**Camp Evolution VIII, December 18-22, 2022, abstracts**

Evening talk, Sunday Dec 18, 2022

**Dynamics of adaptive variation generation and maintenance under very prolonged resource exhaustion**

[Ruth Hershberg](https://hershberg.net.technion.ac.il/), Department of Genetics, The Ruth and Bruce Rappaport Faculty of Medicine, Technion.

Many non-sporulating bacterial species can survive for years within exhausted growth media in a state termed long-term stationary phase (LTSP). In July 2015 we initiated a set of long-term evolutionary experiments aimed at probing the dynamics of *Escherichia coli* adaptation under LTSP. These ongoing experiments reveal that *E. coli* genetically adapts in a continuous, rapid and convergent manner, at least up to six years under resource exhaustion. In my talk I will describe some of the lessons we have learned so far from these experiments, regarding the convergence with which adaptation occurs, the dependence of many adaptations on the occurrence of other adaptations (historical contingency), and on the consequences of early adaptation on the population level maintenance of a genetic ‘memory’ of prior conditions.

Evening talk, Monday Dec 19, 2022

**Admixture between Neandertals, Denisovans and Ancient Modern Humans**

[Viviane Slon](https://www.tau.ac.il/~viviane/), Department of Anatomy and Anthropology and Department of Human Molecular Genetics and Biochemistry, Sackler Faculty of Medicine, Tel Aviv University, Israel, and the Dan David Center for Human Evolution and Biohistory Research, Tel Aviv University.

In the past years, DNA retrieved from ancient human remains have been instrumental in furthering our understanding of our own evolutionary past, as well as that of our closest extinct relatives, the Neandertals and the Denisovans. One of the main insights stemming out of the study of ancient genomes is that members of distinct ancient human groups interbred - multiple times and in multiple places. Here I will review the evidence for the occurrence of archaic admixture, and present case studies highlighting the effects of past admixture events on our current gene pool.

Evening talk, Tuesday Dec 20, 2022

**Extremely rapid evolution in the wild - are gene drives a good idea?**

[Gili Greenbaum](https://www.greenbaumlab.com/), Department of Ecology, Evolution and Behavior, Hebrew University of Jerusalem.

Gene drive is a revolutionary genetic engineering technology that allows genetic modification of entire populations and species in the wild within a few generations. This is achieved by inducing a violation of Mendel's Laws of inheritance, generating a rapid evolutionary process in which an engineered allele takes over. This technology promises to usher in a new age of large-scale genetic biocontrol, with applications to malaria and invasive species eradication. However, alongside the great promises, this new technology presents significant risks, including spillover of the gene drive to non-target populations or species, and counter-evolution of resistance. In addition to these ecological and evolutionary issues, entire-species genetic engineering presents novel ethical dilemmas. So - are gene drives a good idea?

Evening talk, Wednesday Dec 21, 2022

**Simulation-Based Inference with Neural Networks in Experimental Evolution**

[Yoav Ram](http://www.yoavram.com), School of Zoology, The George S. Wise Faculty of Life Sciences, Tel Aviv University

Evolutionary experiments often produce a time-series of genotype or phenotype frequencies. Standard statistical inference from such time-series is challenging, because the underlying generating model (e.g., Wright-Fisher model) is stochastic and non-linear, and therefore the likelihood function in intractable and  model parameters may be correlated. Thus, likelihood-free, simulation-based inference methods, such as approximate Bayesian computation (ABC), are used, together with advanced sampling algorithms such as Markov Chain Monte Carlo (MCMC) or Sequential Monte Carlo (SMC). Recently, new approaches for simulation-based inference have been developed that apply artificial neural networks to directly approximate the likelihood or posterior density functions from simulated data. These methods do not require a summary statistic or a distance function, and moreover, allow for amortized inference. These approaches have been applied in particle physics, cosmology, and neuroscience, but not in evolution.

I will introduce our results using a neural-network simulation-based inference method to infer the rate and fitness effect of copy-number variation in yeast and point mutations in viruses, both in the context of adaptation during lab evolution. Our results demonstrate that these new methods are more efficient and precise then state-of-the-art ABC methods and allow for fast and flexible inference from evolutionary empirical data.