

BAPG Fall 2023

Bay Area Population Genomics Conference

Stanford, 12/02/2023

Welcome to the site for the 22nd Bay Area Population Genomics (#BAPGXXII) Conference at Stanford hosted by the Petrov Lab! The conference will be held on December 2, 2023 at the [Huang Engineering Center](#) on Stanford Campus. Parking is free on campus on weekends. The closest parking structure is the [Via Ortega Garage](#). Registration is free (but required) and will include coffee/breakfast and lunch. **Talk/poster submissions are now closed, but you can still register [here](#)**

Schedule

8:30-8:55: Check-in and breakfast

9:00-9:05: Welcome Remarks - Dmitri Petrov, Stanford University

9:05-10:25: Talk Session 1 - Moderator: Dmitri Petrov, Stanford University

- 9:05-9:25: **Challenges in ARG inference and applications: how to interpret and can we fix them?** - Yun Deng, UC Berkeley Graduate Student, Nielsen Lab and Song Lab
- 9:25-9:45: **The Genetic Architecture of Bronchopulmonary Dysplasia in Extremely Preterm Infants.** - Miguel Guardado, UCSF, Graduate Student, Hernandez Lab and Torgerson Lab
- 9:45-10:05: **Contextual Embedding-Based Weighted Relevance Scoring for Improved Clinical Trial Matching** - Mozhgan Saeidi, Stanford University
- 10:05-10:25: **Population genetics models of complex trait variation** - Roshni Patel, Stanford University, Graduate Student, Pritchard Lab

10:25-11:00: Coffee Break

11:00-12:30: Talk Session 2 - Moderator: Jean Vila, Stanford University

- 11:00-11:20: **Covarying Levels of Water Pollution and Admixture in a Swordtail Fish**

Hybrid Zone - Ben Moran, Stanford University, Graduate Student, Schumer Lab

- 11:20-11:40: **Archaic introgression into present-day humans: Insights into human history and biology** - Laurits Skov, UC Berkeley, Postdoc, Moorjani lab
- 11:40-12:00: **High-resolution lineage tracking of within-host evolution and transmission of a prominent gut symbiont across ecological scales** - Daniel Wong, Stanford University, Graduate Student, Good Lab
- 12:00-12:20: **Prolonged delays in human microbiota transmission after a controlled antibiotic perturbation** - Katherine Xue, Stanford University, Postdoc, Relman Lab and Petrov Lab

12:20-1:30: Lunch

1:30-2:30: Talk Session 3 - Moderator: Sophie Jean Walton, Stanford University

- 1:30-1:50: **Leveraging ARGs for the estimation of selection coefficients and allele histories from ancient DNA** - Andrew Vaughn, UC Berkeley Graduate Student, Nielsen Lab
- 1:50-2:10: **The effectiveness of selection drives the direction of protein evolution** - Hanon McShea, Stanford University, Graduate Student, Welander Lab
- 2:10-2:30: **Fluctuating selection reveals extreme granularity and parallelism of adaptive tracking** - Mark Bitter, Stanford University, Postdoc, Petrov lab

2:30-3:00: Keynote Talk - Moderator: Dmitri Petrov, Stanford University

- **Building cell atlases** - Barbara Engelhardt, Stanford University/Gladstone Institutes

3:00-5:00: Poster session and happy hour

- **Mitochondrial haplotype and mito-nuclear matching drive somatic mutation and selection throughout aging** - Isabel Serrano, UC Berkeley, Sudmant Lab
- **Recovering signatures of ghost admixture using ancestral recombination graphs** - Yulin Zhang, UC Berkeley, Moorjani Lab
- **Elucidating the population genetics of structural variants with 68 chromosome-level long-read genomes of *Drosophila melanogaster*** - James Hemker, Stanford University, Petrov Lab
- **Enhancing Sediment DNA Analysis: An Automated Pipeline for Genomic Analysis** - Jierui Xu, UC Berkeley, Moorjani Lab
- **Revisiting the Evolution of Lactase Persistence: Insights from South Asian Genomes** - Meaghan Marohn, UC Berkeley, Moorjani Lab
- **Large genotype frequency fluctuations are linked to decorrelated offspring number**

- stochasticity** - Joao Ascensao, UC Berkeley, Hallatschek Lab
- **Bacterial Recombination Overwhelms the Signal of Purifying Selection in dN/dS Dynamics** - Zhiru Liu, Stanford University, Good Lab
- **Genetic diversity loss continues long after habitat destruction ends** - Kristy Mualim, Stanford University, Exposito-Alonso Lab
- **Reconstructing the locations of genetic ancestors for a recombining sequence** - James Kitchens, UC Davis, Coop Lab
- **Tracking barcoded transposon mutants of a plant pathogen** - Milo Johnson, UC Berkeley / Lawrence Berkeley National Lab, Deutschbauer Lab, Arkin Lab, and Koskella Lab
- **Mating system variation influences gene expression across the male reproductive tract in *Peromyscus* mice** - Erin Voss, UC Berkeley, Nachman Lab
- **Simulation-Based Evaluation of f-statistics to Detect Admixture in Ancient Human Genomes** - Sarah Johnson, UC Berkeley, Moorjani Lab
- **snpArcher: A fast, reproducible, high-throughput variant calling workflow for population genomics** - Cade Mirchandani, UCSC, Corbett-Detig Lab
- **Detecting Admixture Tracts From the Origin Population of the TCC>TTC Mutation “Europulse”** - Philippa Steinberg, University of Washington, Harris Lab
- **Gene regulatory network structure affects the distribution of expression heritability** - Matthew Aguirre, Stanford University, Pritchard Lab
- **Simple model with resistance acquisition and negative selection explains coexistence of resistant and susceptible strains** - Pleuni Pennings, SFSU
- **The evolutionary history of 17q21.31 structural haplotypes in ancient and modern humans** - Samvardhini Sridharan, UC Berkeley, Sudmant Lab
- **Newly Sequenced Genomes Reveal Patterns of Gene Family Expansion in select Dragonflies (Odonata: Anisoptera)** - Christopher Beatty, Stanford University
- **How Old Is It: Molecular Dating for Ancient eDNA Samples** - Maya Lemmon-Kishi, UC Berkeley, Nielsen Lab
- **The dynamics of Pareto fronts underlying natural resource specialization in *S. cerevisiae*** - Elisa Visher, Stanford University, Petrov Lab
- **Navigating Climate Resilience: Genomic Strategies for Kelp Ecosystem Management and Restoration** - Roy Roberts, UCSC, Pinsky Lab
- **The dynamics of accumulation of gametic segregation distorters in *Arabidopsis*** - Christopher Condon, UCSC
- **Early warning signs of kidney disease in PKD1 and PKD2 loss of function carriers** - Natalie Telis, Helix
- **Phylogenomics reveals microgeographic population structuring in a genus of California trapdoor spiders and an enigmatic new species (*Euctenizidae*: *Promyrmekiaphila korematsui* sp. nov.)** - James Starrett, UC Davis, Bond Lab
- **Adaptive immune response as a platform for experimental evolution** - William DeWitt,

UC Berkeley, Song Lab

- **Testing the Levene Model using experimental evolution of herbivorous Drosophilidae** - Diler Haji, University of Connecticut
 - **Differences in CNV calling methods drive variation in CNVs more than population structure or assembly choice** - Lucia Bazan-Williamson, UC Merced, McTavish Lab
 - **Creating a Global Reference Phylogeny of the Mycobacterium Tuberculosis Complex** - Lily Karim, UCSC, Corbett-Detig Lab
 - **Tracing genealogical ancestors in Mexican populations** - Juan Esteban Rodriguez Rodriguez, Stanford University, Rosenberg Lab
 - **The evolution of structural variants in sulfide adapted fishes** - Kara Ryan, UCSC, Kelley Lab
 - **TBA** - Elena Zavala, UC Berkeley, Moorjani Lab and Rohlf's Lab
 - **TBA** - Alexander Starr, Stanford University, Fraser Lab
 - **TBA** - Meaghan Marohn, UC Berkeley, Moorjani Lab
 - **TBA** - Chandler Sutherland, UC Berkeley, Krasileva Lab
 - **TBA** - Zehua Zhou, UC Berkeley,
 - **TBA** - Kaleda Denton, Stanford University, Feldman Lab
 - **TBA** - Megan Ruffley, Stanford University, Exposito-Alonso Lab
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