BAPG XIX

Bay Area Population Genomics XIX Stanford University, 4/30/22

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We are excited to announce the 19th iteration of the Bay Area Population Genomics Conference, sponsored by [Personalis Genomics](#).

If you registered on line you are all set! Please also join the BAPG google group to stay in the loop in the future!

COVID19 policy: We expect everyone to be vaccinated and if possible to take a rapid test before coming to BAPG. While inside the building we encourage everyone except the speaker to wear a mask. It is optional for the speakers.

PARKING: is free on the weekends at all A and C parking spots. Please check the map: https://drive.google.com /file/d/1gXviAXUVCCgZrXvvz4c9pIe4qnxtrLGO/view

Roth Way and Roth Way Garage are particularly close places to park.

Location: Sapp Center for Science Teaching and Learning, Stanford University
Address: 376 Lomita Dr, Stanford, CA 94305
Time: 9:30am-4:30pm, Saturday April 30th.

Schedule:

8:30-9:25am: **Check-in & breakfast, Location: Courtyard Behind Sapp**

9:25-11am: **Welcome Remarks & Session 1**, Moderator, Dmitri Petrov

9:30- 9:50AM   **Moises Exposito Alonso**, Carnegie Institution for Science & Stanford University, **"The population genetics of species range loss in the Anthropocene"**
9:50 - 10:10AM   **Alyssa Lyn Fortier**, Jonathan Pritchard Lab, Stanford University, **"Ancient Trans-Species Polymorphism at the Major Histocompatibility Complex in Primates"**
10:10 - 10:30AM   **QinQin Yu**, Oskar Hallatschek Lab, UC Berkeley, **"Lineage frequency time series reveal elevated levels of genetic drift in SARS-CoV-2 transmission in England"**

10:30 - 10:50AM   **Rishi De-Kayne**, Simon Martin Lab, University of Edinburgh, **"Stepwise supergene evolution in a butterfly: multiple duplications preceded multiple inversions"**

10:50-11:30am: **Coffee Break,** Location: Courtyard Behind Sapp

11:30am - 1pm: **Session 2** , Moderator Benjamin Good

11:30- 11:50AM   **Patricia Lang**, Dominique Bergmann Lab, Stanford University, **"Functional variation in stomata genes through time"**
11:30 - 12:10AM   **Jeffrey Groh,** Graham Coop Lab, UC Davis, **"The temporal and genomic scale of selection against introgressed ancestry"**

selection against introgressed ancestry

12:10 – 12:30AM   **Kaleda Denton**, Marc Feldman Lab, Stanford University, **"Models of evolution under conformity and anti-conformity"**

12:30 - 12:50AM   **Krzysztof M. Kozak**, Michael Nachman Lab, Museum of Vertebrate Zoology, UC Berkeley and California Conservation Genomics Project, **"Winding paths to convergence in an iconic mimicry system"**

12:50 pm-2pm: **Lunch**

2-2:30pm: **Keynote talk**
Uri Alon, Weizmann Institute, "Theory of evolutionary tradeoffs"

2:30-4:30pm: **Poster Session & Happy Hour**

Poster presenters:

- **Jose Aguilar-Rodriguez**, Stanford University, **"The modulation of a natural genotype-phenotype map by global epistatic modifiers"**

- **Jameel Ali** & **Meris Johnson-Hagler**, San Francisco State University, **"Predicting Antibiotic Resistance Through the Utilization and Comparison of Machine Learning Algorithms"**

- **MaryGracy Antony**, San Francisco State University, **"Estimating the rate of antibiotic resistance using phylogenetic trees"**

- **Mara Baylis**, UC Santa Cruz, **"Selection against mitochondrial mutations occurs across life stages in Drosophila"**

- **Lorena Benitez-Rivera**, San Francisco State University, **"Finding patterns of antibiotic-resistant infections through the diversity of pathogenic sequence types"**

- **José Cerca,** Norwegian University of Science and Technology, **"The genomic basis of repeated evolution in Hawaiian Tetragnatha"**

- **Lucas Czech,** Carnegie Institution for Science, **"Efficient analysis of allele frequency variation from whole-genome pool-sequencing data"**

- **Oskar Hallatschek,** UC Berkeley, **"Who acquires infection from whom? Neutral allele frequency fluctuations can tell"**

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

- **Meixi Lin,** UCLA, **"Inference of the distribution of fitness effects of new mutations in the fin whale, a large-bodied mammal"**

- **David Manahan,** UC Berkeley, **"Regulation of adaptive gene expression through alternative splicing in temperate and subtropical house mice"**

- **Jaime Morin,** Norwegian University of Science and Tecnhology, **"What does the feather say? ...chaeogenomics in Arini parrots"**

- **Hakhamanesh Mostafavi**, Stanford University, **"Why GWAS hits are not eQTLs"**

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- **Shaila Musharoff,** Stanford University, **"Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits"**
- **Evlyn Pless**, UC Davis, **"Predicting environmental and ecological drivers of human population structure"**
- **Megan Ruffley,** Carnegie Institution for Science at Stanford, **"Mapping genetic constraints of drought adaptation strategies in the eco-evolutionary model, Arabidopsis"**
- **Prajjval Pratap Singh,** Banaras Hindu University, **"Genomic Diversity of Bangladeshi Populations"**
- **Susanne Tilk,** Stanford University, **"Cancers adapt to their mutational load by buffering protein misfolding stress"**
- **Florentine van Nouhuijs,** San Francisco State University, **"Using phylogenies to determine antibiotic resistance in E. coli"**

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