

CEHG16



Annual Symposium of the Center for Computational,
Evolutionary and Human Genomics

MONDAY, FEBRUARY 29

8:00 – 9:00 AM | Breakfast and Check-in

SESSION ONE

9:00 – 9:15 AM | Marcus Feldman // Opening Remarks

9:15 – 9:40 AM | Shripad Tuljapurkar // Finding the E in Heritability

9:40 – 10:05 AM | Christina Curtis // Quantifying and predicting tumor evolutionary dynamics

10:05 – 10:20 AM | Arbel Harpak // Effects of mutation rate and epistasis on the distribution of allele frequencies in humans

10:20 – 10:40 AM | Coffee Break

10:40 – 11:30 AM | Christine Kenneally // Keynote: *The Invisible History of the Human Race*

11:30 – 12:30 PM | Lunch

SESSION TWO

12:30 – 12:55 PM | Mattias Jakobsson // The genomic footprints of Neolithic Europeans

12:55 – 1:20 PM | Molly Przeworski // Of mice, men and birds: Recombination with and without PRDM9

1:20 – 1:35 PM | Hugo Hilton // What functional factors underlie the adaptive introgression of archaic immune system genes into modern humans?

1:35 – 1:55 PM | Coffee Break

1:55 – 2:20 PM | Tandy Warnow // Genome-scale estimation of the Tree of Life

2:20 – 2:35 PM | Kelley Harris // The genetic cost of Neanderthal introgression

2:35 – 3:00 PM | Panel Discussion: Building a Career in Academia

SESSION THREE

3:00 – 3:25 PM | John Novembre // Testing directional selection on polygenic traits using ancient DNA

3:25 – 3:50 PM | Yaniv Erlich // Genetic media

3:50 – 4:05 PM | Avanti Shrikumar // Not just a black box: Interpretable deep learning for genomics and epigenomics

4:05 – 4:25 PM | Coffee Break

4:25 – 4:50 PM | Martin Blaser // Role of the early life microbiota in metabolic and immunological development

4:50 – 5:05 PM | Ben Callahan // Improving the accuracy and resolution of microbiome analysis

5:05 – 6:30 PM | Poster Session and Reception

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TUESDAY, MARCH 1

8:00 – 9:00 AM | Breakfast and Check-in

SESSION FOUR

- 9:00 – 9:25 AM | Rasmus Nielsen // The genetic basis of physiological adaptation in humans
- 9:25 – 9:50 AM | Dana Pe'er // Finding structure in single cell transcriptomics
- 9:50 – 10:05 AM | Can Cenik // Integrative analysis of RNA, translation and protein levels reveals distinct regulatory variation across humans
- 10:05 – 10:25 AM | Coffee Break
- 10:25 – 10:50 AM | Nicholas Katsanis // One plus one equals zero
- 10:50 – 11:15 AM | Hunter Fraser // Pooled ChIP-seq identifies QTLs affecting transcription factor binding and histone modification
- 11:15 – 11:30 AM | Linda Szabo // Statistical discovery of circular and linear RNA splicing
- 11:30 – 12:55 PM | Lunch presented by SAP Personalized Medicine

SESSION FIVE

- 12:55 – 1:20 PM | Michael Eisen // What makes an enhancer an enhancer?
- 1:20 – 1:35 PM | Patrick Dolan // Dissecting population structure and fitness in adapting dengue virus populations
- 1:35 – 1:55 PM | Coffee Break
- 1:55 – 2:20 PM | Tadashi Fukami // Nectar microbes: Towards the genomics of community assembly
- 2:20 – 2:35 PM | Dvir Aran // Systematic pan-cancer analysis of tumour purity
- 2:35 – 3:00 PM | Panel Discussion: Opportunities and Challenges Starting a Genomics Company

SESSION SIX

- 3:00 – 3:25 PM | Uma Ramakrishnan // Genetic and genomic data identify population units for wild tigers in the Indian subcontinent
- 3:25 – 3:50 PM | Nicole King // Choanoflagellate colonies, bacterial signals, and animal origins
- 3:50 – 4:05 PM | Trevor Martin // Coordinated evolution of gene expression across 309 marine microbial species
- 4:05 – 4:25 PM | Coffee Break
- 4:25 – 4:50 PM | Stephen Palumbi // Personalized medicine for corals during climate change
- 4:50 – 5:15 PM | Ryan Haasl // Real-time invasion dynamics and genetics of Japanese hop (*Humulus japonicus*) along its frontal wave of expansion in southwestern Wisconsin
- 5:15 – 5:30 PM | Cody M. Sam // Closing Remarks

WEDNESDAY, MARCH 2

9:30 – 11:15 AM | AncestryDNA Seminar: Genomics at Scale (Registration required)

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