Speaker affiliation:

Ilan Gronau, postdoctoral research associate at the Siepel computational genomics lab
Department of Biological Statistics and Computational Biology, Cornell University

Title:

Individual Genomes Reveal Deep Population Histories and Uncover the Evolutionary Roles
of Non Coding DNA

Abstract:

High throughput DNA sequencing has transformed the landscape of genomic data
and is expected to revolutionize our knowledge of evolution and genomic function.
However, the abundant sequence data also poses serious computational challenges,
and realizing its full potential requires developing efficient and reliable
computational and statistical inference methods. This talk will cover work that
I have done as part of my postdoctoral research, utilizing newly emerging genomic
data sets and population genetic models to examine several open questions in
evolution. I will start by describing a study I conducted of ancient human population
demography in Africa, focusing on one of the deepest population divergence events in
human history, dating roughly 130 thousand years ago. I will then present work I did
as part of a large-scale collaborative effort to study the early evolution of dogs
using the complete genome sequences of two dogs and three gray wolves. I will show
how we were able to settle several longstanding debates revolving around the origins
of dogs using these genomes and an innovative computational approach I developed.
Lastly, I will describe a parallel line of research I have been recently conducting,
trying to understand the evolutionary roles of non coding regulatory elements in the
human genome. The talk will describe the computational challenges involved in these
three studies. I will outline the methods developed to address these challenges, and
present the main findings and their significance. I will conclude with a short
survey of my ongoing research, and a map of the opportunities and challenges we face
in the study of evolution in a world of rapidly evolving genomic data sets.

Note: the talk does not require any prior biological knowledge.

Short bio:

Ilan Gronau is a computational biologist studying evolution and population genetics.
Ilan received his PhD from the Computer Science department at the Technion and has
a Masters degree in Bioinformatics from the Weizmann Institute. Since 2009, Ilan has
been a postdoctoral fellow in Adam Siepel's computational genomics lab in Cornell.
Ilan developed algorithms and statistical inference methods for solving a wide range
of fundamental tasks in molecular evolution, such as phylogenetic reconstruction,
demography inference, and detection of recent natural selection. His work combines
innovative computational approaches and cutting edge genomic data sets to examine
central open questions in evolution.

Select publications:
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* Gronau I, Hubisz MJ, Gulko B, Danko CG, Siepel A. Bayesian inference of ancient human
  demography from individual genome sequences. Nature Genetics 43:1031–1034, 2011

* Gronau I, Arbiza L, Mohammed J, Siepel A. Inference of Natural Selection from Interspersed
  Genomic Elements Based on Polymorphism and Divergence. Mol Biol Evol, 30(5):1159â/ˆ1171, 2013

* Arbiza L, Gronau I, Aksoy BA, Hubisz MJ, Gulko B, et al. Genome-wide inference of natural
  selection on human transcription factor binding sites. Nature Genetics, 45:723–729, 2013

* Freedman A, Gronau I, Schweizer RM, Han E, Ortega-Del Vecchyo D, et al. Genome Sequencing
  Highlights the Dynamic Early History of Dogs. PLoS Genetics. in press.

Speaker's website:
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http://compgen.bscb.cornell.edu/~igronau/