UCLA Institute for Quantitative & Computational Biosciences

Wednesday, September 30, 2020

Click here for Zoom Link

Welcome

The QCB Community extends a warm welcome to all. Our annual retreat is an opportunity to welcome new faculty, postdocs, and students, but also to take stock of where we are, to set goals, and define agendas.

In this craziest of years, I am really, really proud to say that we as a community have not only adapted to the challenges of the COVID pandemic and associated lockdown, but we have addressed it and excelled in several important ways: Our labs not only transitioned to remote research, meetings, and seminars, but many tackled important and diverse research questions to address the biology, the public health, and public policy challenges of the pandemic. The Collaboratory stepped up to provide skills-focused workshops to a record >900 workshop participants in the Spring quarter, and students organized collaborative sessions with experimentalists suddenly shut out from their wet labs.

To top this, we managed not only to hold the B.I.G. Summer Undergraduate Research Program this year (unlike most such programs at UCLA or nationally) but further, we expanded it to 74 students, hosted by 38 laboratories! The Program was a remarkable success for the QCB community and a model for UCLA. BIG Thank Yous to our student and faculty mentors, and the support of departments, foremost Computational Medicine, but also Human Genetics, Statistics, Medical Imaging and Informatics, Engineering Departments, and the Life Science Departments of MCDB, EEB, MIMG, and IBP!

More generally, we are in the middle of a Biosciences revolution, as was again emphasized by our recent survey: whereas <10% research effort in Biosciences was computational in the year 2000, a representative sample of the >600 UCLA laboratories now report that on average 53% of their research effort is computational. At this point about 30% of the personnel is entirely dry lab, but even experimentalists spend an increasing amount of time on computational data analysis, database queries and modeling. The consequences of this revolution cannot be overstated. Leading research universities such as UCLA must transform their research training programs at postdoctoral, graduate and undergraduate levels.

UCLA is in fact brimming with graduate training and undergraduate research opportunities in quantitative and computational biosciences across its multitude of departments. We are therefore launching the UCLA Graduate Programs Navigator in Computational Biosciences, and expanding the Undergraduate Research Portal for long supported by Eleazar Eskin. The former helps prospective student navigate the ecosystem of relevant, complementary graduate programs; the latter connects faculty to undergraduate students, an amazing human resource for driving research forward and for training future leaders. And those future leaders should be more diverse than ever, elevating the scientific enterprize through diverse questions, approaches, viewpoints rooted in diverse racial, ethnic, and cultural experiences.

Quantitative and Computational Biosciences encompasses diverse approaches ranging from data processing and analysis, to data-driven and knowledge-based modeling, to achieve prospective prediction and gain insight about complex biological systems. By coordinating our efforts in research, research training, and the substantially expanding educational programs in Bioinformatics and Computational Biology we are striving for Excellence in our own activities, and are thereby also establishing UCLA as the place to be.

Despite the Retreat being relegated to zoom this year, we hope for an exciting afternoon – I invite everyone to contribute ideas for agenda items for the coming academic year. QCB is here to support you!

Special thanks to Caroline Baron for organizing the Retreat this year! Alexander Hoffmann

Agenda

1:30 p.m. **SESSION I**

WELCOME

STATUS REPORTS

- **Alexander Hoffmann**, Director, QCBio, BIG Summer
- **Matteo Pellegrini**, Director, QCBio Collaboratory
- **Eleazar Eskin**, Director of Bioinformatics Minor, Computational Genetics Summer Institute
- **Van Savage**, Director of Computational and Systems Biology Major
- **Eric Deeds**, Associate Chair of Life Science Core, Freshman Math

2:00 p.m. **KEYNOTE**

- **Loes Olde Loohuis,** Assistant Professor of Psychiatry & Biobehavioral Sciences
  "Leveraging longitudinal electronic health records for psychiatric research"

2:20 p.m. **SELECTED TALKS**

- **James Boocock**, Genetics & Genomics Ph.D. student, Kruglyak Lab
  "Genomic epidemiology of the Los Angeles COVID-19 outbreak"
- **Soo Bin Kwon**, Bioinformatics Ph.D. student, Ernst Lab
  "Learning a genome-wide score of human-mouse conservation at the functional genomics level"
- **Kristina Garske**, Genetics & Genomics Ph.D. student, Pajukanta Lab
  "Increased BMI between monozygotic twins impacts subnuclear compartmentalization and higher-order genome structure"
- **Gabriel Hassler,** Biomathematics Ph.D. student, Suchard Lab
  "Fast Phylogenetic Factor Analysis"

3:00 p.m. **SESSION II**

STATUS REPORTS

- **Grace Xiao**, Director, Bioinformatics Interdepartmental Ph.D. Program
- **Alex Bui**, Director, Medical Informatics Ph.D. Program Home Area
- **Paivi Pajukanta**, Director, Genetic & Genomics, Ph.D. Program
- **Eric Sobel**, Director, Biomathematics, Ph.D. Program

3:25 p.m. **KEYNOTE**

- **Harold Pimentel**, Assistant Professor, Departments of Computational Medicine and Human Genetics
  "Model driven design and analysis of quantitative phenotype screens"

3.45 p.m. **SELECTED TALKS**

- **Shamus Cooley,** Bioinformatics Ph.D. student, Deeds Lab
  "Unbiased analysis of scRNA-Seq data reveals cancer stem cells in small cell lung cancer cell lines"
- **Amy L. Cummings, M.D.**, Hematology & Oncology, Medical Imaging & Informatics Ph.D. student, Bui Lab
  "Mutational landscape influences immunotherapy outcomes among non-small cell lung cancer patients with human leukocyte antigen supertype B44"
- **Peter Schuette**, NSIDP graduate student, Kao & Adhikari Labs
  "Long-term characterization of hippocampal remapping during contextual fear acquisition and extinction"

4.20 p.m. **SESSION III**

BREAKOUT DISCUSSION

1: Ideas for scientific symposia or workshops **2**: Ideas for seminar series and speakers **3**: Ideas for supporting the goals of graduate students x **4**: Ideas for supporting the goals of postdoctoral fellows **5**: Ideas for better supporting remote research **6**: Ideas for fostering the remote mentor/mentee relationship **7**: Ideas for supporting the community aspects during lockdown	**8**: Ideas for good practices in remote teaching and TA'ing **9**: Ideas on how to make virtual self-learning more efficient **10**: Ideas for supporting mental health aspects during lockdown **11**: Ideas for improving the inclusivity of our community **12**: Ideas for recruiting more diverse trainees **13**: Ideas for engaging the broader LA community

4:50 p.m. **BREAKOUT REPORTS (one-minute reports)**

5:15 p.m. **CONCLUDING REMARKS**

Breakout Sessions: how it is going to work…

The QCBio Retreat Breakout session is a time to get to know some other members of our broader community. One great way is to engage around topics of mutual interest and generate some recommendations to share with all.

Each room has been assigned a specific topic:

- **Breakout 1:** Ideas for scientific symposia or workshops
- **Breakout 2:** Ideas for seminar series and speakers
- **Breakout 3:** Ideas for supporting the goals of graduate students
- **Breakout 4:** Ideas for supporting the goals of postdoctoral fellows
- **Breakout 5:** Ideas for better supporting remote research
- **Breakout 6:** Ideas for fostering the mentor/mentee relationship during lockdown
- **Breakout 7:** Ideas for supporting the community aspects during lockdown
- **Breakout 8:** Ideas for good practices in remote teaching and TA'ing
- **Breakout 9:** Ideas on how to make virtual self-learning more efficient
- **Breakout 10:** Ideas for supporting mental health aspects during lockdown
- **Breakout 11:** Ideas for improving the inclusivity of our academic community
- **Breakout 12:** Ideas for recruiting more diverse trainees
- **Breakout 13:** Ideas for engaging the broader LA community

Based on your answers from the registration form, you have been pre-assigned to 1 of the 13 Breakout rooms

A scribe has been selected to take notes of the discussion in each room.

Instructions:

Starting at 4:20pm, participants in each breakout room will have 20 minutes to discuss their assigned topic.

Participants will then all be brought back together and the scribe of each group will have ONE minute to share with the audience a summary of their group's discussion.

For this to work, please make sure:

- **That your Zoom software is updated:**

https://support.zoom.us/hc/en-us/articles/201362233-Upgrade-update-to-the-latest-version

- **The e-mail address you provided corresponds to your Zoom account**

Selected Talks

Genomic epidemiology of the Los Angeles COVID-19 outbreak

Longhua Guo*[1], James Boocock*[1], Evann E. Hilt[2], Sukantha Chandrasekaran[2], Yi Zhang[1], Chetan Munugala[1], Laila Sathe[2], Noah Alexander[1], Valerie A. Arboleda[1], Jonathan Flint[1], Eleazar Eskin[3], Chongyuan Luo[1], Shangxin Yang[2], Omai B. Garner[2], Yi Yin[1], Joshua S. Bloom[1], Leonid Kruglyak[1]
[1] Department of Human Genetics, David Geffen School of Medicine, UCLA
[2] Department of Pathology & Laboratory Medicine, David Geffen School of Medicine, UCLA
[3] Department of Computational Medicine, David Geffen School of Medicine, UCLA

Los Angeles (LA) County has sustained a large outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). To learn about the transmission history of SARS-CoV-2 in LA County, we sequenced 142 viral genomes from unique patients seeking care at UCLA Health System. 86 of these genomes are from samples collected before April 19, 2020. We found that the early outbreak in LA, as in other international air travel hubs, was seeded by multiple introductions of strains from Asia and Europe. We identified a US-specific strain, B.1.43, which has been found predominantly in California and Washington State. While samples from LA County carry the ancestral B.1.43 genome, viral genomes from neighboring counties in California and from counties in Washington State carry additional mutations, suggesting a potential origin of B.1.43 in Southern California. We quantified the transmission rate of SARS-CoV-2 over time, and found evidence that the public health measures put in place in LA County to control the virus were effective at preventing transmission, but may have been undermined by the many introductions of SARS-CoV-2 into the region. Our work demonstrates that genome sequencing can be a powerful tool for investigating outbreaks and informing the public health response. Our results reinforce the critical need for the U.S. to have coordinated inter-state responses to the pandemic.

Unbiased analysis of scRNA-Seq data reveals cancer stem cells in small cell lung cancer cell lines

Shamus Cooley[1], Timothy Hamilton[2], Samuel Aragones[2], Sarah Maddox Groves[3], Carlos Lopez[3], Eric Deeds[2]
[1]Bioinformatics Interdepartmental Graduate Program, UCLA
[2]Department of Integrative Biology and Physiology, UCLA
[3]Department of Biochemistry, Vanderbilt School of Medicine

Small Cell Lung Cancer (SCLC) is a debilitating disease with a poor prognosis, and high probability of relapse. Methods of treatment have seen little advance over the last three decades. Heterogeneity of cancer cells is a key factor by which tumors resist treatment, and previous studies of bulk RNA sequencing data have suggested that SCLC assumes one of four subtypes, each with a distinct gene expression signature. Here, we use a new approach to analyze single-cell gene expression data from eight immortalized SCLC cell lines. While our analysis supports the existence of the four classic distinct SCLC subtypes, we found that each cell line is actually made up of highly heterogenous sub-populations, one of which represents a distinct, stem-like group of proliferative cells. This suggests the existence of significant heterogeneity within SCLC that cannot be captured by bulk RNA sequencing experiments. This heterogeneity is likely of clinical relevance for the treatment of SCLC and other cancers, and consideration of these newly discovered subpopulations will likely be critical for the development of effective therapeutics.

Mutational landscape influences immunotherapy outcomes among non-small cell lung cancer patients with human leukocyte antigen supertype B44.

Cummings AL,[1] Gukasyan J,[1] Lu HY,[1] Grogan T,[1] Sunga G,[3] Fares CM,[1] Hornstein N,[1] Zaretsky J,[1] Carroll J,[1] Bachrach B,[1] Akingbemi WO,[1] Li D,[1] Noor Z,[1] Lisberg A,[1] Goldman JW,[1] Elashoff D,[1] Bui AAT,[2] Ribas A,[1] Dubinett SM,[1] Rossetti M,[3] Garon EB[1].
[1] Department of Medicine David Geffen School of Medicine, UCLA
[2] Department of Radiology, David Geffen School of Medicine, UCLA
[3] Department of Pathology & Laboratory Medicine, David Geffen School of Medicine, UCLA

Human leukocyte antigen (HLA)-B has been recognized as a major determinant of discrepancies in disease outcomes, and recent evidence suggests a role in immune checkpoint blockade (ICB) efficacy. The B44 supertype, which features an electropositive binding pocket that preferentially displays peptides with negatively charged amino acid anchors, associated with improved survival in ICB-treated melanoma. Yet this effect was not seen in ICB-treated non-small cell lung cancer (NSCLC). Here we show that mutations leading to glutamic acid substitutions occur more often in melanoma than NSCLC based on mutational landscape. We additionally show stratifying B44 based on the presence of somatic mutations that lead to negatively charged glutamic acid anchors identifies NSCLC patients with ICB benefit similar to that seen in melanoma. We anticipate these findings could improve assessment of HLA-related outcomes and prediction of ICB benefit in those with B44, representing approximately half of the world's population.

Increased BMI between monozygotic twins impacts subnuclear compartmentalization and higher-order genome structure

Kristina M. Garske[1], David Z. Pan[1,2], Caroline Comenho[1], Yash V. Bhagat[1], Gregory Rosenberg[1], Brunilda Baillu[3], Janet S. Sinsheimer[1,2,3], Kirsi H. Pietiläinen[4,5], Päivi Pajukanta[1,2,6]
[1]Department of Human Genetics, David Geffen School of Medicine at UCLA, Los Angeles, California, USA.
[2]Bioinformatics Interdepartmental Program, UCLA, Los Angeles, CA, USA.
[3]Department of Computational Medicine, David Geffen School of Medicine at UCLA, Los Angeles, California, USA.
[4]Obesity Research Unit, Research Programs Unit, Diabetes and Obesity, University of Helsinki, Biomedicum Helsinki, Helsinki, Finland
[5]Obesity Center, Endocrinology, Abdominal Center, Helsinki University Central Hospital and University of Helsinki, Helsinki, Finland
[6]Institute for Precision Health, David Geffen School of Medicine at UCLA, Los Angeles, California, USA.

Adipocyte hypertrophy is induced by obesity and leads to insulin resistance and chronic low-grade inflammation. Dysregulated preadipocytes (PAd) that do not differentiate properly can drive adipose tissue toward hypertrophy (fewer, larger adipocytes), rather than the metabolically more protective phenotype, hyperplasia (more, smaller adipocytes). We hypothesized that the obesogenic cellular microenvironment disrupts the proper function of preadipocytes through altered genomic programming and subnuclear compartmentalization resulting from changes in the higher-order structure of the genome and epigenomic signatures involved in gene regulation. We performed ATAC-seq and RNA-seq in the primary preadipocytes from 10 pairs (n=20) of monozygotic (MZ) twins discordant body mass index (ΔBMI>3 kg/m^2). To test for genome-wide differences in genome structure between the leaner and heavier MZ siblings, we first identified the A/B subnuclear compartments using ATAC-seq co-accessibility at 100-kb resolution in all PAd samples. We found that the genome-wide connectivity of the A/B compartments is significantly higher in the leaner compared to heavier groups ($p_{\text{pairedMWW}}$=3.2x10^{-71}), indicating a global breakdown of coordinated mechanisms to maintain higher-order genome structure and subnuclear compartmentalization in conditions of increased BMI. Overall, we discovered that obesity impacts subnuclear compartments of the genome and characterized the cellular genomic programming in human primary PAd, an understudied cell type that is important for understanding obesity and its comorbidities.

Fast phylogenetic factor analysis

Gabriel Hassler[1], Max R. Tolkoff[2], Zhenyu Zhang[2], Andrew Holbrook[2], Marc A. Suchard[1,2,3]
[1]Department of Computational Medicine, David Geffen School of Medicine, UCLA
[2]Department of Biostatistics, Fielding School of Public Health, UCLA
[3]Department of Human Genetics, David Geffen School of Medicine, UCLA

Phylogenetic comparative methods study the evolution of phenotypes along a phylogenetic tree. However, many of the most relevant phenotypes, such as plant/animal domestication or viral virulence, are inherently complex and multidimensional and are not directly observable. Rather, these phenotypes are formed from interactions of numerous observable phenotypes. Linear dimension reduction, such as factor analysis, allows researchers to summarize these complex traits as a linear combination of observable traits. In the phylogenetic context, however, the evolutionary relationships between taxa induce statistical dependence between the latent factors, complicating statistical inference. Existing solutions to this problem rely on data augmentation and scale poorly with increasing taxa. We propose an inference strategy that avoids costly data augmentation and scales linearly in both the number of taxa and traits. These techniques reduce inference times by up to 100-fold. We apply these methods to study the domestication of brewer's yeast and clinically-relevant genomic interactions in HIV.

Learning a genome-wide score of human-mouse conservation at the functional genomics level

Soo Bin Kwon[1,2], Jason Ernst[1,2,3,4,5,6,7]
[1] Bioinformatics Interdepartmental Program, University of California, Los Angeles, CA 90095, USA
[2] Department of Biological Chemistry, University of California, Los Angeles, CA 90095, USA
[3] Eli and Edythe Broad Center of Regenerative Medicine and Stem Cell Research at University of California, Los Angeles, CA 90095, USA
[4] Computer Science Department, University of California, Los Angeles, CA 90095, USA
[5] Department of Computational Medicine, University of California, Los Angeles, CA 90095, USA
[6] Jonsson Comprehensive Cancer Center, University of California, Los Angeles, CA 90095, USA
[7] Molecular Biology Institute, University of California, Los Angeles, CA 90095, USA

Identifying genomic regions with functional genomic properties that are conserved between human and mouse is an important challenge in the context of mouse model studies. To address this, we take a novel approach and learn a score of evidence of conservation at the functional genomics level by integrating large-scale information in a compendium of epigenomic, transcription factor binding, and transcriptomic data from human and mouse. The computational method we developed to do this, Learning Evidence of Conservation from Integrated Functional genomic annotations (LECIF), trains a neural network, which is then used to generate a genome-wide score in human and mouse. The resulting LECIF score highlights human and mouse regions with shared functional genomic properties and captures correspondence of biologically similar human and mouse annotations even though it was not explicitly given such information. LECIF will be a resource for mouse model studies.

Long-term characterization of hippocampal remapping during contextual fear acquisition and extinction

Peter J. Schuette[1]*, Fernando M.C.V. Reis[1]*, Sandra Maesta-Pereira[1], Meghmik Chakerian[1], Anita Torossian[1], Garrett Blair[1], Weisheng Wang[1], Hugh T. Blair[1], Michael S. Fanselow[1], Jonathan C. Kao[2]**, Avishek Adhikari[1]**
* Equal contributions
**Equal contributions
[1] Department of Psychology, University of California, Los Angeles, Los Angeles, CA, 90095, USA.
[2] Department of Electrical and Computer Engineering, University of California, Los Angeles, Los Angeles, CA, 90095, USA.

Hippocampal CA1 place cell spatial maps are known to alter their firing properties in response to contextual fear conditioning—a process called 'remapping'. We recently used chronic calcium imaging to examine contextual fear-induced remapping over an extended period of time and with thousands of neurons. We demonstrate that hippocampal ensembles encode space at a finer scale following fear memory acquisition. This effect is strongest near the shock grid. We also characterized the long-term effects of shock on place cell ensemble stability, demonstrating that shock delivery induces a several day period of high fear and low between-session place field stability, followed by a new, stable spatial representation that appears after fear extinction. Finally, we identified a novel group of CA1 neurons that robustly encode freeze behavior independently from spatial location. Thus, following fear acquisition, hippocampal CA1 place cells sharpen their spatial tuning and dynamically change spatial encoding stability throughout fear learning and extinction.

Keynote Speakers

Harold Pimentel
Assistant Professor, Departments of Computational Medicine and Human Genetics

Harold wants to understand the link between genes, RNA, and disease. Scientists know that psychiatric and autoimmune diseases, for example, have complicated genetic roots. But teasing out a role for RNA has been difficult. Harold is interested in how people's genetic variation affects RNA splicing and how splicing relates to changing gene regulatory networks. He's developing computational tools to design and analyze CRISPR-based experiments as well as large genetic data sets from patients. The underlying goal is to link these two data types to understand which genes depend on each other so that future treatments can fix broken dependencies. Research in the lab is rooted in using computer science and high-dimensional statistics to solve biologically relevant problems.

Model driven design and analysis of quantitative phenotype screens

Increasingly, CRISPR screens are coupled with flow cytometry (FACS) to sort cells and quantify the impact of genetic perturbations on a continuous phenotype. While FACS provides much more quantitative information than simple survival screens, it introduces a number of experimental and statistical challenges. Furthermore, as experimentalists push these screens in limited primary cells or in vivo, they lack principled guidelines on how different experimental parameters including multiplicity of infection, coverage per guide RNA, or FACS bin cutoffs affect statistical power. We present models for both experimental design of experimental parameters and inference of gene regulation in these screens. With our cell-level hierarchical design model we show that commonly used parameters are far from optimal and screens can be performed with a 20 times reduction in cells at comparable accuracy. Our inference procedure models many components of the experiment, models biological replicates, infers the latent protein distribution, and infers relevant experimental parameters. To our knowledge it is the first model that infers the bin cutoffs while allowing multiple bins and a bimodal FACS distribution which is often observed in real data. Together these analyses provide a holistic framework for designing and analyzing highly parallel FACS screens.

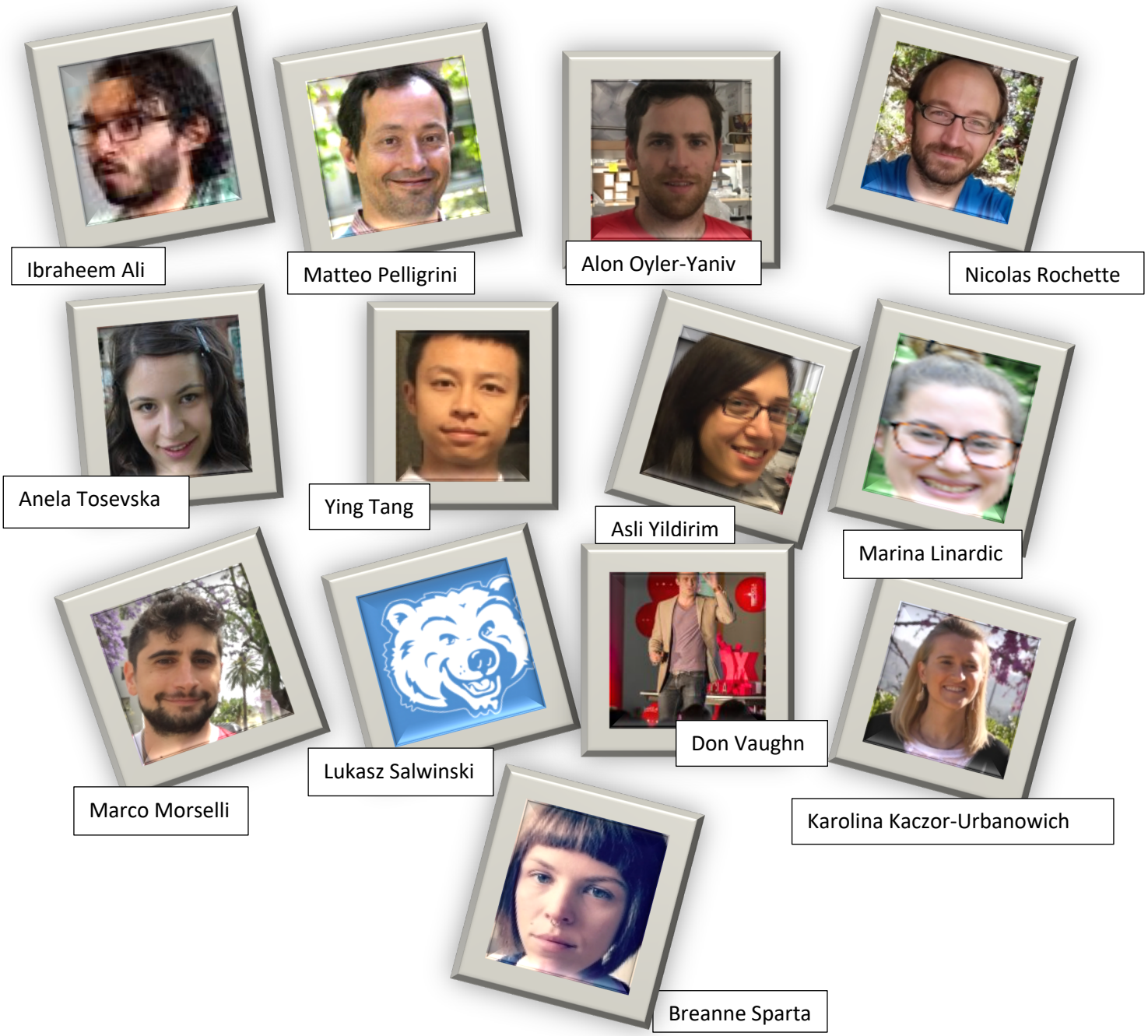
Loes Olde Loohuis
Assistant Professor of Psychiatry & Biobehavioral Sciences

Dr. Loes Olde Loohuis' lab studies the underlying molecular mechanisms of severe mental illness. In recent years, genetic studies have achieved tremendous success in identifying numerous common variants robustly associated with psychiatric disorders, and the aggregated results of these studies have begun to transform our understanding of disease risk. However, most studies focus on broadly defined disease categories and case-control designs, and have yet to yield any tools that can readily be applied in clinical practice. However, with the increased sample sizes in genetics as well as the availability of multi-level data (including clinical phenotypes, health records and molecular phenotypes) psychiatric genetics is at a point where we can begin to address clinically precise questions using targeted approaches. Loes' lab uses and develops genetic and machine learning approaches to do exactly this. Specifically, the lab aims to characterize and predict psychiatric disease trajectories using genetic and high-dimensional phenotypic data resources. The lab has a special focus on the study of populations from Latin America.

Leveraging longitudinal electronic health records for psychiatric research

During this talk, I will present our ongoing investigations of the longitudinal health record data from a psychiatric hospital in Manizales, Colombia. Specifically, I will present i) strategies for extracting a wide range of phenotypes, including symptoms and behaviors ii) geostatistical analyses identifying geographic heterogeneity of both treatment utilization and incidence of severe mental illness; and iii) summarize our efforts to characterize and predict disease trajectories.
These efforts enable and inform genetic analyses in the Latin American Biobank for Severe Mental Illness (LAB-SM): a biobank and databank including 100k participants we are creating to reverse the underrepresentation of Latin American populations in psychiatric genetics research.

Collaboratory Fellows 2020-2021



https://qcb.ucla.edu/collaboratory/people/

Please visit our website to learn more about the Collaboratory, our classes offered, and class schedule and of course to learn more about our Postdoctoral Fellows.

http://qcb.ucla.edu/collaboratory

Welcome our Incoming Bioinformatics Students!

Caroline Chen
BS-Biochemistry, Cal State Los Angeles and MD, University of Miami

Matthew Heffel
BS-Computer Science and MS-Genetics, Kansas State University

Ran Hu
BEng-Computer Science and Engineering, Chinese University of Hong Kong in Shenzhen

Elaine Huang
BS-Neuroscience and BA- Philosophy, Lafayette College

Helen (Xin) Huang
BS-Biology, UCLA
B.I.G. SUMMER 2019 ALUMNA

Huiling Huang
BS-Computational and Systems Biology and MS in Bioinformatics, UCLA
B.I.G. SUMMER 2018 ALUMNA

Jonathan Mah
BS-Biochemistry and Microbiology, University of Washington
B.I.G. SUMMER 2019 ALUMNUS

Jamie Matthews
BS-Animal Science, Cali Polytechnic State University

Kathie Ngo
BS- Biomedical Engineering, UC Davis

Jonathan Perrie
BS-Computer Science and Statistics, Dalhousie University and MMath-Computer Science, University of Waterloo

Trevor Ridgley
BS-Biomolecular Engineering & Bioinformatics, UC Santa Cruz
B.I.G. SUMMER 2019 ALUMNUS

Harold Wang
BS-Animal Science, Cali Polytechnic State University

Ye Wang
BS-Chemistry, Nankai University and PhD-Chemical Biology, Peking University

Angela Wei
BS- Biotechnology and Mathematics, University of Kentucky
B.I.G. SUMMER 2018 ALUMNA

Mark (Yankai) Xiang
BS-Biology and Mathematics, University of Massachusetts-Amherst
B.I.G. SUMMER 2019 ALUMNUS

Albert Xue
BS-Math and Computer Science, Duke University

Welcome our Incoming Medical Informatics Students!

Al Rahrooh
BS, Biomedical Sciences, University of Central Florida

David Zheng
BS, Computer Science, UCLA

Mingzhou (Joy) Fu
BS, Clinical Medicine, Shanghai Jiaotong University, China
MPH, Epidemiology & Health Informatics, University of Michigan, Ann Arbor

Dylan Steinecke
BS, Biological Sciences, California State University San Marcos

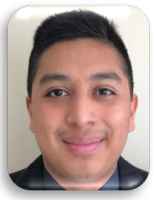
Welcome our Incoming Biomathematics Students!

Ellen Visscher: Bachelor of Engineering (Mechanical), Bachelor of Science (Mathematics); The University of Queensland

Apeksha Singh (MSTP student): Bachelor of Arts (Applied Mathematics, Molecular and Cell Biology); UC Berkeley

Xiangting Li (differing to Spring 2021): Bachelor of Science (Integrated Science); Peking University, China

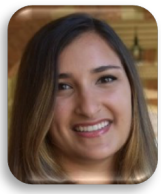
Welcome our Incoming Genetics & Genomics Students!



Alexander Espinoza
BS-Biology, University of La Verne
B.I.G. SUMMER 2019 ALUMNUS

Jennifer Grundman
BS-Physiology and Neuroscience, University of San Diego

Isabella Lin (MSTP)
BA-Genetics and Genomics, UC Berkeley
DGSOM Medical School, UCLA



Laila Sathe (deferring for the Fall)
BS-Molecular, Cell and Developmental Biology, UCLA

Ye Yang
BA-Engineering, Hefei University of Tech, China

Nicole Zeltser
BS-Animal Science, Cali Polytechnic State University
B.I.G. SUMMER 2019 ALUMNA

Welcome new Faculty!

Nanibaa' Garrison (Diné)
Associate Professor, Institute for Society and Genetics, Institute for Precision Health, and the Division of General Internal Medicine & Health Services Research

Nanibaa' Garrison, Ph.D. is an Associate Professor in the Institute for Society and Genetics and the Division of General Internal Medicine & Health Services Research at the University of California, Los Angeles. She is on the faculty for the UCLA Institute for Precision Health and the UCLA genetic counseling master's program. Dr. Garrison earned her Ph.D. in genetics at Stanford University, and completed a postdoctoral fellowship in bioethics at the Stanford Center for Biomedical Ethics and the Center for Integration of Research on Genetics & Ethics at Stanford University. Her research focuses on the ethical, social, and cultural implications of genetic and genomic research in Indigenous communities. Using community-based research approaches, she engages with tribal communities to develop policies and guidance for tribes.

Abigail Bingham
Associate Professor of Anthropology

Dr. Abigail Bigham is an Associate Professor of Anthropology at UCLA. Abby received her B.A. from the University of Arizona and her PhD from The Pennsylvania State University. She completed a postdoctoral fellowship at the University of Washington. Prior to joining UCLA, Abby was on the faculty at the University of Michigan. Her current research is focused on understanding human genetic adaptation to environmental pressures and how these adaptations affect the range of modern human phenotypic diversity.

Daniel Tward
Assistant Professor, Departments of Computational Medicine and Neurology

Dr. Daniel Tward's research focuses on building computational tools that use imaging data to understand how disease affects the brain's structure. One application is studying neurodegeneration in the earliest stages of Alzheimer's disease, connecting information in clinical MRI with microscopy data from autopsy. Daniel obtained his Ph.D. in biomedical engineering from Johns Hopkins University, and completed postdoctoral training in biomedical engineering and neuropathology at the Kavli Neuroscience Discovery Institute. He holds a joint appointment in the Department of Computational Medicine, and the Department of Neurology as part of the Brain Mapping Center.

Harold Pimentel
Assistant Professor, Departments of Computational Medicine and Human Genetics

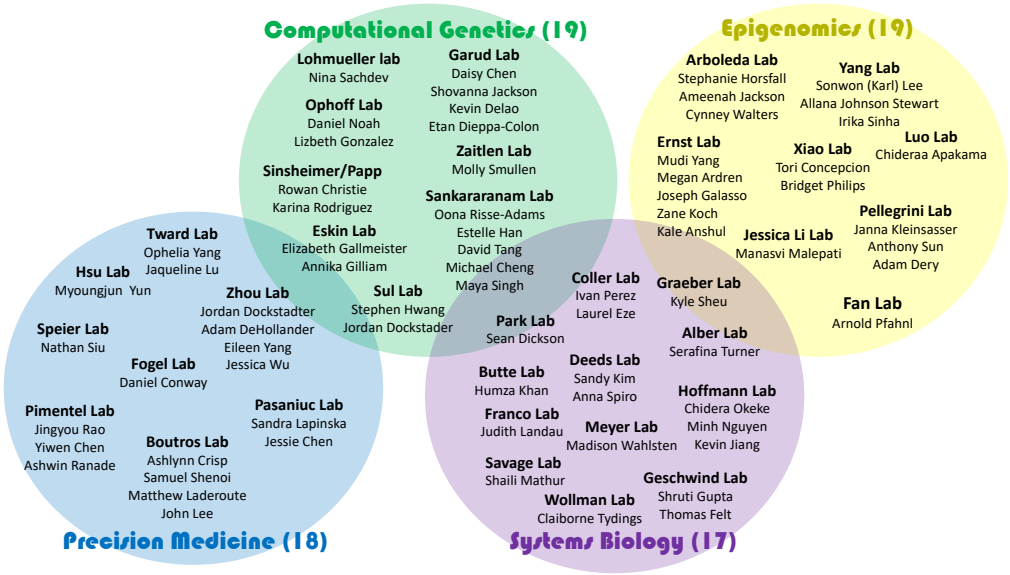
Harold received an MA in statistics and a PhD in computer science from UC Berkeley with Lior Pachter working on ultrafast pseudoalignment and small sample estimation with RNA-seq data. In his postdoc at Stanford with Jonathan Pritchard he worked on methods for integrating human genetics and gene regulation estimation. At UCLA he is continuing the focus of combining gene regulation and human genetics by developing models for screen inference, experimental design, network inference, and improving pseudoalignment approaches.

Loes Olde Loohuis
Assistant Professor of Psychiatry & Biobehavioral Sciences

Dr. Loes Olde Loohuis' lab studies the underlying molecular mechanisms of severe mental illness. Specifically, the lab aims to characterize and predict psychiatric disease trajectories using genetic and high-dimensional phenotypic data resources, such as electronic health records. The lab has a special focus on the study of populations from Latin America.

A B.I.G. Thank you

To all mentors for a successful 2020 Program!



- June 22 to August 14, 2020
- 5th Annual Program
- 370+ applications
- 74 admitted students
- 38 faculty mentors
- 38 direct research mentors
- 54 mentors nominated by their mentees for outstanding mentorship!

Talks & Abstracts Posted on the QCBio Website at https://qcb.ucla.edu/big-summer/big2020/

B.I.G. SUMMER – Bruins-In-Genomics

Bruins-In-Genomics (B.I.G.) Summer Research Program is an 8-week full-time immersion program for undergraduates interested in learning how to read and analyze genes and genomes. Through this program students have the opportunity to experience graduate-level-cutting-edge research in UCLA laboratories and learn some of the latest research methods to solve real-world problems.
Please visit our website to learn more: https://qcb.ucla.edu/big-summer/