on Twitter? Use our hashtag #gss15 and tweet us at @StanfordCEHG. Also, you can follow our designated tweeters, Rajiv McCoy at @rajivmccoy and Jeremy Hsu at @Hsubox.

If you have any questions or concerns at the event, please feel free to stop by the CEHG registration table or ask anyone wearing a blue "Organizing Committee" ribbon. Planning committee members and symposium volunteers will be ready to help you in any way we can. When you return your name badge, don't forget to submit a feedback form.

MONDAY OVERVIEW

8:00am	*Breakfast*
9:00am	Introduction by Director Carlos Bustamante
9:10am	**DNAnexus Keynote: Gene Myers**
10:10am	Devaki Bhaya
10:40am	Nicolas Alcala, Fellow
11:00am	Stephen Montgomery
11:30am	Natasha O'Brown, Fellow
11:50am	*Lunch*
1:00pm	**Keynote: Ed Green**
2:00pm	Julia Salzman
2:30pm	Rachel Goldfeder, Fellow
2:50pm	*Break*
3:10pm	**Keynote: Michelle Mello**
3:50pm	Anna Rychkova, Fellow
4:10pm	Mike Cherry
4:40pm	Oren Kolodny, Fellow
5:00pm	*Reception and Poster Session*

TUESDAY OVERVIEW



8:00am	*Breakfast (Workshop registration required)*
9:00am	Workshops (Registration required)
10:30am	Dennis Wall
11:00am	Mike Snyder
11:30am	Stuart Kim
12:00am	*Lunch*
1:00pm	**Keynote: Ami Bhatt**
1:40pm	Susan Holmes
2:10pm	Rachael Bay, Fellow
2:30pm	Christopher McFarland, Fellow
2:50pm	*Break*
3:20pm	Carlos Bustamante
3:50pm	Kathy Xie, Fellow
4:10pm	Josh Knowles
4:40pm	Closing Remarks by Director Marc Feldman
5:00pm	*Faculty Reception*

SESSION ONE

9:00 - 12:00PM MONDAY, APRIL 13

Symposium Introduction by **Carlos Bustamante**

DNAnexus Keynote: "The Resurrection of *de novo* DNA Sequencing" **Gene Myers**

"Diversity and conflict in microbial communities" **Devaki Bhaya**

"Measuring the genetic differentiation of populations: What the most commonly used statistics do and do not tell us" **Nicolas Alcala**

"Rare regulatory variation in human families" **Stephen Mongomery**

"Searching for the Molecular Basis of Human Brain Expansion" **Natasha O'Brown**

DNAnexus®
The Global Network For Genomic Medicine™

SESSION ONE BIOS

Carlos Bustamante

Dr. 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. From 2002-2009, he was on the faculty at Cornell University in the Departments of Statistical Sciences and Biology Statistics and Computational Biology where he was promoted to full professor in 2008. 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 a Marshall-Sherfield Fellowship (2001-2), the Sloan Research Fellowship (2007), and a John D. and Catherine T. MacArthur Fellowship (2010). He is one of the Principal Investigators of the recently announced $25M ClinGen project to build the country's National Database of Clinically Relevant Genomic Variants.

Gene Myers

Dr. Gene Myers is the founding director of a new Systems Biology Center at the Max-Planck Institute of Molecular Cell Biology and Genetics. Previously, he served as a group leader at the HHMI Janelia Farm Research Campus, a faculty member at U.C. Berkeley and the University of Arizona, and Vice President of Informatics Research at Celera Genomics. Voted the most influential in bioinformatics in 2001 by Genome Technology Magazine, Dr. Myers has received numerous awards, including the ACM Kanellakis Prize in 2002 and the International Max-Planck Research Prize in 2004. In 2006, he was inducted into Leopaldina, the German Academy of Science.

Dr. Myer's research interests include the design and analysis of algorithms for problems in computational molecular

biology, bioimage analysis and light microscopy with a focus on building models of the cell and cellular systems from imaging data. He is best known for: the development of BLAST, the most widely used tool in bioinformatics; the paired-end whole genome shotgun sequencing protocol; and the assembler he developed at Celera that delivered the fly, human and mouse genomes in a three-year period.

Devaki Bhaya

Dr. Devaki Bhaya is a research scientist in the Department of Plant Biology at the Carnegie Institution of Science with a courtesy appointment in the Department of Biology at Stanford University. Her research interests focus on cyanobacteria, an ancient and important phylum of photosynthetic microorganisms. Currently, she is working on the genomic diversity of phototrophic microbial communities in extreme environments and their response to stressors and phages. She also has a longstanding interest in dissecting and modeling the complex signaling and biochemical networks that govern phototaxis in microbes.

Nicolas Alcala

Dr. Nicolas Alcala is a postdoctoral researcher in Noah Rosenberg's lab at Stanford. He received his Master's degree in Bioinformatics and Modelling from The National Institute of Applied Sciences (INSA) in Lyon, France and his Ph.D in Biology from the University of Lausanne, Switzerland. During his Ph.D, he investigated the transient impact of changes of population structure on patterns of genetic diversity. Dr. Alcala is now working on the development of statistical methods for the interpretation of population genetic data. In particular, he investigates the properties, interpretation and uses of genetic differentiation statistics.

SESSION ONE BIOS

Stephen Montgomery

Dr. Stephen Montgomery is Assistant Professor of Pathology, Genetics and, by courtesy, Computer Science at Stanford. His research focuses on applying innovative data in genomics and methods in computer science to understand how genetic variation influences genome function to define disease. His work was among the first genetics of gene expression studies using RNA-sequencing and the first with comparisons to full genomes.

Natasha O'Brown

After receiving her B.S. degree in Biology from Davidson College in 2010, Natasha O'Brown moved to the Developmental Biology Department at Stanford for her Ph.D. studies. For her thesis work in David Kingsley's lab, Natasha has used genetic and genomic approaches to both stickleback fish and laboratory mice, identifying specific molecular events contributing to vertebrate evolution. Her work identifying the DNA base pair changes responsible for repeated armor plate evolution in sticklebacks was recently published in eLIFE. After completing her graduate work this summer, Natasha plans to begin studying the molecular basis of blood brain barrier development as a postdoc in Chenghua Gu's lab at Harvard.

SESSION TWO

1:00 - 5:00PM MONDAY, APRIL 13

Keynote: "A simple approach for highly contiguous genome assemblies" **Ed Green**

"Dynamic expression of circular RNA revealed by statistically based splicing detection" **Julia Salzman**

"Clinical Genome Sequencing: Challenges and Opportunities" **Rachel Goldfeder**

Keynote: "Data Sharing: What Might the Future Hold?" **Michelle Mello**

"Improving Computational Prediction of Missense Variants Pathogenicity for Clinically Relevant Genes" **Anna Rychkova**

"Do you have everything you need? How do you know?" **Mike Cherry**

"Evolution in leaps: the stepwise accumulation of cultural innovation" **Oren Kolodny**

SESSION TWO BIOS

Ed Green

Dr. Richard (Ed) Green was born in 1972 in Atlanta, Georgia. He graduated from the University of Georgia with a BS in Genetics in 1997 and then taught math in the Peace Corps in Barentu, Eritrea. He did his PhD with Steven Brenner at the University of California, Berkeley and worked on alternative splicing and sequence analysis methods. He was an NSF Fellow in Biological Informatics with Svante Paabo at the Max Planck Institute in Leipzig, Germany. During this time, he headed the analysis consortium responsible for publishing the draft genome sequence of Neanderthal.

Since 2010, Dr. Green has been Assistant Professor in Biomolecular Engineering at UC Santa Cruz. His current research interests include genome sequencing, assembly, sex-determination, ancient DNA, forensics and human evolution.

Julia Salzman

Dr. Julia Salzman is an Assistant Professor of Biochemistry. As a post-doc, she used statistical methods to discover that circular RNA is a ubiquitous product of eukaryotic gene expression and constitutes the major isoform in hundreds of human genes. Her research focuses on circular RNA and developing novel statistical, bioinformatic and experimental methods to quantify RNA structural variation and its regulation. She has been named a Sloan Fellow and is the recipient of a Baxter Faculty award and a Howard Temin Pathway to Independence Award from the NIH.

SESSION TWO BIOS

Rachel Goldfeder

Rachel Goldfeder is an NSF and CEHG fellow in the Biomedical Informatics PhD Program who is interested in applications of genomics to medicine. Before coming to Stanford, she earned her bachelor's degree in Biomedical Engineering from Washington University in St. Louis and then continued her training at the National Human Genome Research Institute (NHGRI). Currently, Rachel is working in Dr. Euan Ashley's lab, developing methods for medical-grade variant detection with the long-term goal of enabling personalized genomic medicine.

Michelle Mello

Dr. Michelle Mello is Professor of Law at Stanford Law School and Professor of Health Research and Policy at Stanford University School of Medicine. She conducts empirical research into issues at the intersection of law, ethics and health policy. She is the author of more than 140 articles and book chapters on the medical malpractice system, medical errors and patient safety, public health law, research ethics, the obesity epidemic, pharmaceuticals, and other topics.

From 2000 to 2014, Dr. Mello was a professor at the Harvard School of Public Health, where she directed the Program in Law and Public Health. She currently serves as a Key Consultant to the National Program Office of the Robert Wood Johnson Foundation's Public Health Law Research Program. In 2013, she was elected to the Institute of Medicine.

Anna Rychkova

Dr. Anna Rychkova joined Carlos Bustamante's Stanford lab as a postdoctoral fellow in September 2013. Previously, she received her training in biophysics (with an MS in Biophysics from Lomonosov Moscow State University) and computational

chemistry (with a PhD in Chemistry from the University of Southern California). Dr. Rychkova is particularly interested in human genetics and its application to human health and personalized medicine. She is currently working on the ClinGen project, where she uses information about protein structure to improve methods for variant pathogenicity assessment.

Mike Cherry

Dr. Mike Cherry came to Stanford Genetics in 1993. He directs a group of Scientific Biocurators, Software Engineers, Data Wranglers and Bioinformatic Analysts that serve the biological research and teaching communities via public resources. The Cherry lab maintains SGD and Gene Ontology as premier resources, provides manually curated gold standard annotations, creates and maintains the ENCODE Portal with association programmatic submission systems, and creates tools for curation and Portal interfaces for the newly funded ClinGen Project.

Oren Kolodny

Dr. Oren Kolodny is a postdoc in Marc Feldman's lab. He studies the joint evolution of the microbiome and its host, focusing on adaptations that are brought about by changes to the microbiome on an evolutionary timescale. He also works on other topics, such as the accumulation of culture by hominids. Oren studied physics and molecular evolution in the Hebrew University and did his PhD in Tel Aviv University, exploring the evolution of learning mechanisms. Outside of his academic life, Dr. Kolodny has been involved in the establishment of a breeding center for endangered amphibians and is father to an exceptionally cute toddler.

SESSION THREE

9:00 - 12:00PM TUESDAY, APRIL 14

Workshop (Registration Required): "Science, Stories, and Society: Science writing for non-science audiences" **Thomas Hayden**

Workshop (Registration Required): "Contemporary problems in statistical genetics" **Kenneth Lange** and **Chiara Sabatti**

"Machine learning and big data to decode autism" **Dennis Wall**

"What makes us different: Variation in regulatory information among humans" **Mike Snyder**

"Genetics of Extreme Human Longevity" **Stuart Kim**

SESSION THREE BIOS

Thomas Hayden

Thomas Hayden teaches science and environmental communication in Stanford University's School of Earth, Energy and Environmental Sciences. He has been an oceanographer, a staffer at Newsweek, and a senior editor at US News & World Report. His cover stories have appeared in Wired, National Geographic, Smithsonian, and many other publications. He is coauthor of *On Call in Hell*, a national bestseller about battlefield medicine, and *Sex and War*, about the biological and social evolution of warfare. He is coeditor of *The Science Writer's Handbook: Everything You Need to Know to Pitch, Publish, and Prosper in the Digital Age.*

Kenneth Lange

Dr. Kenneth Lange is the Rosenfeld Professor of Computational Genetics and Chair of the Department of Human Genetics at the University of California, Los Angeles. He previously served as chair of the UCLA Department of Biomathematics. From 1994 to 1998, he was Professor of Biostatistics and Mathematics and the Pharmacia & Upjohn Foundation Research Professor at the University of Michigan. He has authored four advanced textbooks and published more than 200 scientific papers in the areas of genetic epidemiology, population genetics, membrane physiology, demography, oncology, medical imaging, stochastic processes, and optimization theory. Many of his landmark papers predate, by a decade or more, the current flood of biological applications of hidden Markov chains, Markov chain Monte Carlo and high-dimensional optimization.

SESSION THREE BIOS

Chiara Sabatti

Dr. Chiara Sabatti grew up in Italy, where she attended Liceo Classico Arnaldo in Brescia, and obtained a master's degree in "Economics and Social Sciences" (DES) from the Luigi Bocconi University in Milan in 1993. Her final research project, supervised by Eugenio Regazzini, was on applications of finite exchangeability to population sampling. In the same year, she was awarded a Bocconi Fellowship for advanced studies. She came to Stanford in 1994 to pursue a PhD in Statistics, and worked with Jun Liu on multiscale MCMC methods. Between 1998 and 2000 she was a post-doctoral scholar with Neil Risch in the Department of Genetics, also at Stanford. In 2000, she joined the facutly at UCLA in the newly established departments of Human Genetics and Statistics. She received the NSF Career award in 2003. Dr. Sabatti now leads a research group housed in the Biostatistics and Statistics Departments at Stanford, and pursues her interest in the statistical challenges presented by high-throughput genomics data.

Dennis Wall

Dr. Dennis Wall is Associate Professor in the Department of Pediatrics and the Division of Systems Medicine at Stanford, where his lab is developing novel approaches in systems biology to decipher the molecular pathology of autism spectrum disorder and related neurological conditions. He is the recipient of numerous awards, including the Fred R. Cagle Award for Outstanding Achievement in Biology, the Vice Chancellor's Award for Research, three awards for excellence in teaching, the Harvard Medical School Leadership award, and the Slifka/Ritvo Clinical Innovation in Autism Research Award for outstanding advancements in clinical translation.

SESSION THREE BIOS

Mike Snyder

Dr. Mike Snyder is the Ascherman Professor and Chair of the Stanford Genetics Department and the Director of the Center of Genomics and Personalized Medicine. He is a leader in the field of functional genomics and proteomics and one of the major participants of the ENCODE project. Seminal findings from the Snyder lab include the discovery that much more of the human genome is transcribed and contains regulatory information than was previously known and a high diversity of transcription factor binding occurs between and within species. Dr. Snyder has also combined different state-of–the-art "omics" technologies to assess disease risk and monitor disease states for personalized medicine.

Stuart Kim

Dr. Stuart K. Kim is Professor of Developmental Biology and Genetics at Stanford University. His research interests include functional genomics and aging. He has recently used genome-wide analyses to look at the process of aging in both C. elegans and humans. In worms, he found that aging is caused by drift of a transcriptional network. In humans, Dr. Kim has sequenced the genomes of the world's oldest people.

SESSION FOUR

1:00 - 5:00PM TUESDAY, APRIL 14

Keynote: "Bugs, drugs, and cancer" **Ami Bhatt**

"Statistical and Computational Challenges from the Human Microbiome" **Susan Holmes**

"The genomic basis of thermal tolerance in reef-building corals" **Rachael Bay**

"Measuring the effects of deleterious passengers in mice models and cancer genomics" **Christopher McFarland**

"Opportunities and challenges in population genomics and human identification" **Carlos Bustamante**

"DNA fragility and adaptive evolution in natural populations" **Kathleen Xie**

"Identification and characterization of NAT2 as an insulin resistance gene" **Joshua Knowles**

Closing Remarks by **Marc Feldman**

SESSION FOUR BIOS

Ami Bhatt

Dr. Ami Bhatt is an Assistant Professor of Medicine and Genetics at Stanford University. She received her MD and PhD (Biochemistry & Molecular Biology) at UCSF and completed residency, chief residency and Hematology/Oncology at Brigham and Women's Hospital and Dana-Farber/Partners Cancer Center. Thereafter, she carried out her post-doctoral studies at MIT and the Broad Institute of Harvard.

Dr. Bhatt seeks to improve outcomes in patients with hematological malignancies by exhaustively characterizing the dynamics of the microbiome in immunocompromised individuals and exploring how changes in the microbiome are associated with idiopathic diseases in this population. Her recent work, demonstrating the discovery of a novel bacterium using sequence-based analysis of a diseased human tissue, has been presented nationally and internationally and was published in 2013 in the New England Journal of Medicine.

Susan Holmes

Dr. Susan Holmes is Professor of Statistics and a BioX faculty member at Stanford. She specializes in visualization and analysis of complex biological multi-table data and works on integrating image data and covariates in the context of the longitudinal study of the human brain, ant interaction networks, and studies of the immune system. She recently received an NIH High Risks, High Rewards grant with David Relman for the study of Resilience in the Human Microbiome. She is wedded to the principles of Reproducible Research, makes all her work available as R packages and teaches the BIOS 221 summer crash course: Modern Statistics for Modern Biology using BioConductor.

SESSION FOUR BIOS

Rachael Bay

Dr. Rachael Bay recently completed her PhD in Steve Palumbi's lab at Hopkins Marine Station. Her general research interests center around how human activities alter the evolutionary trajectories of organisms and how we can use this type of information to inform conservation plans. She received a bachelor's degree from the University of Miami and a master's degree in computational biology from Dalhousie University in Nova Scotia. For her dissertation, she investigated the evolutionary and physiological determinants of heat tolerance in reef-building corals.

Christopher McFarland

Dr. Christopher McFarland obtained his PhD in Biophysics from Harvard University in 2014, where he developed evolutionary models of cancer progression and incorporated the effects of deleterious passengers. Under the guidance of Professor Dmitri Petrov in the Department of Ecology, Evolution and Conservation at Stanford, Dr. McFarland is continuing his efforts, in several burgeoning projects, to understand cancer from an evolutionary perspective.

Kathy Xie

Kathy Xie grew up in Boston and attended MIT. There, she worked in David Bartel's lab and helped establish that RNAi is prevalent in budding yeasts, even though our favorite model species, Saccharomyces cerevisiae, has lost the ability to do RNAi. She developed an interest in the gain and loss of traits in natural populations and, once at Stanford, joined the lab of David Kingsley to study evolution, using stickleback fish. Today, she will talk about how variation in mutagenic processes may affect the path of evolution.

SESSION FOUR BIOS

Joshua Knowles

Dr. Joshua W. Knowles obtained his MD-PhD at the University of North Carolina while working in the lab of Nobuo Maeda and (Nobel Laureate) Oliver Smithies. He completed his Internal Medicine and Cardiovascular Medicine training at Stanford. For the last several years, his work has focused on using large-scale genomic studies to identify the genes associated with complex cardiovascular conditions including insulin resistance. The ultimate goal is to understand the genes and gene networks that underlie insulin resistance, thereby leading to new therapeutic possibilities. The American Heart Association and the NIH have funded his research and he has over 65 publications broadly related to genetics and cardiovascular disease.

Marcus Feldman

Dr. 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. 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.

Dr. Feldman is a fellow of the American Academy of Arts and Sciences and of the California Academy of Science. He has written more than 335 scientific papers and four books on evolution, ecology, and mathematical biology. He received a BSc in mathematics and statistics from the University of Western Australia, an MSc in mathematics from Monash University (Australia), and a PhD in mathematical biology from Stanford. He has been a member of the Stanford faculty since 1971.

ORGANIZING COMMITTEE

Bridget Algee-Hewitt

Dr. Bridget Algee-Hewitt is a biological anthropologist and CEHG Postdoctoral Fellow in the Rosenberg Lab in the Department of Biology at Stanford. Her research focuses on the study of human biological variation at the global scale and the estimation of the key parameters of identity in individual forensic case analysis. She is especially interested in the inference of geographic ancestry from skeletal and genetic data. Dr. Algee-Hewitt is strongly committed to social justice work and has an active research program on genetic variation among undocumented migrant populations.

Anand Bhaskar

Dr. Anand Bhaskar is a postdoctoral fellow in the Department of Genetics at Stanford University, where he develops and applies rigorous methods from computer science, applied mathematics, and statistics to challenging problems in evolutionary biology and population genetics. He received a Ph.D. in Computer Science and an M.A. in Statistics, both from the University of California, Berkeley, and M.Eng. and B.S. degrees in Computer Science from Cornell University. His research has been supported by a Berkeley fellowship, a Simons-Berkeley Fellowship, a JSPS Postdoctoral Fellowship, and a Stanford CEHG Postdoctoral Fellowship.

Yang Li

Dr. Yang Li is a postdoctoral scholar in the Department of Genetics. Advised by Professor Jonathan Pritchard, Dr. Li works on population genomics with a special focus on gene regulation. Previously, he was at the University of Oxford where he studied evolutionary genomics with Professor Chris Ponting. Outside work, he enjoys rock climbing and cooking.

ORGANIZING COMMITTEE

Katie Kanagawa

Dr. Katie M. Kanagawa is the Communications Coordinator for Stanford's Center for Computational, Evolutionary and Human Genomics and Administrative Associate in the Bustamante Lab. She received her Ph.D. in Literature from the University of California, Santa Cruz in 2009 and worked as a lecturer and adjunct faculty member in the Department of Women and Gender Studies at San Francisco State University. Before joining the Stanford community, she worked on the Communications team of San Francisco-based nonprofit organization, Breast Cancer Action.

Cody M. Sam

Cody M. Sam is the Business Manager for the Stanford Center for Computational, Evolutionary and Human Genomics and Bioinformatics Coordinator for the Clinical Genomics Resource Consortium (ClinGen). He joined the Center in 2013 after graduating from Stanford with a B.S. in Chemistry. When he is not working, Cody enjoys traveling and spending time at home in New Orleans.

SPECIAL THANKS

The GSS15 Organizing Committee would like to thank everyone who helped us plan this event: Directors Carlos Bustamante and Marcus Feldman, the CEHG Executive Committee, Chris Gignoux, Alexandra Adams, Maude David, Angela Anderson, Trish Gilfoil, Serafim Batzoglou, Rajiv McCoy, and Jeremy Hsu.

NOTES

NOTES

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Stanford Center for Computational, Evolutionary and Human Genomics

VENUE

Paul Brest Hall
555 Salvatierra Way
Stanford, CA 94305

PARKING

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MAP