

BAPG Fall 2022

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UC Berkeley, 10/15/22

We are very excited to announce the 20th Bay Area Population Genomics (BAPG) Conference at UC Berkeley! Thank you to everyone who has signed up to present either a talk or a poster. We have posted the speakers, talk titles, and poster presenters on the schedule below.

Thank you to our sponsors [Ancestry](#), [Variant Bio](#), [D2G Oncology](#), and [Personalis](#) for helping us put on this great conference!



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Time: 7:30am - 5pm, Saturday, October 15 (Breakfast and check-in begins at 8:30am)

Transportation to UC Berkeley: For those planning on driving to Berkeley, visitor parking is available at a number of campus-owned parking lots. The closest ones to Stanley Hall will be the [La Loma Parking Structure](#), the [Lower Hearst Parking Structure](#), and the [Foothill Lot](#). Visitor parking on the weekends is \$2 per hour. See [Berkeley's visitor parking page](#) for more details. Please follow all posted signs and directions for campus parking lots, which all look something like [this](#). For those looking to take public transportation, [BART](#) stops one block west of campus at the Downtown Berkeley station. From there, it is a [very scenic walk](#) up through campus to Stanley.



BAPG Fall 2022

8:30-9:30am Check-in and breakfast, atrium of Stanley Hall

9:30-10:30 Session 1

9:30-9:45: **Silu Wang**, Coop Lab, UC Davis, "**On the synthesis of Recombination Effect, Large X Effect, Snowball Effect underlying speciation**"

9:45-10:00: **Frederik Filip Vinggaard Staeger**, Section for Computational Biology, University of Copenhagen, "**The unique genetic architecture of common diseases in Greenland**"

10:00-10:15: **Elise Kerdoncuff**, Moorjani Lab, UC Berkeley, "**Reconstructing patterns of admixture through time: Insights from whole genome sequencing of South Asian populations**"

10:15-10:30: **Nicolas Lou**, Sudmant Lab, UC Berkeley, "**Time-series data reveal the genomic ramifications of a fishery collapse**"

10:30-11:00 Coffee Break, Stanley Hall Atrium

11:00-12:00 Session 2

11:00-11:15: **Tristram Dodge**, Schumer Lab, Stanford, "**The genetic architecture of sexual mimicry in swordtail (Xiphophorus) fishes**"

11:15-11:30: **Lenore Pipes**, Nielsen Lab, UC Berkeley, "**Estimating the relative proportions of SARS-CoV-2 haplotypes from wastewater samples**"

11:30-11:45: **Xiran Liu**, Rosenberg Lab, Stanford, "**A Dirichlet model of alignment cost in mixed-membership clustering results of ancestry inference**"

11:45-12:00: **Serena Caplins**, Bay Lab, UC Davis, and Williams Lab, UC Berkeley, "**A life-history polyphenism along temporally and geographically shifting environmental factors in the sea slug *Alderia willowi***"

12:00-1:30 Lunch, Stanley Hall Atrium

1:30-2:30 Session 3

1:30-1:45: **Joao Ascensao**, Hallatschek Lab, UC Berkeley, "**Adaptive landscapes after diversification: what do they look like and what do they do?**"

1:45-2:00: **Zhiru Liu**, Good Lab, Stanford, "**Dynamics of bacterial recombination in the human gut microbiome**"

2:00-2:15: **Hakhamanesh Mostafavi**, Pritchard Lab, Stanford, "**Limited overlap of eQTLs and GWAS hits due to systematic differences in discovery**"

2:15-2:30: **William Dewitt**, Song Lab, UC Berkeley, "**Evolutionary dynamics of antibody affinity maturation in replica germinal centers**"

2:30-3:00 Keynote Talk

Chuck Langley, UC Davis, "Haplotypes spanning the centromere proximal regions of *Drosophila* and humans"

3:00-5:00 Poster Session and Happy Hour, Stanley Hall 1st Floor Atrium

Alexander Ioannidis - "**Ancestry-specific methods in population genetics**"

Allison Gaudinier - "**Characterizing *Mimulus guttatus* adaptation to serpentine soil**"

Artemisia Lyulina - "**Linkage equilibrium between rare alleles**"

Arjun W Vaughn - "**Bayesian inference of admixture graphs on Native American and Arctic populations**"

Daniel Wond - "**Quantifying the adaptive landscape of commensal gut bacteria using high-resolution lineages**"

BAPG Fall 2022

James Ferrare - **Evolution of Evolvability in Adapting Populations**

Kaleda Denton - **"Re-examining the evolution of altruism"**

Maike Morrison - **"FSTruct: An Fst-based tool for quantifying ancestry variability"**

Marianna Karageorgi - **"Adaptive tracking in response to seasonal insecticide pressure in *Drosophila*"**

Matthew Aguirre - **"Simulating effects from genetic and experimental perturbations to gene regulatory networks"**

Maya Lemmon-Kishi - **"A Penalized Likelihood Approach for Estimating Haplotypes from Environmental DNA"**

Nico Ayala - **"Inferring Non-Additive Multi-Locus Selection in Admixed Populations Using Hidden Markov Model"**

Noah Simon - **"Evidence for polygenic, directional cis-regulatory evolution in Southeast Asian mice"**

Olivia Ghosh - **"Emergent evolutionary forces in spatial models of luminal growth in the human gut microbiota"**

Ren Hamm - **"Evolutionary dynamics of stress-activated mobile elements in *Mimulus guttatus*"**

Sophie Jean Walton - **"Within-host evolution and strain dynamics in the human gut microbiome during and after antibiotic perturbations"**

Sylvia Durkin - **"Gene regulatory basis of parallel environmental adaptation in house mice (*Mus musculus domesticus*)"**

Yulin Zhang - **"Recovering signatures of ghost admixture using ancestral recombination graphs"**

Yun Deng - **"A new framework for efficiently inferring ancestral recombination graph"**

Yuval Simons - **"Simple scaling laws control the architectures of complex traits"**

