18th Annual Biomedical Computation at Stanford Symposium

Stanford University

April 19, 2018

2018 University Sponsors

STANFORD BIO-X

Stanford | BIOENGINEERING

Stanford
Cancer Institute

Stanford | MEDICINE

STANFORD CSB

bmi

CEHG

CCB | CENTER FOR COMPUTATIONAL BIOLOGY

2018 Corporate Sponsors

AncestryDNA

BCATS Symposium Schedule

Thursday April 19, 2018 | Li Ka Shing Center, Paul Berg Hall (2nd floor)
For event details and a list of our 2018 sponsors, please visit: **www.bcats.stanford.edu**

Session 1

8:30 AM **Sign-in & Breakfast**

9:00 AM **Opening Remarks**

9:15 AM **Keynote Address: Nathan Price, PhD**

Institute of Systems Biology
Mining personal, dense, dynamic data clouds to enhance health and drive discovery

10:00 AM **Emily Flynn**

Meta-analysis of sex-differential gene expression in human liver

10:15 AM **Erika Bongen**

KLRD1 expressing NK cells may protect against influenza infection

10:30 AM **Coffee Break**

Session 2

10:45 AM **Pratheepa Jeganathan**

The block bootstrap method for longitudinal microbiome data

11:00 AM **Boxiang Liu**

Genetic regulatory mechanisms of smooth muscle cells map to coronary artery disease risk loci

11:15 AM **Keynote Address: Jason Ernst, PhD**

University of California, Los Angeles
Computational approaches for interpreting the epigenome and non-coding genome

12:00 PM **Lunch**

Session 3

1:00 PM **Keynote Address: Priya Moorjani, PhD**

University of California, Berkeley
Genetic insights into South Asian population history and disease

1:45 PM **Winn Haynes**

Gene annotation bias impedes biomedical research

2:00 PM **David Gokhman**

Reconstructing Denisovan anatomy using DNA methylation maps

2:15 PM **Keynote Address: Ryan Hernandez, PhD**

University of California, San Francisco
How evolutionary forces shape the genetic architecture of complex traits

3:00 PM **Snack Break**

Session 4

3:15 PM **Industry Panel**

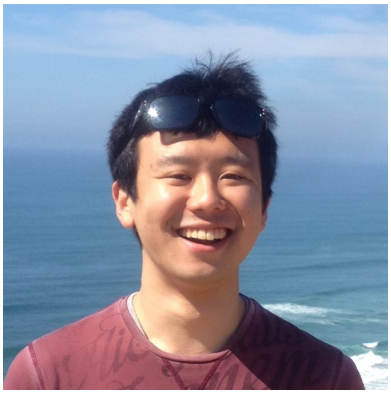
- 3T Biosciences: Dr. Marvin Gee
- AncestryDNA: Drs. Eurie Hong, Natalie Telis
- Cardinal Analytx Solutions: Drs. Brian Maples, Joe Davis
- IBM: Dr. Ban Kawas

4:00 PM **Closing Remarks**

4:15 PM **Poster Session & Happy Hour**

Paul Berg Hall, Room A

About Us



Yosuke Tanigawa
2nd year, Biomedical Informatics
Rivas & Bejerano Labs

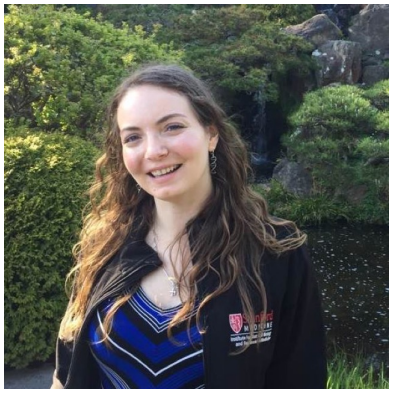
Yosuke is a 2nd year Ph.D. student in Biomedical Informatics Training Program after he received BS in Bioinformatics and Systems Biology from University of Tokyo. He is jointly advised by Dr. Manuel Rivas and Dr. Gill Bejerano and working on methods development for large-scale human genetics dataset. He enjoys swimming, running, and playing the piano.

Nicole Ferraro
2nd year, Biomedical Informatics
Montgomery Lab

Nicole received a dual BS/MS in Biomedical Engineering from Drexel University in Philadelphia, PA in 2016. She is currently a second year in the Stanford Biomedical Informatics training program. As a member of the Montgomery Lab, Nicole works on methods development to understand the genetic influences underlying gene expression, and incorporate multi-omics data modalities to characterize the impact of rare variation. She enjoys running, vegetarian cooking, and exploring new cities.

Irene Li
2nd year, Cancer Biology
Plevritis Lab

Irene is a second-year in the Cancer Biology program and received her bachelors in Molecular Genetics and Global Public Health at Michigan State University. She investigates metabolic shifts and progressions in the tumor microenvironment in the Plevritis Lab. Shes an avid painter, piano & ukulele player, and hiker.



Samantha Piekos
3rd year, Stem Cell Biology & Regenerative Medicine
Oro Lab

Samantha received her BS in Biological Sciences and Psychology from the University of Notre Dame. Currently, she is a third year PhD student in the Stem Cell Biology & Regenerative Medicine and is advised by Dr. Anthony Oro. Her research focuses on understanding how the chromatin landscape changes during early skin differentiation. In her free time, Samantha enjoys spending time outdoors whether it be hiking or traveling. She also enjoys rock climbing and is an avid cook.

Lawrence Bai
2nd year, Immunology
Habtezion & Khatri Labs

Lawrence graduated with a BS in Microbial Biology from UC Berkeley in 2016 before joining the Immunology Program at Stanford University. He is currently in his second year, where he works on better understanding inflammatory bowel disease from a systems biology perspective. He is jointly advised by Dr. Aida Habtezion and Dr. Purvesh Khatri. In his spare time, Lawrence enjoys going on food adventures with his friends, whether it be exploring new restaurants or cooking at home. He also enjoys listening to music and traveling around the world to better understand other cultures (including cuisines, language, and customs).

Gautam Machiraju
Incoming 1st year, Biomedical Informatics
Mallick Lab

Gautam is an incoming Ph.D. Student in the Biomedical Informatics program after receiving his B.A. in Applied Mathematics from University of California, Berkeley. Under the mentorship of Dr. Parag Mallick, he currently works on mathematical models of biomarker shedding kinetics in early-stage tumors, NLP of PubMed biomarker dark data, and deep learning of multi-omic time-series patient profiles. He enjoys Bay Area events, camping trips, and traveling on a budget.

Organizer Remarks

We are proud to host and have you here at the 18th annual symposium for Biomedical Computation at Stanford (BCATS). Every year, members of the organizing committee and our generous sponsors provide a platform for scientific interaction between students, faculty and members of the industry involved in solving computational problems in biology, biomedicine, and healthcare. In the past, our affiliates and attendees have been involved in some of the most cutting edge discoveries and technologies that continue to drive great breakthroughs in these fields and beyond. This year, our participants include students and faculty from Stanford University, UC San Francisco, UC Berkeley, UC Los Angeles, UC Santa Cruz, and University of Washington. Our keynote speakers will be speaking on topics such as Personalized Medicine, Systems Regulomics, and Population & Statistical Genetics, with overarching themes in Data Mining, Machine Learning and computational methods development. Our industry panel includes esteemed speakers from a mix of the Bay Area's dynamic startups and biotech giants including 3T Biosciences, Cardinal Analytx Solutions, AncestryDNA, and IBM. We are generously supported by various departments within Stanford, the Li Ka Shing Center for Learning and Knowledge and also our industry affiliates in the Bay Area.

Your organizing committee,

Nicole Ferraro, Lawrence Bai, Irene Li, Gautam Machiraju, Samantha Piekos, Yosuke Tanigawa

Keynote Speakers

Nathan Price, PhD
Professor & Associate Director
@ *Institute of Systems Biology*
Affiliate Faculty, Departments of Bioengineering, Computer Science & Engineering, and Molecular & Cellular Biology
@ *University of Washington*
Talk title: Mining personal, dense, dynamic data clouds to enhance health and drive discovery

Dr. Nathan Price's group leverages systems biology to make fundamental contributions to human health. Focusing on the data-driven processes of wellness optimization, treatment development, and diagnosis precision, the group has pioneered many unique approaches to analyzing clinical data to optimize therapeutic and diagnostic interventions. Central to these goals are 1) the 100K Wellness Project, which aims to detail quantifiable metrics of wellness via analysis of longitudinal clinical data, 2) refining Systems Medicine models to search for diagnostic and therapeutic targets, and 3) integrating biochemical network models into unified computational pipelines to further streamline genotype-to-phenotype associations.

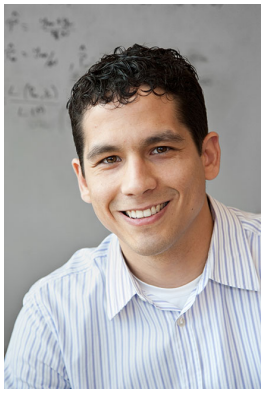
Jason Ernst, PhD
Assistant Professor, Departments of Biological Chemistry and Computer Science
@ *University of California, Los Angeles*
Talk title: Computational approaches for interpreting the epigenome and non-coding genome

Dr. Jason Ernst joined the faculty at UCLA in the Department of Biological Chemistry, the Computer Science Department, and the Bioinformatics Program in 2012. His lab is interested in developing and applying computational methods, in particular machine learning methods, for the analysis of high-throughput experimental data to address problems in epigenomics and gene regulation. A primary interest of his is developing computational approaches to use epigenomic and other high-throughput datasets to better understand the non-coding portions of the human genome and its role in disease. Dr. Ernst pioneered computational approaches to learn chromatin states from genome-wide maps of multiple epigenetic marks to systematically annotate the human genome. His group's research is often conducted in close collaboration with experimental groups.

Priya Moorjani, PhD
Assistant Professor, Department of Molecular & Cell Biology, Center for Computational Biology
@ *University of California, Berkeley*
Talk title: Genetic insights into South Asian population history and disease

Recently arriving to UC Berkeley in 2018, the Moorjani Lab focuses on using statistical and computational approaches to study questions in human genetics and evolutionary biology. A central aim in the lab is to understand the impact of evolutionary history on genetic variation and to apply this knowledge to learn about human history and biology. They use genetic data from ancient specimens and present-day humans and primates to learn about: (1) how different evolutionary processes such as mutation rate evolve across primates, (2) when key events (such as introgression and adaptations) occurred in human history, and (3) how to leverage these patterns to identify genetic variants related to human adaptation and disease. The research in the lab involves both development of new methods and large-scale genomic data analysis.

Ryan Hernandez, PhD
Associate Professor, Department of Bioengineering & Therapeutic Sciences
@ *University of California, San Francisco*
Talk title: How evolutionary forces shape the genetic architecture of complex traits



Dr. Ryan Hernandez' lab uses detailed simulations and population genetic modeling to understand the role that natural selection and demography have had on the patterning of variation throughout our genomes. His lab develops novel population genetic simulation techniques in order to unravel and interpret these complex evolutionary patterns. Finally, the Hernandez Lab seeks to exploit population genetic models of demographic history and natural selection to interrogate the genetic basis of disease. By capitalizing on recent theoretical advances, the group builds models of population dynamics that will utilize genomic re-sequencing data to discover novel regions of the genome that underlie genetic susceptibility to disease and drug response.

Student Speakers

Emily Flynn
Meta-analysis of sex-differential gene expression in human liver

Erika Bongen
KLRD1 expressing NK cells may protect against influenza infection

Pratheepa Jeganathan
The block bootstrap method for longitudinal microbiome data

Boxiang Liu
Genetic regulatory mechanisms of smooth muscle cells map to coronary artery disease risk loci

Winn Haynes
Gene annotation bias impedes biomedical research

David Gokhman
Reconstructing Denisovan anatomy using DNA methylation maps

Industry Panel

Marvin Gee, PhD
VP of Research - Target Discovery @ *3T Biosciences*

Eurie Hong, PhD
Senior Director, Genomics @ *AncestryDNA*

Natalie Telis, PhD
Statistical Geneticist @ *AncestryDNA*

Brian Maples, PhD
VP of Data Science @ *Cardinal Analytx Solutions*

Joe Davis, PhD
Data Scientist @ *Cardinal Analytx Solutions*

Ban Kawas, PhD
Research Scientist @ *IBM*

Poster Titles

Alborz Bejnood
Genomic and leukocytic inferences of the tumor microenvironment in the context of node-negative and node-positive disease

Joshua Bloomstein, Rie von Eyben, and Elizabeth Kidd
Identifying a predictive gene expression signature for lymph node involvement in cervical cancers

Bryan Bunning
Age prediction using plasma global metabolic profiles

Claire Donnat
Inferring microbiome networks

Noah Dove
Ascribing an etiology to a mutation signature through logistic regression of cancer genomic RNA expression data

Nicholas Dwork
Automatically detecting disease markers with optical coherence tomography

Michael Gloudemans
Uncovering tissue-specific mediators of disease-causing genotypes

Charles Li
Flexible record linkage tools for data integration of Chinese electronic health records

Greg McInnes
Phenotype prediction using a vectorized representation of genomic variants

Aditya Rao
A novel multi-cohort framework for analysis of host response signatures

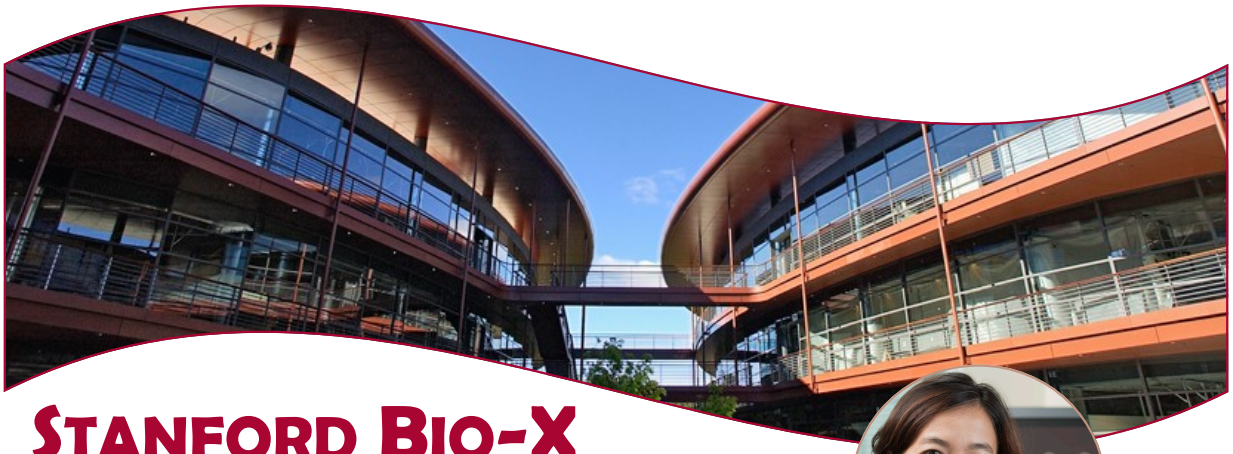
Roger Volden
R2C2: increasing accuracy of MinION sequencing reads

Li Xia
Linked-read, whole genome sequencing reveals pervasive chromosomal-level instability and novel rearrangements in brain metastases from colorectal cancer

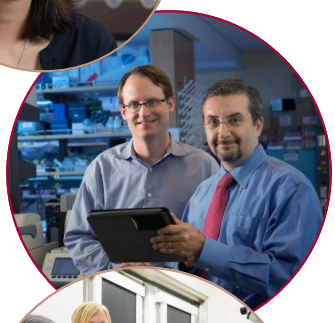
Zheng Yan
Assessing the effects of non-heritable factors on immunological phenotypes

Leeat Yankielowicz-Keren
Characterizing heterogeneity in the tumor immune microenvironment in triple negative breast cancer by multiplexed imaging

Junjie Zhu
Facile generation of single-cell transcriptome and immune repertoire from clinical tumor specimens



STANFORD BIO-X

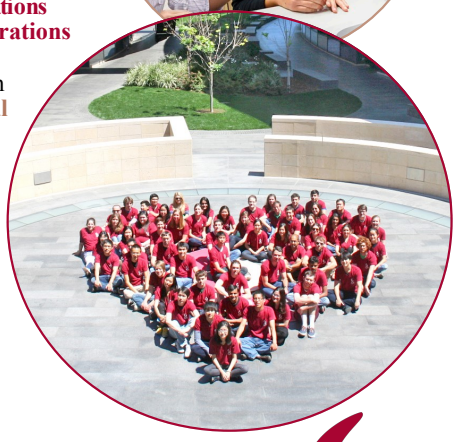


Bio-X is Stanford's pioneering initiative in the interdisciplinary movement at Stanford University. Over the past 18 years, Bio-X has developed into an **impactful institute that brings together biomedical and life science** researchers, clinicians, engineers, physicists, and computational scientists to unlock the secrets of the human body.

Over 800 Stanford faculty from all 7 Stanford schools and 65+ departments are affiliated with Bio-X, and participating in the following **Core Programs**:

- **Interdisciplinary Initiatives Seed Grant Program (IIP)**
- **Ventures**
- **Graduate Student Fellowships and Bio-X Stanford Interdisciplinary Graduate Fellowships**
- **Undergraduate Research Awards**
- **Travel Awards**

In addition, Bio-X establishes numerous **collaborations between the Stanford scientists and large corporations** by being a networking portal and providing opportunities for companies to join and participate in **symposia/seminars/mixers and customized technical summits, developing faculty liaisons,** and more.



The **James H. Clark Center is the hub of Bio-X**, comprising the equipment, resources, and utilities required to conduct breakthrough research at the cutting edge of engineering, science, and medicine.

To learn more about Bio-X, visit our website:

biox.stanford.edu

STANFORD BIO-X

Stanford Biomedical Informatics Training Program

The Biomedical Informatics Training Program (BMI) is an interdisciplinary graduate and postdoctoral training program, part of the Biosciences Program at Stanford University's School of Medicine. We offer MS and PhD degrees, and other coursework and research options.

Full-Time Graduate Programs:

- PhD in Biomedical Informatics
- Research MS degree (primarily, but not exclusively, for those with PhD and/or MD)

Part-Time Distance Education Programs:

- Professional/Honors Cooperative Program MS degree
- Certificate in Biomedical Informatics
- Non-degree option for individual classes

For Stanford Students:

- Coterminal MS degree in Biomedical Informatics in addition to BA/BS
- PhD Minor in Biomedical Informatics for Stanford graduate students

For Stanford Medical Students:

- Coursework and research opportunities through Scholarly Concentration and Medical Scholars programs

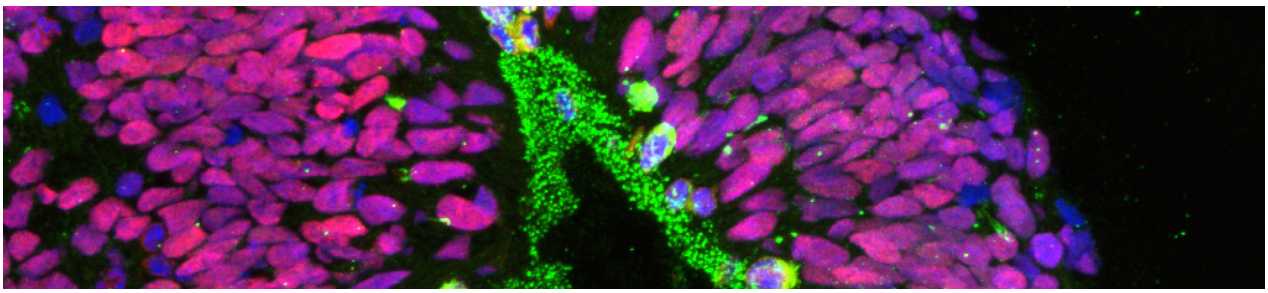
All degree programs require rigorous coursework in Biomedical Informatics core courses, a coherent set of electives from Computer Science, Statistics, Math and/or and Engineering, and training in Social, Legal and Ethical issues.

For more information, contact:

Student Services Officer
Stanford Biomedical Informatics Training Program
Medical School Office Building, Room X-343
1265 Welch Road, Mail Code: 5464
Stanford, CA 94305-5464

Phone: (650) 723-1398
email: bmi-contact@lists.stanford.edu
http://bmi.stanford.edu

Supported by National Library of Medicine Training Grant LM007033



Stanford Neurosciences Institute

We aim to understand how the brain gives rise to mental life and behavior, both in health and in disease. Our research community draws from and informs multiple disciplines, including neuroscience, medicine, engineering, psychology, education and law.

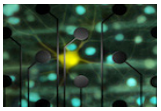
The Neurosciences Institute is shaping the future of neuroscience in three interdisciplinary areas:

NeuroDiscovery - Question-driven discovery about how the brain works

Big Idea NeuroChoice, Understanding and treating addicitve behavior from circuits to policy.

Boxuan Zhao focuses on the development of multiple molecular tools for transcriptome and connectome studies in neuronal systems.

NeuroEngineering - Tools for making novel measurements of brain structure and function

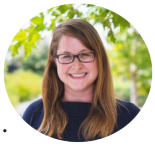


Big Idea Stanford NeuroTechnology Initiative, Creates an incubator for next-generation neural interface platforms.

Sergey Stavisky is developing technology to allow people with paralysis to accurately and intuitively move robotic arms with their minds.

NeuroHealth - Translating neuroscience discoveries into treatments

Big Idea Brain Rejuvenation, Neurodegeneration research focusing on brain maintenance and regeneration, and the role of the immune system in these processes.



Laura Marquardt's focus is on improving cell transplantation therapies after spinal cord injury using novel biomaterial design approaches in order to improve functional regeneration.

Opportunities

Interdisciplinary Research
Big Ideas in Neuroscience
Seed Grants
Visiting Scholars

Training
Interdisciplinary Postdoctoral-Scholar Awards
Stanford Interdisciplinary Graduate Fellowships
Software Carpentry Workshops
Undergraduate Society - coming soon

Engaging our Community
Weekly Seminar Series
Annual Symposium
Retreat
Brain Broadcast Newsletter

Get Involved
http://neuroscience.stanford.edu

Stanford | Neurosciences Institute

Stanford Center for Cancer Systems Biology

Interested in Cancer Systems Biology?

How To Get Involved

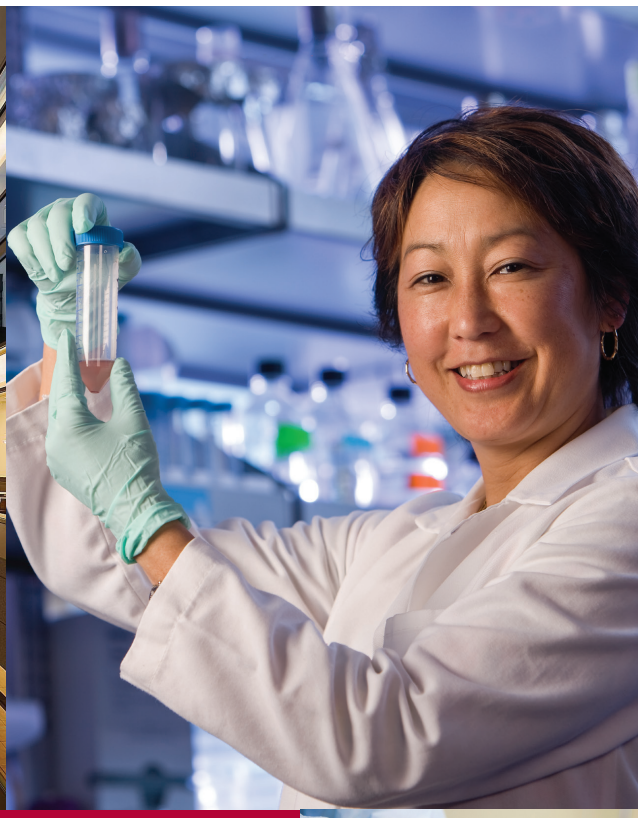
- **CCSB 6th Annual Symposium**
  - May 11, 2018 – LKSC Berg Hall
  - Submit and abstract to be part of our poster session or to be selected for a speaker slot
  - Register Today: ccsb.stanford.edu/events/symposium/symposium2018.html

- **CCSB Monthly Seminars**
  - Subarna Sinha, SRI International, 4/27, 12:30pm – Clark S360
  - Rahul Satija, New York University, 5/18, 11:00am – Clark S360
  - Doug Lauffenburger, MIT, 5/22, – Clark S360
  - Zena Werb, UCSF, 6/8, – Clark S360
  - Additional seminar information at: ccsb.stanford.edu/events/seminars/2018-seminars.html

- **Cancer Systems Biology Scholars (CSBS) Program**
  - Fellowship Opportunity: med.stanford.edu/csbs/news.html
  - CSBS Journal Club: med.stanford.edu/csbs/events/journalclubs.html

- **Join our mailing lists to stay up-to-date with the latest news and event**
  - ccsb-announcements@lists.stanford.edu
  - csbs-journalclub@lists.stanford.edu

For more information, please visit ccsb.stanford.edu



Stanford Cancer Institute

LEADING THE WAY CANCER IS TREATED TODAY AND TOMORROW

The Stanford Cancer Institute (SCI) is committed to giving patients every clinical and technological advantage in the prevention and treatment of cancer. The SCI leverages the expertise of over 300 physicians and researchers working together to unravel cancer's secrets. Stanford's scientific focus includes cancer cell and stem cell biology, immunology, molecular imaging and genetics. Translational medicine is the cornerstone of Stanford's cancer treatment programs, combining new advances with compassionate care and supportive services.

Stanford
Cancer Institute
A National Cancer Institute
Comprehensive Cancer Center

Stanford | MEDICINE

Stanford's Center for Computational, Evolutionary and Human Genomics

Founded in 2012, CEHG supports and showcases the cutting edge scientific research conducted by faculty and trainees in more than 40 member labs across the School of Humanities and Sciences and the School of Medicine. CEHG members collaborate on interdisciplinary research projects at the forefront of the information age of genomics in order to improve human well-being.

Trainee Fellowships:

- Fellowship support is centered on the transition from graduate school to postdoctoral fellowship.
- Fellows receive: financial support during the transition period; conference travel support; opportunities to lead and participate in Center scientific activities; and feature blog interviews.

Symposia and Seminars:

- Annual symposium features faculty and trainee research from member labs and guest keynote/faculty speakers from the Bay Area and beyond.
- Evolgenome seminar series explores Stanford and guest faculty/trainee speaker research on CEHG topics. Meets 2-3 times a month on Wednesdays, during the lunch hour. Food is provided.

Science Education Outreach:

- Curriculum support for lessons in science and genetics, and panel presentations on STEM education and professions, for local middle- and high- school classrooms.
- Coordinated science lab tours for visiting student groups; and trainee-led education outreach events.

Event and Program Partnerships:

- 2018 Event partnerships include the Tinker Symposium on Latin American Research in Biodiversity (2/27), and BCATS 2018 (4/19).

For more information, contact:

Katie M. Kanagawa, Ph.D.
CEHG Program Manager
Littlefield Center, Room 315
365 Lasuen Street, Mail Code: 2069
Stanford, CA 94305-5464

Phone: (971)570-0998
Email: stanfordcehg@stanford.edu
https://cehg.stanford.edu/

Thank You

Monica James

Joan Menees

Ayla Akgul

Linny Le

Joy Morimoto

LKSC staff