PEQG26

Population, Evolutionary and Quantitative Genetics Conference

PROGRAM BOOK

June 9–12, 2026
Pacific Grove, CA | #PEQG26

GSA GENETICS G3

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GSA is an international scientific society representing more than 4,000 researchers and educators around the world. In addition to connecting researchers through conferences and career programs, we publish two peer-reviewed scholarly journals, GENETICS and G3: Genes|Genomes|Genetics. We encourage you to join GSA so you can make use of exclusive member benefits and get involved in the Society's many programs, including professional development training, awards, advocacy, and more. Join us as we work to advance the field and serve our community. Visit genetics-gsa.org for more information.

GENETICS has been innovating since 1916, publishing high quality original research across the breadth of the field.

G3: Genes|Genomes|Genetics is an open access journal that publishes high quality, useful results regardless of perceived impact.

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Genetics Society of America gratefully acknowledges the following sponsors:

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Conference App

Download the GSA Conference App to your smartphone (available on both iOS and Android) to have meeting information at your fingertips. Once you download the App, you will only need access to the internet for program updates. You will not need an internet connection to access previously downloaded information. Full access to the Program is also available through the web version on the conference website.

Your registration badge ID is needed to access the App. The badge ID was sent in a registration confirmation email from the address NoReply@Convention-Mail.com and is on your conference badge.

Wifi Access

Guests of Asilomar will have complimentary Wifi in their rooms as well as in the meeting rooms and Fireside Pavilion.

Network: Asilomar Conference

Password: conference2026 (all lower case)

Registration

Registrants were emailed their badge to print at home. Show your pre-printed badge to the registrar to collect your badge holder and lanyard in Merrill Hall. For admission to the sessions, posters, exhibits, and receptions, you must have your official conference badge.

The Program Book, Abstract Book, and Certificates of Attendance and Participation are all available online. The Registration Desk will be open in Merrill Hall during the hours noted below.

Tuesday, June 9	12:00 p.m.–6:00 p.m.
Wednesday, June 10	8:00 a.m.–3:00 p.m.
Thursday, June 11	8:30 a.m.–1:00 p.m.

Oral Presentations/Speaker Ready Room

All oral session speakers must go to the Speaker Ready Room located in Merrill Hall the day before your session to upload and review your presentation and become familiar with the equipment that will be in the session room. You will not be able to use your own computer or upload your presentation in the session room at the podium. The day of your presentation, arrive 30 minutes before the start of your session (not your talk) to let the session chair know you are there and to get any last-minute instructions. The Speaker Ready Room will be open during the hours noted below.

Tuesday, June 9	12:30 p.m.–3:30 p.m.
Wednesday, June 10	7:30 a.m.–1:00 p.m.
Thursday, June 11	7:30 a.m.–1:00 p.m.
Friday, June 12	7:30 a.m.–12:00 p.m.

Poster Sessions

All posters will be displayed in the Fireside Pavilion located in the garage under the Fred Farr Forum. Display your poster after 8:30 a.m. the day of your presentation. All posters will be up for one day. Posters must be removed at 10:30 p.m. After that time, remaining posters will be removed and recycled. The meeting does not take responsibility for posters that are not removed on time. Authors will present according to the schedule below.

WEDNESDAY, JUNE 10	
8:30 a.m.–10:00 p.m.	Open viewing (All Wednesday posters must be displayed)
8:30 p.m.–9:15 p.m.	Even-numbered poster presentations
9:15 p.m.–10:00 p.m.	Odd-numbered poster presentations
10:00 p.m.	Wednesday posters must be removed
THURSDAY, JUNE 11	
8:30 a.m.–10:00 p.m.	Open viewing (All Thursday posters must be displayed)
8:30 p.m.–9:15 p.m.	Even-numbered poster presentations
9:15 p.m.–10:00 p.m.	Odd-numbered poster presentations
10:00 p.m.	Thursday posters must be removed

Job and Meeting Postings

Individuals and institutions offering or seeking employment and organizers of meetings may post notices and resumes on the Community Notices bulletin board, located in the Fireside Pavilion.

Meals

Meals are not included in the registration fee. Guests staying at Asilomar and those who purchased a meal plan are invited to eat at Crocker Dining Hall. If you prefer to eat outside, you can pick up a to-go meal in Crocker Dining Hall. Phoebe Cafe, located in the Social Hall, has a limited menu available for those that did not purchase a meal plan. Meals are offered at the following times:

Breakfast	7:30 a.m.–9:00 a.m.
Lunch	12:00 p.m.–1:00 p.m.
Dinner	6:00 p.m.–7:00 p.m.

Parking

Parking on the Asilomar Conference Grounds is complimentary.

Security/Lost and Found

For all emergencies and lost and found items, contact Asilomar security by dialing 0 from any house phone. The conference Registration Desk will be able to assist you as well.

Quiet Space

There are living rooms available in Lodge, Afterglow, Pirates Den, and Stuck-Up Inn for those who are looking for a quiet space to recharge.

EXHIBITS

GSA wishes to thank our exhibitor partners. Be sure to visit these companies that have come to support your science and show you how they can help advance your research.

Biomarker Technologies
info@bmk.com
https://www.bmkgene.com/

Founded in 2009, Biomarker Technologies (BMKGENE) is a leading global genomics service provider with over 17 years of dedicated innovation in high-throughput sequencing and bioinformatics. Our strong R&D foundation is demonstrated by over 60 national invention patents and more than 200 software copyrights.

Boster Biological Technology
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Studying evolution, population genetics, or ecology with a non-standard organism? Boster Bio's Custom Polyclonal Production Service generates high-affinity antibodies for virtually any species. Starting at just $600 with full expert support, we take you from antigen design through final validation. Stop letting reagent gaps slow your discovery.

Evolutionary Studies at Vanderbilt University
andrew.j.flick@vanderbilt.edu
www.vanderbilt.edu/evolution/

The aim of Evolutionary Studies at Vanderbilt is to unite a remarkably diverse array of scholars from diverse disciplines with broad interests and expertise in evolution-related fields. Our campus houses scholars that integrate evolution with anthropology, neuroscience, psychological sciences, economics, law, language, paleontology, education, ecology, and medicine.

Genetics Society of America
genetics-gsa@thegsajournals.org
http://genetics-gsa.org

Come explore the resources and opportunities that GSA has to offer; meet members of the GSA staff and leadership; and find out about publishing in GENETICS and G3: Genes|Genomes|Genetics.

GTseek LLC
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GTseek LLC offers an extensive range of services in experiment design, bioinformatics, panel development, and production genotyping, all at competitive prices. Our mission is to continue developing cutting-edge methods and products while utilizing our expertise to aid in our clients' research needs.

National Institute for Theory and Mathematics in Biology
nitmb@nitmb.org
https://www.nitmb.org

The NSF-Simons National Institute for Theory and Mathematics in Biology (NITMB) aims to create a nationwide collaborative research community that will integrate the disciplines of mathematics and biology, transforming the practice of biological research and inspiring new mathematical discoveries.

Code of Conduct

This Code of Conduct covers in-person conferences, online conferences, and other online events hosted by the Genetics Society of America. GSA Conferences include plenary presentations, concurrent sessions, poster presentations, workshops.

GSA Conferences foster an international community of geneticists and provide an opportunity to discuss scientific advances and form new collaborations.

GSA values your attendance and wants to make your experience productive and inspiring by fostering an open exchange of ideas in a professional setting. Our Code of Conduct was established to communicate a transparent set of standards and guidelines for acceptable behavior at GSA Conferences and to provide a positive, safe, and welcoming environment for all attendees, vendors, volunteers, and staff.

All conference participants (regardless of their role) are expected to follow the Code of Conduct while attending any portion of the conference, including but not limited to keynote presentations, concurrent sessions, live poster Q&A sessions, and workshops. Because there is also a virtual nature to the conference, our Code of Conduct extends to communications related to the meeting and its attendees, presenters, exhibitors, sponsors, staff, and vendors. These types of communications include Zoom chat, Zoom Q&A window, live poster Q&A, email, social media, and texts.

Unacceptable Behaviors

Unacceptable behaviors include, but are not limited to:

- Intimidating, harassing, abusive, discriminatory, derogatory, or demeaning speech or actions by any participant and at all related events
- Harmful or prejudicial verbal or written comments or visual images related to gender, gender expression, gender identity, marital status, sexual orientation, race, religion, political orientation, socioeconomic standing, disability or ability status, or other personal characteristics, including those protected by law
- Inappropriate use of nudity and/or sexual images (including presentation slides, posters, Slack channels, or Zoom chat)
- Deliberate intimidation or stalking
- Violating the rules and regulations of the online provider, Zoom
- Sustained disruption of scientific sessions or other events
- Unwelcome and uninvited attention or contact
- Real or implied threat of physical harm

- Real or implied threat of professional or financial damage or harm
- Photographing or reproducing slides of oral presentations and posters without permission
- Recording of scientific and other sessions without permission

Taking Action or Making a Report

To confidentially report a Code of Conduct violation or to file a complaint, including a complaint about a GSA volunteer or GSA staff member, please visit genetics-gsa.ethicspoint.com. Please email Tracey DePellegrin, GSA Executive Director, at tracey.depellegrin@genetics-gsa.org. GSA staff is available to assist participants in making a report.

Consequences of Non-compliance

Anyone asked by GSA staff or an Organizer, Session Chair, Workshop Leader, Moderator, Presenter, or Zoom representative to stop unacceptable behavior is expected to comply immediately. Retaliation toward GSA or toward someone reporting an incident or after experiencing any of the following consequences will not be tolerated and may result in additional sanctions.

The consequences of non-compliance with GSA's Code of Conduct may include:

- Immediate removal from in-person meeting
- Immediate removal from accessing the online meeting
- Immediate removal from Slack channels and the meeting app without warning
- Restrictions from future GSA meeting attendance
- Termination of GSA membership or positions on GSA Boards or Committees
- Incidents may be reported to the proper authorities

Accessibility

GSA is committed to assisting attendees with special needs. If you have accessibility questions or requests, please email gsaconferences@genetics-gsa.org. If you have difficulty walking long distances, consider renting a scooter from Scoot Around. They will deliver your scooter to your hotel and pick it up when you no longer need it. For more details, visit www.scootaround.com or call (888) 441-7575.

Diversity and Inclusion

GSA is committed to foregrounding equity, accessibility, and inclusion alongside scientific content, education, and professional development at each step of conference planning. We seek to create opportunities for all individuals to fulfill their scientific potential, regardless of their background, identity, or circumstances.

A commitment to inclusion leads to innovation by attracting the widest possible talent to the community

and fostering greater diversity of ideas, approaches, and perspectives. The Allied Program Committee and the Community Organizers aim to select speakers and session chairs that represent the breadth and diversity of the discipline and of conference participants. GSA especially encourages the Committee and Organizers to select excellent speakers from groups that have been historically excluded or marginalized in science.

Social Media/Photo/Video Policy

Live posting of presentations on social media is allowed unless the speaker explicitly opts out by stating so at the start of their talk. Taking or sharing photos or videos of posters is permitted only with the presenter's consent during the assigned poster session. Taking photos of posters while the presenter is not present is strictly prohibited. By attending a GSA Conference, you grant GSA the right to use your photograph, video, name, and likeness for use in GSA educational, news, or promotional materials.

Family Policy

PEQG 2026 welcomes attendees with children!

Children are allowed in plenary, concurrent, and poster sessions; this includes babywearing of young children. Those travelling with family members or caregivers who are not in the scientific community and not registered for the meeting can obtain a guest pass from the conference Registration Desk so that they can accompany children into the poster sessions. All guests will be asked to agree to the Conference Code of Conduct and will need a name badge to enter the sessions. Guests must obtain their pass during posted registration hours.

To ensure the safety of all children in attendance and to create a productive and fulfilling meeting atmosphere for all attendees, we ask all parents and caregivers to abide by the following guidelines:

- Children ages 12 and under must be accompanied by an adult in all meeting areas.
- Parents and caregivers should do their best to ensure that children are not disruptive to any sessions they attend (including poster sessions).
- For safety reasons, children are not allowed in the Exhibit/Poster Hall during set-up or break-down times.

General Safety Tips for Attending Meetings

You should practice common sense safety guidelines when attending any conference:

- Be aware of your surroundings at all times, and don't get distracted by your phone.
- Use the buddy system when leaving the hotel, especially during early morning and late evening hours.
- Don't wear your meeting badge outside of the designated meeting space or when you leave the hotel.
- Don't carry a lot of cash or credit cards.
- Don't leave personal property unattended anywhere, at any time.

All times are listed in Pacific Daylight Time (PDT)

Tuesday, June 9		
12:00 p.m.–3:30 p.m.	Speaker Ready Room	Merrill Hall
12:00 p.m.–6:00 p.m.	Registration	Merrill Hall
12:30 p.m.–3:30 p.m.	Evolutionary Applications of Pan-genomes PEQG Doorstep Meeting (separate registration required)	Fred Farr Forum
1:00 p.m.–2:00 p.m.	Conference Success Tips and Welcome from GSA Engagement	Kiln
2:00 p.m.–2:30 p.m.	Getting Involved in GSA's Early Career Professional Development	Kiln
2:30 p.m.–3:30 p.m.	Individual Development Plan (IDP) and Career Exploration Workshop	Kiln
3:45 p.m.–5:00 p.m.	Welcome and Opening Keynote	Merrill Hall
5:00 p.m.–6:00 p.m.	Plenary Session: Initiatives in Education, Pedagogy, Engagement, and Outreach	Merrill Hall
6:00 p.m.–7:00 p.m.	Dinner (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
7:00 p.m.–8:00 p.m.	Mentor/Mentee Meet-up (all are welcome)	Phoebe A Hurst Social Hall
Wednesday, June 10		
7:30 a.m.–1:00 p.m.	Speaker Ready Room	Merrill Hall
7:30 a.m.–9:00 a.m.	Breakfast (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
7:30 a.m.–8:00 a.m.	Netwalking	
8:00 a.m.–3:00 p.m.	Registration	Merrill Hall
8:30 a.m.–10:00 p.m.	Open Poster Viewing	Fireside Pavilion
9:00 a.m.–11:45 a.m.	Plenary Session: Computational and Statistical Genetics	Merrill Hall
12:00 p.m.–1:00 p.m.	Lunch (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
12:00 p.m.–1:00 p.m.	Editorial Board Lunch	Kiln
1:30 p.m.–3:45 p.m.	James F. Crow Early Career Researcher Award Finalist Talks	Merrill Hall
4:15 p.m.–5:30 p.m.	Plenary Session: Human Variation, Health, and Disease	Merrill Hall
6:00 p.m.–7:00 p.m.	Dinner (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
7:30 p.m.–8:15 p.m.	Keynote #2, Jenny Tung	Merrill Hall
7:30 p.m.–10:30 p.m.	Exhibit Viewing	Fireside Pavilion
8:30 p.m.–10:00 p.m.	Photographer Headshots	Fireside Pavilion
8:30 p.m.–10:00 p.m.	Poster Presentations: W Posters (8:30–9:15 p.m. even; 9:15–10:00 p.m. odd)	Fireside Pavilion

Thursday, June 11		
7:30 a.m.–1:00 p.m.	Speaker Ready Room	Merrill Hall
7:30 a.m.–9:00 a.m.	Breakfast (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
7:30 a.m.–8:00 a.m.	Netwalking	
8:30 a.m.–1:00 p.m.	Registration	Merrill Hall
8:30 a.m.–10:00 p.m.	Open Poster Viewing	Fireside Pavilion
9:00 a.m.–12:00 p.m.	Plenary Session: Complex Traits	Merrill Hall
12:00 p.m.–1:00 p.m.	Lunch (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
12:15 p.m.–1:15 p.m.	Genomic History Inference Strategies Tournament Workshop (lunch ticket required)	Woodlands
1:30 p.m.–3:30 p.m.	Plenary Session: Genome Biology	Merrill Hall
4:00 p.m.–5:15 p.m.	Plenary Session: Fitness Landscapes	Merrill Hall
5:00 p.m.–6:00 p.m.	Teaching with Purpose: Implementing the New Genetics Learning Framework	Kiln
6:00 p.m.–7:00 p.m.	Dinner (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
7:30 p.m.–8:15 p.m.	Keynote #3 Jeffrey Ross-Ibarra	Merrill Hall
7:30 p.m.–10:30 p.m.	Exhibit Viewing	Fireside Pavilion
8:30 p.m.–10:00 p.m.	Poster Presentations: T Posters (8:30–9:15 p.m. even; 9:15–10:00 p.m. odd)	Fireside Pavilion
8:30 p.m.–10:00 p.m.	Poster Session and Exhibits	Fireside Pavilion
Friday, June 12		
7:30 a.m.–12:00 p.m.	Speaker Ready Room	Merrill Hall
7:30 a.m.–9:00 a.m.	Breakfast (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
7:30 a.m.–8:00 a.m.	Netwalking	
9:00 a.m.–12:00 p.m.	Plenary Session: Evolutionary Genetics	Merrill Hall
12:00 p.m.–1:00 p.m.	Lunch (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
1:30 p.m.–4:45 p.m.	Keynote #4 (Session Chairs) and Awards	Merrill Hall
6:00 p.m.–7:00 p.m.	Dinner (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall
7:00 p.m.–8:30 p.m.	Closing Mixer	
Saturday, June 13		
7:30 a.m.–9:00 a.m.	Breakfast (for those staying at Asilomar or who purchased a meal plan)	Crocker Dining Hall

Tuesday, June 9, 2026

12:30 p.m.–3:30 p.m.
Fred Farr Forum

Evolutionary Applications of Pan-genomes PEQG Doorstep Meeting (separate registration required)
Led by John Lovell and Avril Harder, Genome Sequencing Center, HudsonAlpha Institute for Biotechnology

The availability of many reference genomes within and across species provides a powerful foundation to discover the causes and consequences of molecular evolution. When integrated into a single resource, these "pan-genomes" can capture the full spectrum of sequence and functional variation across individuals, populations, species, and higher order taxonomic groups. This richer framework can enable more accurate read mapping, variant discovery, and evolutionary inference, particularly in diverse or non-model systems.

This workshop will probe the challenges and benefits of pangenomics, through the lens of evolutionary population and quantitative genetics. Invited presentations, discussions, and hands-on tutorials will cover topics including:
- Pan-genome construction and analysis across very diverse taxa
- Phylogenetic inference in the context of multiple reference genomes
- Annotation of genes, structural variants, and functional effects
- Pan-genome graph construction and quality control

Tuesday, June 9, 2026

1:00 p.m.–2:00 p.m.
Kiln

Conference Success Tips and Welcome from GSA Engagement
The purpose of this event is to help first-time conference attendees and early career scientists make the most of the conference and provide a chance to meet other attendees in an informal setting. Topics covered may include introductions to organizers of the meeting, advice on having meaningful interactions, and an introduction to scientific events and other conference programming.

2:00 p.m.–2:30 p.m.
Kiln

Getting Involved in GSA's Early Career Professional Development
GSA Early Career Leadership Program (ECLP) members will join us in sharing how to get involved in GSA's professional development programming for early career scientists. GSA will walk through upcoming events and programs including how and when to apply to the ECLP.

2:30 p.m.–3:30 p.m.
Kiln

Individual Development Plan (IDP) and Career Exploration Workshop
This workshop will walk participants through the career exploration process by combining self-assessment exercises with IDP-informed strategies to break participants out of the linear career path. Participants will leave with a better understanding of their personal goals and how to ensure that their professional goals align with their values and needs.

Tuesday, June 9, 2026

3:45 p.m.–5:00 p.m.
Merrill Hall

Welcome and Opening Keynote
Session Chairs: Robert Unckless, University of Kansas; and Kirk Lohmueller, University of California, Los Angeles

3:45 p.m. Opening Remarks **Robert Unckless** University of Kansas

3:55 p.m. GSA Welcome and Awards **Jeffrey Ross-Ibarra** University of California

4:05 p.m. GSA Journals Overview **Lauren McIntyre**

1 4:15 p.m. Coalescent structure through time: A non-parametric approach **John Novembre** University of Chicago

Tuesday, June 9, 2026

5:00 p.m.–6:00 p.m.
Merrill Hall

Initiatives in Education, Pedagogy, Engagement, and Outreach
Session Chairs: Kevin Wei, University of British Columbia; and Julia Kreiner, University of Chicago

2 5:00 p.m. Visualizing the shared nature of human genetic variation **James Kitchens** University of California, Davis

3 5:15 p.m. Building an AI-assisted, Quarto-based digital course companion textbook to support a lab-based advanced bioinformatics course **Laurie Stevison** Auburn University

4 5:30 p.m. The Genomics Education Partnership: Leveraging comparative evolutionary genomics to engage biology students through course-based undergraduate research experiences **Laura Reed** The University of Alabama

5 5:45 p.m. Rhapsody of Genetics: An Algorithmic Composition System that Converts Genetics into Music and Web-Based Browser for Genomics Education **Siyuan Feng** University of Wisconsin Madison

Wednesday, June 10, 2026

9:00 a.m.–11:45 a.m.
Merrill Hall

Computational and Statistical Genetics
Session Chairs: Mahul Chakraborty, Texas A&M University; and Joana Rocha, New York University

22 9:00 a.m. A General FST Framework Reveals the Variability of Rare Versus Common Alleles **Maike Morrison** Santa Fe Institute

23 9:15 a.m. Leveraging Ancestral Recombination Graphs to Detect Adaptive Differences Among Gene Duplicates **Charlotte LeMay** University of Texas at Austin

24 9:30 a.m. An Evolutionary Multi-Omic Framework to Assess the Evidence for Adaptive Regulatory Evolution Across Diverse Molecular Traits **Siyuan Feng** University of Wisconsin - Madison

25 9:45 a.m. Increased Genetic Diversity and Residual Stratification Contribute to Polygenic Score Prediction Accuracy **Nicole Kleman** University of Minnesota

26 10:00 a.m. The Impact of Proxy and Missing Contexts on Polygenic Score Calibration **Shevaughn Holness** Brown University

Break
10:15 a.m.–10:45 a.m.

Wednesday, June 10, 2026

Computational and Statistical Genetics (cont'd)
Merrill Hall

27 10:45 a.m. Microevolutionary cophylogeny using ancestral recombination graphs **Rowan Hart** University of Chicago

28 11:00 a.m. Jointly inferring population sizes and the fitness effects of new beneficial mutations **Solomon Sloat** University of North Carolina Chapel Hill

29 11:15 a.m. Quantifying selection on the nonsynonymous human mutation spectrum **Ryan Gutenkunst** University of Arizona

30 11:30 a.m. The dawn of phylogenetic comparative graph neural networks (PCGNNs): Applications to quantitative trait imputation and ancestral state reconstruction **Austin Patton** Arcadia Science

Wednesday, June 10, 2026

1:30 p.m.–3:45 p.m.
Merrill Hall

James F. Crow Early Career Researcher Award Finalist Talks
Session Chairs: Bret Payseur, University of Wisconsin; and Amanda Larracuente, University of Rochester

1:30 p.m. Introduction

31 1:40 p.m. Balanced polymorphism in a floral transcription factor underlies an ancient rhythm of daily reciprocal sex alternation in avocado **Jeffrey Groh** University of California Berkeley

32 2:05 p.m. Uncovering the Dynamics of Population Structure Through Time Using Genome-Wide Genealogies **Yun Deng** Stanford University

33 2:30 p.m. Small population size and isolation drive low genetic diversity, inbreeding depression, and an elevated mutation rate in the endangered Devils Hole pupfish (Cyprinodon diabolis) **David Tian** University of California, Berkeley

34 2:55 p.m. Gene-specific selective sweeps are pervasive across human gut microbiomes **Richard Wolff** University of California, San Diego

35 3:20 p.m. Ultra-soft sweeps drive viral escape from broadly neutralizing antibodies and generate novel diversity signatures **Elena Romero** University of Washington

Wednesday, June 10, 2026

4:15 p.m.–5:30 p.m.
Merrill Hall

Human Variation, Health, and Disease
Session Chairs: Megan Behringer, Vanderbilt University; and Carl Veller, University of Chicago

36 4:15 p.m. Human Y-specific satellite repeat variation is associated with trans-acting modulation of gene expression **Andrew Clark** Cornell University

37 4:30 p.m. Detecting parallel adaptive changes in the gut microbiome **Aina Martinez i Zurita** University of California, Los Angeles

38 4:45 p.m. Recovering signatures of archaic introgression using ancestral recombination graphs **Yulin Zhang** University of California, Berkeley

39 5:00 p.m. Pervasive cryptic selection in the human noncoding genome **Swetha Ramesh** University of California, Los Angeles

40 5:15 p.m. The effects of super-exponential growth on the human site frequency spectrum **Yuval Simons** University of Chicago

Wednesday, June 10, 2026

7:30 p.m.–8:15 p.m.
Merrill Hall

Keynote #2 Jenny Tung
Session Chairs: Erin Kelleher, University of Houston; and Yasir Ahmed-Braimah, Syracuse University

41 7:30 p.m. From individual life outcomes to evolutionary genetic change: lessons from multidecadal field studies of social mammals **Jenny Tung** Max Planck Institute for Evolutionary Anthropology

Thursday, June 11, 2026

9:00 a.m.–12:00 p.m.
Merrill Hall

Complex Traits
Session Chairs: Julia Kreiner, University of Chicago; and Joana Rocha, New York University

42 9:00 a.m. Cis-regulatory change underlies a balanced flower color polymorphism **Zachary Radford** University of South Carolina

43 9:15 a.m. Abundant Recurrent Mitochondrial Mutations and Widespread Mitonuclear Epistasis in *Caenorhabditis elegans* **Tuc Nguyen** New York University

44 9:30 a.m. Single-cell eQTL Mapping Reveals Environment-dependent Genetic Regulation **Akriti Agrawal** New York University

45 9:45 a.m. Unravelling the genetic basis of domestication in a multigenerational experiment with barley **Daniel Koenig** University of California, Riverside

46 10:00 a.m. Shifting Genetic Architecture in Human Complex Phenotypes **Ana Vazquez** Michigan State University

Thursday, June 11, 2026

10:15 a.m.–10:45 a.m.
Break

47 10:45 a.m. The genetic basis of neural circuit evolution for mate preferences **Emily Behrman** Dartmouth College

48 11:00 a.m. Evolution and genomic architecture of male reproductive strategies in swordtail fishes **Gabriel Preising** Stanford University

49 11:15 a.m. The genetic legacy of a single immigrant behind the Big Bird hybrid lineage in Darwin's finches **Rachel Goodridge** Cornell University

50 11:30 a.m. Beyond Fixation: Persistent Genetic Variation Under Intense Selection **Kenneth Arnold** Oregon State University

51 11:45 a.m. Measuring history dependence along evolutionary trajectories **Caroline Holmes** Harvard University

12:15 p.m.–1:15 p.m.
Woodlands

Genomic History Inference Strategies Tournament Workshop
GHIST is an annual forum for the community to test approaches for inferring evolutionary history from genomic data. Each year, the GHIST organizers release simulated population genomic data sets and host a competition to infer various aspects of the processes that generated those data, such as demographic history or selective sweeps. From the competitors' solutions, the community learns which approaches perform well or poorly in particular circumstances, and top competitors earn authorship and modest cash prizes. In this workshop, participants will be introduced to the competition and guided through their first submission. No prior knowledge is required. Please bring a laptop to participate.

Thursday, June 11, 2026

1:30 p.m.–3:30 p.m.
Merrill Hall

Genome Biology
Session Chairs: Mahul Chakraborty, Texas A&M University; and Kevin Wei, University of British Columbia

52 1:30 p.m. Y chromosome evolution shapes male reproduction in the world's highest-dwelling mammal **Daniel Shaw** University of Montana

53 1:45 p.m. PRDM9-Directed Meiotic Breaks are Hotspots for Structural Variants Formation Across Mouse Strains **Hilda Opoku Frempong** The Jackson Laboratory and The University of Maine

54 2:00 p.m. The evolution of structural and single nucleotide mutation across haplotype-resolved vertebrate genome assemblies **R. Nicolas Lou** University of California, Berkeley

55 2:15 p.m. Endogenous Retrovirus Editing Drives Structural Remodeling of Human Acrocentric Chromosomes **Rafael Contreras** University of Alabama at Birmingham

56 2:30 p.m. Strong Negative Selection on Structural Variants of Common Fruit Flies **Jen-Yu Wang** University of California, Irvine

57 2:45 p.m. Transposable elements shape local mutation landscapes through chromatin remodeling **Yuheng Huang** University of California, Irvine

58 3:00 p.m. Selection on telomere homeostasis drives the adaptive evolution of TERT in *Mimulus* **Naseem Samo** University of Kansas

59 3:15 p.m. Tempo and mode of transposon mobilization in the *Drosophila* male germline **Peiwei Chen** Cornell University

Thursday, June 11, 2026

4:00 p.m.–5:15 p.m.
Merrill Hall

Fitness Landscapes
Session Chairs: Julia Kreiner, University of Chicago; and Carl Veller, University of Chicago

60 4:00 p.m. Notes on a model for evolvability at the molecular scale: A reflection on Weinreich et al. 2006 **Brandon Ogbunu** Yale University

61 4:15 p.m. Module-selection balance in the evolution of modular organisms **Sergey Kryazhimskiy** University of California, San Diego

62 4:30 p.m. Massively parallel interrogation of the fitness of natural variants in ancient signaling pathways reveals pervasive local adaptation **Jose Aguilar-Rodriguez** Stanford University

63 4:45 p.m. The emergence of global epistasis from the geometry of the genotype-phenotype-fitness map. **Jhelam Nitin Deshpande** University of California, San Diego

64 5:00 p.m. Nucleotide and amino acid-level effects combine to shape the navigability of protein fitness landscapes **Bryan Gitschlag** Cold Spring Harbor Laboratory

Thursday, June 11, 2026

5:00 p.m.–6:00 p.m.
Kiln

Teaching with Purpose: Implementing the New Genetics Learning Framework

Hosted by the GSA Education Committee, this interactive workshop will help faculty understand and apply the newly updated Genetics Learning Framework in their courses. Participants will be introduced to this resource, engage in collaborative activities to align course content, develop ideas for applications, and share teaching strategies. The session will support faculty from diverse institutions and educational contexts in translating the learning objectives into meaningful classroom practice. Guided questions will structure discussion around what areas of genetics are the most important to a particular course context, how the framing of genetics concepts impacts students' identities and views on topics of societal significance, and more.

Friday, June 12, 2026

9:00 a.m.–12:00 p.m.
Merrill Hall

Evolutionary Genetics
Session Chairs: Megan Behringer, Vanderbilt University; and Kevin Wei, University of British Columbia

6 9:00 a.m. Elevated mutation near crossovers inhibits the evolution of recombination **Bret Payseur** University of Wisconsin-Madison

7 9:15 a.m. The repeated evolution of hybrid melanoma across swordtail fish **Kelsie Hunnicutt** Stanford University

8 9:30 a.m. Following the process of sunflower domestication through space and time with ancient DNA **Benjamin Blackman** University of California, Berkeley

9 9:45 a.m. Comparing the evolutionary consequences of large regions of suppressed recombination in Mimulus and Panicum **David B. Lowry** Michigan State University

10 10:00 a.m. The molecular axis of endemism is governed by the opposing forces of purifying and balancing selection **Alan Bergland** University of Virginia

11 10:45 a.m. Life history adaptation to an extreme habitat via a novel nonstructural supergene **Lila Fishman** University of Montana

12 11:00 a.m. The genetic basis of species persistence in two monkeyflowers with weak reproductive isolation **Henry Arenas-Castro** Yale University

13 11:15 a.m. Introgression and parental conflict shape repeated occurrences of postzygotic isolation **Megan Frayer** Yale University

14 11:30 a.m. Functional connectivity of a threatened avian habitat specialist in a fragmented landscape **Nancy Chen** University of California, Los Angeles

15 11:45 a.m. Dynamics and consequences of co-evolution between *Wolbachia* and *Drosophila recens* **Kelly Dyer** University of Georgia

1:30 p.m.–4:45 p.m.
Merrill Hall

Keynote #4 (Session Chairs) and Awards
Session Chairs: Jenn Coughlan, Yale University; and Justin Fay, University of Rochester

16 1:30 p.m. A draft *Pan*-pangenome reveals the diversity and selection landscape of humans, chimpanzees and bonobos **Joana Rocha** New York University

17 1:55 p.m. From Smeagol to Gollum: the trajectory, drivers, and consequences of Y chromosome degeneration **Kevin Wei** University of British Columbia

18 2:20 p.m. The spatiotemporal dynamics of plant adaptation to anthropogenic environments **Julia Kreiner** University of Chicago

19 3:15 p.m. Navigating Growth–Survival Trade-offs in Fluctuating Environments **Megan Behringer** Vanderbilt University

20 3:40 p.m. Role of genome structural variation in phenotypic diversity and adaptations **Mahul Chakraborty** Texas A&M University

21 4:05 p.m. Chromosome-scale drift under stabilizing selection **Carl Veller** University of Chicago

4:30 p.m. James F Crow Early Career Researcher and GSA Poster Awards

Poster Presentations (8:30 p.m.–9:15 p.m. even, 9:15 p.m.–10:00 p.m. odd)

W = Wednesday Presentation

T = Thursday Presentation

Complex Traits

66W Genetic and temperature variation in anteroposterior (AP) axial patterning of *Drosophila* **Lossie (Elle) Rooney** NC State University

67W A Simple Developmental Trait as a Genetic Entry Point into Complex Behavioral Variation in Drosophila **Sarah Ruckman** University of California, Irvine

68W Exposing the hidden load: Recessive deleterious variation and inbreeding depression in an outcrossing nematode. **Tom Parée** New York University

69W Natural Genetic Variation Shapes Metabolic Outcomes in an Insulin-Deficient *Drosophila* System **Yuyan Chen** University of Arkansas Fayettville

70W Genetic architecture of variation in locomotor senescence in *Drosophila melanogaster* **Bibhu Simkhada** Clemson University

71W FlyPaths: A pangenomic analytic architecture for complex trait mapping in *Drosophila* **Logan Cohen** University of Alabama

Complex Traits (Cont'd)

72W Kinship as a modifier of the transcriptome, epigenetic age predictions and physiological outcomes **Hippokratis Kiaris** University of South Carolina

73W Evolution towards monomorphy leads to a loss of plasticity in wing polymorphic crickets **Lourenco Martins** University of California, Berkeley

74W Wild Barley Cytoplasm Confers Environmental Stability and Modulates the Phenotypic Output of the *ari-e* Semi-Dwarfing Locus **Eyal Fridman** ARO

75W The *TaGSNE*, a *WRKY* transcription factor population genetic analysis indicates adaptive variation in relation to yield contributing traits in the global wheat germplasm **Nadia Khan** University of Karachi

76W Cellular Phenotypes That Mediate Context-Dependent Fitness Effects of Mutation **Kerry Geiler-Samerotte** Arizona State University

77W The Influence of Demographic History and Genetic Architecture on Complex Traits via Runs of Homozygosity **Mingzuyu Pan** Pennsylvania State University

78W High-resolution, meiosis-free mapping of genetic variation with CRI-SPA-Map **Megan Lawler** University of Minnesota

79W Epistasis between gene expression noise and functional mutations shapes cellular fitness **Wei-Han Lin** Institute of Molecular Biology, Academia Sinica

80W Genetic control of phenology and plasticity in sunflower across six diverse field environments **Peter Innes** University of Colorado, Boulder

81T Leveraging Runs of Homozygosity to Identify Recessive Complex Trait Architecture **Tessa Ferrari** University of Southern California

82T Genetic and environmental interactions outweigh mitonuclear coevolution for complex traits in *Drosophila* **David Rand** Brown University

83T Additive genetic control of gene expression underlying wood chemistry in *Populus trichocarpa* **Chanaka Abeyratne** Oak Ridge National laboratory

84T ESCALATOR: an efficient bioinformatics pipeline to harmonize and calculate polygenic scores in large-scale datasets **Meng Lin** University of Colorado Anschutz

85T Inferring selection on complex traits in British individuals using marginal coalescent trees **Obadiah Mulder** University of Southern California

86T Genetic architecture of PFAS toxicity revealed by natural variation in *C. elegans* **Tess Leuthner** Indiana University

87T Complex traits: genetic effects from social partners and from the microbiome **Amelie Baud** Centre for Genomic Regulation

88T *The center for genetics, genomics, and epigenetics of substance use disorders in outbred rats* **Abraham A. Palmer** University of California, San Diego

89T Evolved differences in mitochondrial function between temperate and tropical house mice **Mal Ballinger** Cornell University

90T Elucidating the genomic architecture governing chloroplast-nuclear stoichiometric balance **Evita Chee** University of California, Santa Barbara

Complex Traits (Cont'd)

91T The Limits of PCA: The Origin and Propagation of Residual Confounding in GWAS **Walid Mawass** University of Chicago

92T Thrifty Gene Signatures Underlying Diet-Dependent Variation in Drosophila Development **Xuan Zhuang** University of Arkansas

93T Search for durable wheat stem sawfly resistance QTL in spring wheat **Isha Isha** Montana State University

94T Predicting the body composition change in response to an aerobic exercising intervention on young adults, using genomic DNA, phenotypes and blood metabolomic profile before the intervention. **Yifei Li** Michigan State University

95T Genome-wide association studies of puberty and fertility traits in US beef heifers **Garrett Franklin** University of Missouri

96T Epistatic interactions detected by GWAS in thousands of F1 families establishes the molecular identities of phenotypically impactful natural variants **Brian Dilkes** Purdue University

Computational and Statistical Genetics

97W Representation in genetic studies affects inference about genetic architecture **Jared Cole** University of Texas at Austin

98W Improving polygenic score prediction for non-European ancestry groups through transfer learning. **Hao Wu** Michigan State University

99W The site-frequency spectrum under selection and time-varying demography **Anastasia Lyulina** Stanford University

100W Biobank-scale visualization and interactive exploration of ancestral recombination graphs with Lorax **Pratik Katte** University of California, Santa Cruz

101W Modeling Local Ancestry Covariance to Infer the Timing of Denisovan Admixture Events **Sarah Johnson** University of California, Berkeley

102W Pangenome architecture of quantitative trait loci in Darwin's finches **Jiayang Sun** Cornell University

103W Genome-wide linkage disequilibrium estimation reveals extensive correlations among unlinked sites **Anthony Greenberg** Bayesic Research

104W Predicting Theoretical Linkage Disequilibrium for Arbitrary Genome Sizes **Daniel Liu** University of California, Berkeley

105W GhostBuster: A Multi-Test Framework for Detecting Ghost Introgression **Margaret Wanjiku** San Diego State University

106W Panmap: Scalable alignment, genotyping, and phylogenetic placement on pangenomes at sample and read resolution **Alan Zhang** University of California, Santa Cruz

107W Balancing and Positive Selection Shapes the Spot Patterning Phenotype in the Masai Giraffe **Joy Love** Penn State University

108W Downstream biases introduced by identity-by-descent inference **Aydin Loid Karatas** University of Southern California

109W Using Ancestry Switches to Infer Demography in Admixed Populations **Shengmiao Huang** University of Southern California

Computational and Statistical Genetics (Cont'd)

110W How should we report genetic matches following an investigative genetic genealogy search? **Feriel Ouerghi** University of Southern California

111W Estimating uncertainty in sibling-based genotype-phenotype association **Xinyi Miao** University of Texas at Austin

112W Sex differences in crossover interference in house mice **Andrew Morgan** Duke University Hospital

113W *SaVor* - A Reproducible Structural Variant Calling and Benchmarking Platform from Short-Read Data **Trevor Mugoya** San Diego State University

114W Mutation Rate Heterogeneity Shapes Population-Level Genetic Variation **Mariele Lensink** University of California, Davis

115W Inferring the Breeding Sex Ratio by Comparing Variation on the X Chromosome and the Autosomes **William Spurley** University of Wisconsin-Madison

116W A rarefaction approach for identifying local introgression **Thomas Smith** Pennsylvania State University

117W Extracting quantitative genetic parameters from neural networks using equivalent linear mappings **George Sandler** Arcadia Science

118W Rethinking admixture mapping in terms of marginal coalescent trees **Junjian Liu** University of Southern California

119W Supervised machine learning jointly predicts geographic location and climate of origin from genotypes **Jordan Rodriguez** University of Oregon

120W Quantifying Factors That Influence Structural Variant Detection and Characterization **Diana Tataru** Utah State University

121W Leveraging Factor Analytic Linear Mixed Models for Prediction of Genotype-by-Environment Dynamics in Large-Scale Wheat Breeding Populations **Mitchell Eglinton** The University of Queensland

122W One Nation under a Groove: Ensemble Learning for Demographic Inference **Ananya Kapoor** University of Oregon

123W Information gain as a framework for evolutionary data collection **Ryan York** Arcadia Science

124W Model-based inference of regional African contributions in African-American genealogies using Transatlantic Slave Trade voyage records **Kennedy Agwamba** Stanford University

125W A neural model of linkage disequilibrium decay for recent effective population size inference **Chris Smith** Indiana University

126T Correcting for hematopoietic variation in whole blood sequencing isolates heritable aging signals in multigenerational pedigrees **Alexis Garretson** University of Utah

127T A Comparison of Phylogenetic Genotype to Phenotype Models **Adam Warlen** University of Missouri

128T Tandem Repeats and Adaptive Archaic Introgression in HPRC Individuals **Melody Chang** University of Oregon

129T The effect of missing data on ARG inference in an empirical system **Nicole Adams** University of Michigan

Computational and Statistical Genetics (Cont'd)

130T Cross-population replication analysis of STR-trait associations in the All of Us dataset **Nichole Owen** University of California, San Diego

131T Population genomics in hyper-polymorphic species: pangenomic approaches using the nematode *Caenorhabditis brenneri* **Anastasia Teterina** University of Oregon

132T ARGformer: learning on ancestral recombination graphs with transformers **David Bonet** University of California, Santa Cruz

133T DeepNe, A Novel Deep Learning Approach for Inference of Effective Population Size, Provides Precise Reconstruction of Founder Events Across Oceania **Samuel Sacco** University of California, Santa Cruz

134T Ancient local ancestry inference with a graph transformer **Cole Shanks** University of California, Santa Cruz

135T Predicting Puberty and Fertility Traits in Multi-breed Beef Heifer Cattle **Dotun Olaoye** University of Missouri-Columbia

136T Estimation of marginal geneaology using wavelets and graph convolutional neural networks **Dylan Ray** University of North Carolina at Chapel Hill

137T Beyond Glucose: Machine Learning Identifies Genetic Determinants of Mannose Metabolism Across More Than 1,000 Yeast Species **Benjamin Narh-Madey** Laboratory of Genetics, Wisconsin Energy Institute, Center for Genomic Science Innovation, J.F Crow Institute for the Study of Evolution, University of Wisconsin-Madison

138T Larger polygenic effects on health outcomes in groups with lower socioeconomic status **Olivia Smith** University of Texas at Austin

139T Dating large ARGs, with clinical applications **Peter Ralph** University of Oregon

140T Identifying multi-allelic quantitative trait loci using empirical haplotypes **Katelyn McInerney** University of North Carolina at Chapel Hill

141T Interrogating the role of gene-environment interactions in polygenic score portability **Roshni Patel** University of Oregon

142T Scalable Local Ancestry Inference Using Genotype Representation Graphs **Gordon Mei** Cornell University

143T Polygenic risk and association beyond linearity **Christophe Thomassin** Stanford University

144T Population Genetic Analysis of highly degraded ancient-DNA data **Benjamin Peter** University of California, Los Angeles

145T Neural networks preferentially learn additive models for genomic prediction **Aaron Kusmec** Kansas State University

146T Functional and evolutionary determinants of protein divergence in Drosophila **Anthony Jacob Joson** Temple University

147T A Statistical Framework to Infer the Mutation Model of Tandem Repeat Variants via The Ancestral Recombination Graph **Sebastián Iturbe** University of Oregon

148T Integrating GGE-Biplot Analysis with Genome-Wide Association for Multi-Scale Genetic Dissection of Biomass Stability and Adaptation in Switchgrass **Jonathan Concepcion** Michigan State University

149T How do Recurrent Bottlenecks Shape Selection in Structured Populations? **Kendra Zwonitzer** University of North Carolina at Chapel Hill

Computational and Statistical Genetics (Cont'd)

150T Can neutral coalescent models capture the quirks of site-frequency spectra in Atlantic cod? **Jack Edwards** Harvard University

151T Quantifying turnover in microbial communities using the traveling salesperson problem **Chloe Shiff** Stanford University

152T A moment projection framework for computing the expected site frequency spectrum under exact discrete Wright-Fisher dynamics **Jeremy J. Berg** University of Chicago

153T Eco-evolutionary Inference for Valley Fever **Julian Gottfried** Stanford University

Conservation and Ecological Genetics

154W Non-invasive genetic monitoring of a Ugandan elephant population using simulation-based spatially explicit close-kin mark-recapture **Gilia Patterson** University of Montana

155W Ancient Bottleneck events, varied patterns of selection, and increased risk of maladaptation shape the past, present and future population structure of a widespread conifer **Sean Collins** Northern Arizona University

156W Isolation in real-time: the demographic and fitness consequences of declining immigration **Jeremy Summers** Virginia Tech

157W Genetic early-warning signals of habitat fragmentation in dynamic migration networks **Ryan Chaffee** Cornell University

158W Comparative mutation load in the California Conservation Genomics Project **Anne Nakamoto** University of California, Santa Cruz

159W Population genomics of the stony coral *Acropora millepora* and its symbionts across the Great Barrier Reef **Daria Bykova** Columbia University

160W Population genomic health of an entire community of California wildlife **Erik Enbody** Cornell University

161W A unified theory of genetic and species diversity **Meixi Lin** University of California, Berkeley

162W The Population Genomics of Invasion: Founder effects, local adaptation, and chromosomal inversions shape the rapid evolution of an invasive migratory fish **Azwad Iqbal** Cornell University

163W Nothing to see here? Population and species level comparisons highlight lack of parallelism in polygenic trait evolution **Claire Schraidt** Yale University

164W Genomic diversity across 200 plant species of variable Red List status **Jules Perez** University of California, Berkeley

165W Local Environmental and Regional Oceanographic Factors Shape Genetic Structure for *Crassadoma gigantea* Across Natural and Anthropogenic Reefs **Hayley Goss** University of California, Santa Barbara

166W Population genomics of ʻōpaeʻula (*Halocaridina rubra*): conservation implications for highly structured populations of the state shrimp of Hawaii **Russell Fitzgerald-Cook** The University of Texas at Austin

167W Genomic insights into equids at the edge of extinction **Arielle Fogel** Cornell University

168W Higher genomic offset in planted forests of the UK reveals maladaptation risks under climate change **Guillermo Friis** Royal Botanic Gardens, Kew

Conservation and Ecological Genetics (Cont'd)

169W Genetic diversity loss in the Anthropocene **Moises Exposito-Alonso** University of California Berkeley, Howard Hughes Medical Institute

170W The genetics of inbreeding depression in a pedigreed wild population of Florida Scrub-Jays **Faye G. Romero** University of Rochester

171T Realized relatedness in a wild baboon population and its implications for kin discrimination **Carlota Galán-Plana** Max Planck Institute for Evolutionary Anthropology

172T Understanding the genomic architecture of inbreeding in the endangered mountain gorilla **Aditi Prasad Bangalore Venkateshwara** Max Planck Institute for Evolutionary Anthropology

173T Population genomic analyses reveal asexual reproduction may facilitate spread in a recently introduced sea anemone **Keira Monuki** University of California, Davis

174T Phylogenetic Modeling of the Endangered Pacific Pocket Mouse Using Mitochondrial Genomes **Jackson Wolfe** San Diego State University

175T Recombination and divergent selection shapes the genome architecture of the Hawai'i Island *Metrosideros* speciation **Askhan Shametov** University of Kansas

176T A genetic characterization of the elusive elephants of the Lisima highlands (Angola) **Carla Hoge** University of Chicago

177T The genomics of urban adaptation in house mice in the northeastern United States **Rene Clark** Drexel University

178T Assessing the response of giant kelp to marine heatwaves using temporal genomics **Meaghan Clark** University of California, Santa Cruz

179T Uncovering the genetic architecture of herbicide resistance in the agricultural weed *Amaranthus tuberculatus* using popGWAS **William Yaeger** University of Chicago

180T Using century-old fish collections to study rapid adaptation across space and time in the epicenter of marine diversity **Marianne Dehasque** University of California, Santa Cruz

181T Evolution and diversity of major histocompatibility complex II gene *DRB* in yellow-tailed woolly monkeys (*Lagothrix flavicauda*) **Chloe Leaman** Boston University

182T From Fragmentation to Near-Complete: A Framework for Managing Genetic Diversity in the Spoon-billed Sandpiper **Rachel Davis** Cornell University

183T Decoding the population structure and history of the world's deadliest cat **Victoria Grant** Stanford University

184T Genomic Offset Predicts Allele Frequency Changes but Not Always Population Fitness: Insights from Forward-Time Simulations **Andrew McCracken** University of Vermont

185T The contribution of introgression to local adaptation in North American jackrabbits **Jessica Scales** University of Montana

186T Museum genomics clarifies the evolutionary history and taxonomic status of the extinct Lotis blue butterfly (Lycaeides anna lotis) **Alia Donley** Utah State University

187T Longitudinal population genetics of the cooperatively breeding Acorn Woodpecker (*Melanerpes formicivorus*) **Chi Wei** Old Dominion University

Evolutionary Genetics

188W Genetic and environmental basis of Allen's rule in tropical and temperate house mice (*Mus musculus domesticus*) **Sylvia Durkin** University of California, Berkeley

189W Early life-stage thermal resilience is determined by climate-linked regulatory variation **Joaquin Nunez** University of Vermont

190W Fitness effects of mitonuclear incompatibilities in Swordtail (Xiphophorus) hybrids **Nemo Robles** Stanford University

191W There are no unlinked loci: How pedigrees couple neutral genealogies across the genome **Maximillian Newman** University of Chicago

192W High-resolution mapping of a rapidly evolving complex trait reveals genotype-phenotype stability and an unpredictable genetic architecture of adaptation **Jessica Smiley-Rhodes** Stanford University

193W Hidden in plain sight: How Ks histogram dynamics can reveal and obscure ancient whole genome duplications. **Tamsen Dunn** University of Arizona

195W Parallel Molecular Evolution Across Replicated *Anolis* Lizard Adaptive Radiations **Aryeh Miller** Washington University in St. Louis

196W Collateral fitness effects of mutation are not commonly caused by protein misfolding **Natalie Quan** Arizona State University

197W Population genomics and shell morphometrics of a coastal dogwhelk identify history of glacial refugia **Emily Longman** University of Vermont

198W Origin and evolutionary history of an urban underground mosquito **Yuki Haba** Columbia University

199W Evolutionary adaptation proceeds through a small number of phenotypic modules **Mohammad Hossein Donyavi** Arizona State University

200W Rapid genome-wide introgression reveals fitness advantage of immigrant genotypes **Benjamin Flanagan** University of Connecticut

201W Bugs in the balance: local adaptation and balancing selection shape amino acid variation in *Anopheles* **Clara Rehmann** University of Oregon

202W Fixation Probabilities of Mutant Alleles in an Ecological Context **Kunaal Joshi** Arizona State University

203W Mutation load at active tRNA genes in three nematode species **Avery Bell** Georgia Institute of Technology

204W Harnessing citizen science to contextualize adaptation mechanism discovery **Xianran Li** USDA-ARS

205W Increased male frequency in *Caenorhabditis briggsae* intra-species hybrids occurs by genetic incompatibility that produces X nondisjunction **Joseph Ross** California State University, Fresno

206W Can the Z:A ratio serve as a genomic index of sexual selection strength? **H. Luke Anderson** Cornell University

207W Modes of natural selection on maternal and zygotic gene expression in *Drosophila melanogaster* embryos **Brent Lockwood** University of Vermont

Evolutionary Genetics (Cont'd)

208W New insights into the nature of genetic variation revealed by highly-resolved longitudinal studies **Mark Bitter** Stanford University

209W Evolutionary and Functional Conservation of Topologically Associating Domain Boundaries in Rice Genomes **Owen Geyman** New York University

210W The evolutionary and functional impact of the human-specific acyl-CoA thioesterase (*ACOT1*) gene duplication **Carsyn Bonesteel** University at Buffalo

211W The genetic basis of intrinsic postzygotic reproductive isolation in necrotic Mimulus **Pia Franziska Schwarz** Yale University

212W Population Genetics of Source–Sink Dynamics **Ziyang Xia** Cornell University

213W Analytical expectations for ancestry junction accumulation in admixed genomes **Shirin Nataneli** University of Southern California

214W Simple and complex: mapping the genetic basis of insecticide resistance across genotypes and environments to predict resistance evolution **Seth Rudman** Washington State University

215W Disentangling Reticulated Evolution: Genomic Signatures of Introgression in Darwin's Finches **Gerardo Cendejas Mendoza** Cornell University

216W Study pollinator syndrome switches through evolution experiment with *Mimulus* **Foen Peng** Haverford College

217W Genetic incompatibilities and compensatory adaptation drive hybrid genome evolution in yeast **Gregory Lang** Lehigh University

218W Microsyntenic Divergence with Conserved Protein Domains of *chico* Across *Drosophila* Subgenera During Species Radiation **Elizabeth Wasson** University of Alabama

219W A Molecular Evolution Analysis of *Phosphoinositide-dependent-kinase-1 (Pdk1)* Orthologs Across *Drosophila* **Emie Vandiver** University of Alabama

220W Sex differences in recombination in house fly, *Musca domestica* **Basanta Bista** University of Houston

221W Theory of Epimutation-Selection Balance **Gregory Chernomas** University of Guelph

222W Integrating competition into quantitative genetics **Yasmine McDonough** University of British Columbia

223W Deer mice (*Peromyscus maniculatus*) of California: Investigating evolutionary history, conservation genomics of island populations, and patterns of co-diversification with Sin Nombre hantavirus **Tommy Herrera** University of California Berkeley

224W Premature hair-greying caused by melanocyte-specific gene regulation in American black bears **Emily Puckett** University of Memphis

225W Massively parallel evolution reveals a scaling law between cell size and cell density **Alexander Sastokas** Arizona State University

226W Molecular and In Silico Characterization of Xylanase Enzyme in *Sordaria fimicola* **Muhammad Saleem** University of the Punjab

Evolutionary Genetics (Cont'd)

227W Adaptive Dynamics of Repeated Local Adaptation in *Amaranthus* **Elizabeth Polston** University of Chicago

228W Spontaneous un-selected mutation patterns in *Candida albicans* reveal the relative stability of alternative ploidy states **Nathaniel Sharp** University of Wisconsin-Madison

229W Comparative single-cell analysis of transcriptional bursting reveals the role of genome organization in de novo transcript origination **UnJin Lee** Rockefeller University

230W Rare intronic variants drive high variance in human ancestral fitness under a high deleterious mutation rate **Ulises Hernandez** University of Arizona

231W Evolutionary genomics of *Paramecium* mitochondrial genomes **Ravina Telkar** Arizona State University

232W Sex, DNA Repair, and the germline mutational landscape in *Drosophila melanogaster* **Rob Melde** University of Wisconsin-Madison

233W Investigating the effect of mild heat stress on pollen viability in multiple species across a variety of scales **Derek Denney** Michigan State University

234W Genomic and transcriptomic signatures of proto-neo-Y chromosome evolution in *Drosophila americana* **Zethus Avery** Syracuse University

235W Lineage specific selection in the mound-building mouse Mus spicilegus **Mara Baylis** University of California, Berkeley

236W A chromosomal inversion underlies life history divergence on a microhabitat scale in yellow monkeyflower **Madison Plunkert** Michigan State University

237W Turtles reveal novel insights into PRDM9's role in recombination rate landscape evolution **Laurie Stevison** Auburn University

238W Insect Compound Eye Cell Type Evolution Across a Speciation Continuum **Wei Lu** University of Chicago

239W A comparative genomic view of Tandem Repeat evolution in primates **Carolina de Lima Adam** University of Oregon

240W The Genetic Basis of the Repeated Postzygotic Isolation in *Mimulus* **Hagar Soliman** Yale University

241W Contemporary sex-differential selection across organisms and life stages **Matthew Ming** University of Texas at Austin

242W Inferring models of ancient introgression with single unphased genomes and a two-locus statistic **Nicholas Collier** University of Wisconsin-Madison

244W k-mer counts in pooled sequencing data rapidly estimate frequencies of known alleles in a pangenome graph **Miles Roberts** University of California, Berkeley

245W Chromosome-level assembly and annotation of the genomes of two Antarctic pinniped sister species: the leopard seal (*Hydrurga leptonyx*) and the Weddell seal (*Leptonychotes weddellii*). **Juan Pablo Aguilar Cabezas** Hampton University

246W Resolved globally, conflicted locally: Multi-scale genetic architecture of intralocus sexual conflict in human metabolism **Anasuya Chakrabarty** Ashoka University

247W Pangenome-based investigation of genomic diversity in *Kaolinonychus*: A harvestmen lineage with deep admixture history and troglophilic adaptation (Arachnida, Opiliones, Paranonychidae) **Choongwon Jeong** Seoul National University

Evolutionary Genetics (Cont'd)

248W Detecting Positive Selection Using Spatial Autocorrelation and Haplotype Structure in Populations with Limited Dispersal **Amatur Rahman** Pennsylvania State University

249W Gene Expansion and Regulatory Rewiring Shape Sex-Biased Evolution of the Mouse Submandibular Gland **Luane Jandira Bueno Landau** University at Buffalo

250W MHC class II DQB heterozygosity confers transgenerational fitness advantage in wild dolphins **Oliver Manlik** United Arab Emirates University

251W Selective sweeps of recessive beneficial alleles in populations with continuous spatial structure **Freya Kailing** Cornell University

252W Characterizing genomic structural variation within and between populations of *Aedes aegypti* **Gabriela Valente-Almeida** University of North Carolina Chapel Hill

253W Evolution of mutational fitness effects in island populations **Emma Howell** University of Wisconsin-Madison

254W Comparative Population Genetics of Octopus Sister Species **Silas Tittes** University of Oregon

255W Regulation of gene expression shapes genotype x environment interactions in switchgrass **Colette Berg** Michigan State University

256W Reused Genes and Divergent Paths: Genomic Predictability in Stickleback Ecotypes **Diana Rennison** University of California, San Diego

257W From Monogamy to Polygamy: Mating Systems as Drivers of Sex-Biased Gene Evolution in Syngnathids **Morjina Solaiman** University of Idaho, Department of Biological Science

258W Germline mutation rate evolution in species with contrasting mating systems **Ivanna Ostapchuk** Columbia University

259W Evolution of gene expression in the trout retina **Emily Kopania** University of Pittsburgh

260W Sequence context and methylation interact to shape germline mutation rate variation at CpG sites **Sheel Chandra** University of Pennsylvania

261W The genomic landscape of structural variation during parallel divergence in three-spined stickleback **Matthew Farnitano** University of California, San Diego

262W Adaptation vs sexual selection: Exploring the genes and selective pressures underlying a pheromone difference between natural Drosophila populations **Myron Child** University of Wisconsin-Madison

263W The genetics of gene expression divergence in wild baboons **Shuyu He** Duke University

264W Numerical challenges when inferring selection and population size history from the site frequency spectrum **Jonathan Wiese** University of Chicago

265W Genomic analysis of *Solanum polygamum* suggests convergent evolution of sex determination via a response regulator gene **Aldo Carmona Baez** North Carolina State University

266W Spatial population structure in the hyperpolymorphic Pacific acorn barnacle **Angel Rivera-Colon** University of Oregon

267W Using an extinction-recolonization framework to model *P. falciparum* populations **Cobi Henry** University of North Carolina at Chapel Hill

Evolutionary Genetics (Cont'd)

268W Population history and migration in sub-Saharan African *Drosophila melanogaster* **Austin Daigle** University of North Carolina at Chapel Hill

269W The harmonic mean recombination rate: properties, measurement, and implications **Tyler Kent** University of Chicago

270W Identifying key adaptations facilitating functional differentiation of duplicate genes **Liaoyi Xu** University of Texas at Austin

271W Decoupling Migration from Coalescence under the Structured Serial Coalescent **Hao Shen** University of Chicago

272W Spatial Transcriptomics to Characterize a Novel Pigmentation Trait in Swordtail Fish **Rhea Sood** Stanford University

273T Integrating Pan-Genome and AI to Identify Adaptive Causal Variants for Maize Environmental adaptation **Wei-Yun Lai** Cornell University

274T The influence of abiotic factors on a selfish centromere **Findley Finseth** Scripps, Pitzer, and Claremont McKenna Colleges

275T Mapping the Genomic Landscape of Convergent Dietary Adaptation Across Mammalian Liver Transcriptomes **Gwendolyn Johnson** Lehigh University

276T Detecting Convergent Evolution Beyond Individual Genes: Insights from Cluster-Level Selection **Ethan Talley** University of Arkansas

277T Population Structure and Genetic Divergence in Marine Threespine Sticklebacks Along the Western Coast of North America **David Ferranti** University of California, San Diego

278T A statistical method to estimate mutational variance in humans **Arun Durvasula** University of Southern California

279T The rights and wrongs of rescaling in population genetics simulations **Parul Johri** University of North Carolina at Chapel Hill

280T A catalog of structural variation in sample of high-quality *Culex quinquefasciatus* genome assemblies **Daniel Schrider** University of North Carolina at Chapel Hill

281W Differentiating shared ancient origin and recent admixture for genetic similarities between populations **Eaaswarkhanth Muthukrishnan** University of Southern California, Keck School of Medicine

282T Pangenome reveals diverse structural variants underlying repeated evolution of herbicide resistance in *Amaranthus tuberculatus* **Jacob Montgomery** University of Chicago

283T A Simple Genetic Basis for Necrosis in *Mimulus guttatus* **Erin Howard** University of Georgia

284T The genetic basis of two melanic pigmentation traits in *Xiphophorus nezahualcoyotl* **Lyle Given** Stanford University

285T Re-interpreting Deleterious Variant Burden in Populations with Elevated Runs of Homozygosity **Leqi Tian** University of Southern California

286T Transgenerational inheritance of thermal tolerance reveals generation-specific gene-expression responses to environmental change **Melissa Pespeni** University of Vermont

287T Investigating the role of interspecific introgression in flowering time variation in *Capsella bursa-pastoris* **Maya Wilson Brown** Michigan State University

Evolutionary Genetics (Cont'd)

288T A diffusion framework for the steady-state allele frequency distribution under fluctuating selection and population size **Hisham Ali** Arizona State University

289T The trans-Pacific voyage that shaped the pattern of genetic variation and enrichment of functional alleles in Native Hawaiians **Ji Tang** University of Southern California

290T Disentangling the biogeography of multiple fermentative yeast species **Yu-Chen Yeh** Academia Sinica

291T Heavy-tailed dispersal and its impact on local adaptation: Revisiting the British peppered moth **Sherif Negm** University of Chicago

292T Convergent genome- and gene-level constraints shape repeated environmental adaptation in grasses **Sheng-Kai Hsu** Institute for Genomic Diversity, Cornell University

293T Population-level divergence in 3D genome organization revealed by comparative chromatin contact matrix analysis in threespine stickleback **Fahad Gilani** University of Connecticut

294T Comprehensive Genomic Landscape and Selection History of Adaptive Introgression in Peruvians **Susanna Gutierrez** University of Michigan

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308T Rapid Adaptation and Extinction In Synchronized Outdoor Evolution Experiments of Arabidopsis thaliana **Xing Wu** University of California, Berkeley

309T A Coalescent Framework to Model Pathogen Evolution as a Metapopulation **James Crescenzi** University of North Carolina at Chapel Hill

310T Population Structure, Ancestry, and Demographic History of House Mice in the Northeastern United States **Zade Alafranji** Drexel University

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312T Inferring unknown spatial locations with genome-wide genealogies **Alexander Lewanski** Michigan State University

313T The Extent of Sparsity In The Genotype-Phenotype-Fitness Map **Reza Ghelich** Arizona State University, Biodesign Center for Mechanisms of Evolution

314T Differential adaptation and genic divergence related to drought tolerance among rattlesnakes within a phylogenetic framework **Austin Biddy** University of Alabama at Birmingham

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318T Quantifying the Genome-Wide Effect of Polygenic Selection over a Single Generation **Gabriele Sgarlata** University of California, Davis

319T Does polygenic adaptation leave a molecular trace? **Dandan Peng** University of Southern California

320T An *FT* paralog causes photoperiod divergence between closely related *Mimulus* **Logan Scott** University of Georgia

321T Contribution of locally adapted variation to adaptive potential in experimental cages of *Drosophila melanogaster* **Jamie Freeman** University of Wisconsin-Madison

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327T The counteracting effects of hitchhiking and repulsion of deleterious alleles during a selective sweep **Maya Weissman** University of California, Los Angeles

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331T BLInG: Enabling Population Genomic and Evolutionary Studies of Unicellular Organisms Through High-Throughput Single-Cell DNA Sequencing **Parker Crossland** Arizona State University

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334T A pedigree study in rhesus macaques reveals a large fraction of early embryonic germline mutations **Anastasia Stolyarova** Columbia University

335T Novel gene content and meiotic drive in *Mimulus guttatus* **Evan Stark-Dykema** University of Montana

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342T An exapted transposase suppresses the *Mu*-suppressible lesion-forming Uroporphyrinogen III Synthase mutant allele **Rajdeep Khangura** University of Wisconsin-Madison

343T High-throughput analysis of the eco-evolutionary dynamics over 75,000 generations in the E. coli long-term evolution experiment using a novel barcoding system **Jenya Belousova** Harvard University

344T The polygenic basis of ecogeographic isolation maintains species distinction despite ongoing introgression **Julia Harencar** University of California, Davis

345T Unveiling the genetic basis of water stress resilience in *Fragaria vesca* through high-resolution genome-wide association mapping **Sebastian Arenas** Swedish University of Agricultural Sciences

346T Evolutionary Flexibility of *Daphnia* Ribosome **Man Lin** Arizona State University

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347T Not All Roads Lead to Red: The genetics of sexual dichromatism in the northern cardinal (Cardinals cardinalis) **Miranda Wade** The University of Hong Kong

348T Living with a killer: how coevolved *Saccharomyces cerevisiae* become killer toxin resistant **EmilyClare Baker** University of Michigan Medical School

349T Genomic signatures of spatially heterogeneous selection in evolving *Pseudomonas fluorescens* populations **Chimaroke Onyeaghala** Clarkson University

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351T The role of structural variants in *Formica* ant supergenes **Zul Alam** University of California, Riverside

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356T Quantifying anthropogenic effects on maize genetic diversity **Samantha Snodgrass** University of California, Davis

357T Local adaptation in *Mimulus guttatus* **Katherine Toll** University of South Carolina

358T Natural variation reveals hidden divergence in the evolution of a polyphenism **Stephen Dreyer** Indiana University

359T Inference of polygenic selection on thermal performance variation in a marine invertebrate **Lawrence Uricchio** Tufts University

Fitness Landscapes

360W Finding order in evolution: how fitness reveals hidden biological modules **Kara Schmidlin** Arizona State University

361W Deconstructing empirical fitness seascapes across scales of granularity **Swathi Nachiar Manivannan** Yale University

362W Ascertainment biases empirical fitness landscapes **Maryn Carlson** NSF-Simons National Institute for Theory and Mathematics in Biology

363W Global epistasis constrains evolution across environments. **Jhelam Nitin Deshpande** University of California, San Diego

364W Interpreting empirical fitness landscapes under a combinatorial fitness-landscape model **Shoshana Elgart** Stanford University

365T The genetic architecture of an ancestral neofunctionalization **Jose Fabricio Lopez Hernandez** University of Chicago

366T The distribution of fitness effects of new mutations in regulatory regions of *D. melanogaster* **Austin Daigle** University of North Carolina at Chapel Hill

Fitness Landscapes (Cont'd)

367T Beyond Misfolding: How Cellular Context Reshapes a Deep Mutational Fitness Landscape **Ashley Brown** Arizona State University

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369T Temperature Seasonality and Water Vapor Pressure as Selective Drivers of Local Adaptation in the Woodland Strawberry **Oluwafemi Alaba** University of California, Riverside

Genome Biology

370W Unusual population frequencies of transposable element in *Drosophila Affinis* and *Drosophila Algonquin* **Mark Xu** University of California, Irvine

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386T The rapid evolution of centromeric satellite sequences in house mouse lineages **Jitendra Thakur** Emory University

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Human Variation, Health, and Disease

399W Antimicrobial activity characterization of a novel anticancer peptide **Ahmed Ibrahim** The American University in Cairo

400W APOE ε4 risk allele accelerates episodic memory and mental status decline in women faster than men **Yanyan Wu** University of Hawaii at Manoa

401W Large-effect drivers of gene-expression variation across individuals **Alber Aqil** University of Michigan

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403W Unraveling the contribution of mutational rate variation to observed patterns of driver mutations in human cancer **Diljeet Kaur** University of Pennsylvania

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405W The Genomic Legacy of Neanderthal and Denisovan Ancestry Across 50,000 Years of Evolutionary History in East Asia **Sophie Joseph** University of California, Berkeley

Human Variation, Health, and Disease (Cont'd)

406W Identifying Germline Mutation Hotspots and Their Determinants in Human Genomes **Nathan Cramer** University of California, Berkeley

407T Cross-population discovery and lung cancer risk prediction using TOPMed imputation and mixed-effect models **Yafang Li** University of New Mexico

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410T Genetics of Stroke in Sickle Cell Disease Patients **Anvita Kulshrestha** Duke University

411T Gene regulation changes associated with a chromosome 15q13.3 deletion **Adeena Rahman** University of California, Davis

412T Translating Sequence to Structure: Defining the Biophysical Fitness Landscape of the HDAC6 Catalytic Domain **Paul Fong** Duke University

Initiatives in Education, Pedagogy, Engagement, and Outreach

413W Engaging Undergraduates in Evolutionary Genomics through Biocontrol Agents at a Rural PUI: A Scaffolded Research Pipeline **Amanda Stahlke** Colorado Mesa University

414T Efficient Repetition in Molecular Evolution: Integrating Frequent Practice Across Discussion Sections, Online Homework, and Problem-Based Review Sessions **Hayley Goss** University of California, Santa Barbara

Microbial and Host/Microbial Genomics

415W Community coalescence reveals strong selection and coexistence within species in complex microbial communities **Sophie Walton** Stanford University

416W Uniform bacterial genetic diversity along the gut **Michael Wasney** University of California, Los Angeles

417W Using strain-resolved metagenomics to track microbiome transmission in a wild primate **Reena Debray** Max Planck Institute for Evolutionary Anthropology

418W How does environmental difference, distance, and dimensionality shape Pareto fronts? **Elisa Visher** Stanford University

419W Microbial single-cell RNA sequencing data reveal opposing transcriptional relationships at population and single-cell scales **Leandra Brettner** Arizona State University

420W Capture, characterization, and experimental evolution of barcoded mobile genetic elements **Milo Johnson** University of California, Berkeley

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422T Mapping the landscape of viral-immune coevolutionary dynamics **Tatiana Ruiz-Bedoya** Harvard University

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Microbial and Host/Microbial Genomics (Cont'd)

424T Comparative Gut Viromes of Wild Lowland (*Lagothrix lagotricha tchudii)* and Yellow-tailed Woolly Monkeys (*Lagothrix flavicauda*) **Reese Hotten-Somers** Boston University

425T Adaptations spreading across human gut microbiomes arise from complex multisite adaptive architectures **Peter Laurin** University of California, Los Angeles

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Phylogenetics

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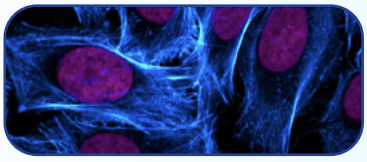
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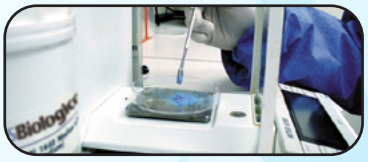
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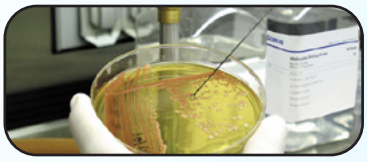
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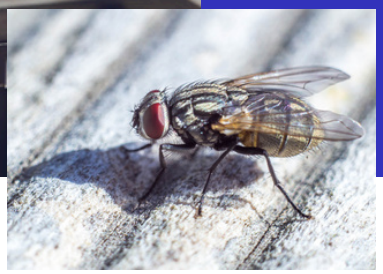

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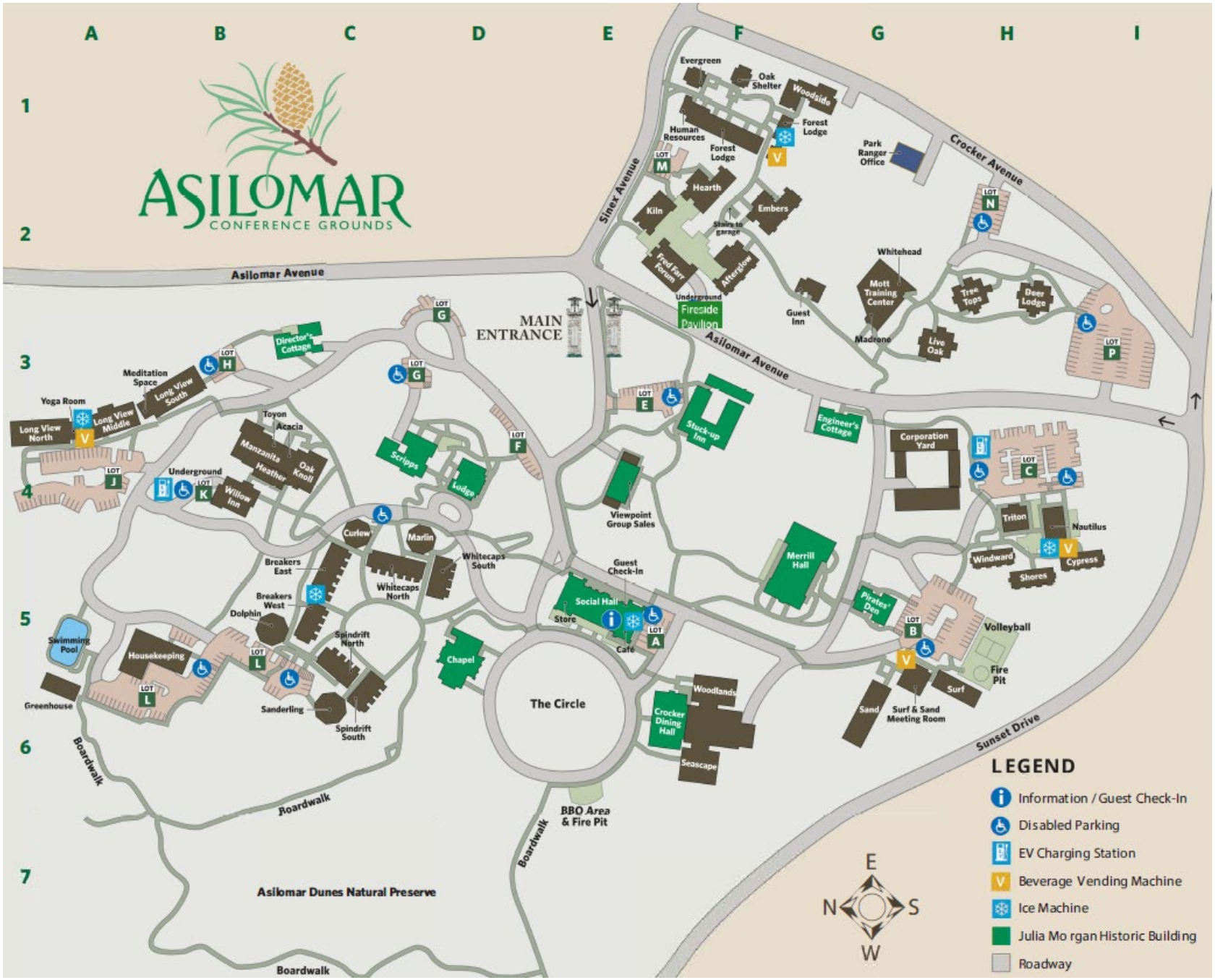
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