

Sunday, March 24th

All talks are 23 min + 7 min for Q&A

3:00 pm Check-in

6:00 pm Reception (*Lobby*)

7:00 pm Dinner

8:00 pm Welcome and opening remarks (Sean Eddy)

8:05 pm Session 1: Ancestral genome reconstruction
Chair: Adam Siepel

8:05 pm **Mathieu Blanchette**, McGill University
Ancestral mammalian genome reconstruction and its uses toward annotating the human genome

8:35 pm **David Haussler**, HHMI/University of California, Santa Cruz
Generalizations of the Fourier Transform to Gelfand Pairs provide a continuous time Markov model for the evolution of genomes via rearrangements and substitutions

9:05 pm Refreshments available at Bob's Pub

NOTE:

Meals are in the **Dining Room**
Talks are in the **Seminar Room**
Posters are in the **Lobby**

Monday, March 25th

- 7:30 am Breakfast (*service ends at 8:45am*)
- 9:00 am Session 2: Comparative genomics**
Chair: Katherine Pollard
- 9:00 am **Philip Green**, University of Washington
How much of the human genome is functional?
- 9:30 am **Gerton Lunter**, University of Oxford
Modeling the coalescent with selection, without trees
- 10:00 am **Adam Siepel**, Cornell University
Inference of natural selection from interspersed genomic elements based on polymorphism and divergence
- 10:30 am Break
- 11:00 am Session 3: Polymorphisms**
Chair: Reed Cartwright
- 11:00 am **Serafim Batzoglou**, Stanford University
Genome evolution during progression to breast cancer
- 11:30 am **Ingo Ruczinski**, Johns Hopkins University
On study designs and statistical analyses in sequencing studies
- 12:00 pm **Barbara E. Engelhardt**, Duke University
Efficient Bayesian structured sparsity models to discover multiple regulatory genetic variants
- 12:30 pm Lunch
- 1:15 pm Tour (*optional – meet at reception*)

- 2:15 pm** **Session 4: Population history**
Chair: Ryan Hernandez
- 2:15 pm **Graham Coop**, University of California, Davis
Using identity by descent to learn about recent population history
- 2:45 pm **Kelley Harris**, University of California, Berkeley
Inferences of demography from identity by descent tract distributions
- 3:15 pm **Yun S. Song**, University of California, Berkeley
Gene genealogies when the sample size is very large
- 3:45 pm Break
- 4:15 pm** **Session 5: Poster blitz!** (5 minutes / 3 slides per talk)
Chair: Katherine Pollard
- Anand Bhaskar**, University of California, Berkeley
Reed Cartwright, Arizona State University
Ryan Hernandez, University of California, San Francisco
Heng Li, Broad Institute
Siavash Mirarab, University of Texas at Austin
Luay Nakhleh, Rice University
Alejandro Ochoa, Princeton University
Benedict Paten, University of California, Santa Cruz
Chaolong Wang, Harvard University
Daniel Zerbino, EMBL
- 5:05 pm Poster Reception
- 6:45 pm Dinner
- 8:00 pm** **Session 6: Efficient algorithms**
Chair: Heng Li
- 8:00 pm **Anders Krogh**, University of Copenhagen
Mapping of short DNA reads
- 8:30 pm **Richard Durbin**, Wellcome Trust Sanger Institute
Suffix array based methods for efficient analysis of genetic variation data
- 9:00 pm Refreshments available at Bob's Pub

Tuesday, March 26th

- 7:30 am Breakfast (*service ends at 8:45am*)
- 9:00 am Session 7: Models of sequence evolution**
Chair: Sean Eddy
- 9:00 am **Manolo Gouy**, Centre National de la Recherche Scientifique (CNRS)
A branch-heterogeneous model of protein evolution for efficient inference of ancestral sequences
- 9:30 am **Marc A. Suchard**, University of California, Los Angeles
Learning about evolutionary processes from big data
- 10:00 am **Elena Rivas**, Janelia Farm Research Campus/HHMI
Remote homology searches combining an affine insertion model of evolution with profile HMMs
- 10:30 am Break
- 11:00 am Session 8: Functional genomics**
Chair: Thomas Mailund
- 11:00 am **Uwe Ohler**, Duke University
Integrating sequence and chromatin information for prediction of functional binding sites
- 11:30 am **Olga Troyanskaya**, Princeton University
Identifying cell-lineage specific gene expression and function on the genome scale
- 12:00 pm **Jotun J. Hein**, University of Oxford
Regulatory annotation using a large number of sequences using k -restricted spanning trees
- 12:30 pm Lunch

- 2:00 pm** **Session 9: Regulatory sequences**
Chair: Shaun Mahony
- 2:00 pm **Ivan Ovcharenko**, National Institutes of Health
Computational identification and sequence analysis of enhancers
- 2:30 pm **Katherine Pollard**, University of California, San Francisco
Human accelerated regions drive unique expression patterns during embryonic development
- 3:00 pm **Saurabh Sinha**, University of Illinois
Quantitative models for function and evolution of cis-regulatory modules
- 3:30 pm Break
- 4:15 pm** **Session 10: Recombination history**
Chair: Matthew Rasmussen
- 4:15 pm **Mikkel Schierup**, Aarhus University
Fine scale recombination maps in ancestral species
- 4:45 pm **Asger Hobolth**, Aarhus University
Discrete space Markov models for the coalescent with recombination along two sequences
- 5:15 pm Poster Reception
- 6:45 pm Dinner
- 8:00 pm** **Session 11: Multiple alignment and phylogeny**
Chair: Des Higgins
- 8:00 pm **Ari Löytynoja**, University of Helsinki
Sequence alignment in evolutionary analysis
- 8:30 pm **Tandy Warnow**, University of Texas at Austin
Three statistical methods for ultra-large alignment and phylogeny estimation
- 9:00 pm Refreshments available at Bob's Pub

Wednesday, March 27th

- 7:30 am Breakfast (*service ends at 8:45am*)
- 9:00 am Session 12: Metagenomes**
Chair: Daniel Zerbino
- 9:00 am **Ian Holmes**, University of California, Berkeley
Statistical phylogenetics for predicting SNP phenotypes
- 9:30 am **Curtis Huttenhower**, Harvard School of Public Health
High-precision functional profiling of metagenomes and metatranscriptomes using unique marker sequences
- 10:00 am Break
- 10:30 am Session 13: Protein and RNA sequence models**
Chair: Luay Nakhleh
- 10:30 am **Johannes Soeding**, University of Munich
Sensitive protein sequence searching and regulatory motif discovery
- 11:00 am **Christopher Langmead**, Carnegie Mellon University
Structured probabilistic models of proteins across fitness landscapes
- 11:30 am **Sean R. Eddy**, Janelia Farm Research Campus/HHMI
Acceleration of profile HMM and profile SCFG methods for remote homology search
- 12:00 pm Lunch and Departure
- 12:30 pm First shuttle to Dulles
1:30 pm Second shuttle to Dulles
2:30 pm Last shuttle to Dulles