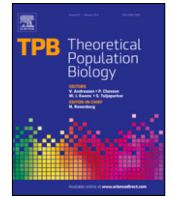




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Editorial

The 2022 Feldman Prize

The Feldman Prize is awarded to one or two outstanding articles published in *Theoretical Population Biology* during a two-year interval. Each prize includes an award of \$500 from the publisher.

This year's prize covers 2019 and 2020, an eventful period for the journal. We reported a special issue in honor of Marc Feldman's 75th birthday (Ramachandran et al., 2019) and a special issue for the 50th anniversary of *TPB* (Rosenberg, 2020), and many researchers in the *TPB* community devoted much of their scientific energy in 2020 to the population biology of the COVID-19 pandemic (Rosenberg, 2021). We are grateful to the Feldman Prize committee of Reinhard Bürger (chair), Michael Desai, and Claudia Neuhauser for their close examination of papers nominated by the handling editors from among the 106 research articles published in *TPB* in 2019 and 2020.

The winning articles are Baake et al. (2019) and Agarwala and Fisher (2019).

Modelling and simulating Lenski's long-term evolution experiment.

Ellen Baake, Adrián González Casanova, Sebastian Probst, Anton Wakolbinger.

Theoretical Population Biology 127: 58–74 (2019).

“Baake, González Casanova, Probst, and Wakolbinger develop a population-genetic Markov chain model, a so-called Cannings model with mutation and selection, to analyze the fitness increase in Lenski's famous long-term evolution experiment. Motivated by, and partially based on previous approaches, they construct their model to mimic the serial-transfer protocol by taking into account much of the underlying biology. Among these are finite-population effects, details of growth-dynamics within and between days, random fitness increments, and clonal interference. One of the completely novel results is that the observed diminishing fitness increase during the experiment, whose power law had been estimated previously by heuristic means, is partially due to a run-time effect, i.e., the shortening of the daily growth period, and not exclusively caused by diminishing-returns epistasis. The thorough mathematical analysis provides a precise and biologically intuitive meaning to the parameters in this previously derived power law. In fact, this power law is derived rigorously from the microscopic model by assuming a large-population limit. The model also allows for parameter estimation, in particular of the epistasis parameters. This approach breaks new ground, both conceptually as well as mathematically. It shows impressively that deep and rigorous mathematics can provide important new insights into the findings of a seminal evolution experiment.”

Adaptive walks on high-dimensional fitness landscapes and seascapes with distance-dependent statistics.

Atish Agarwala, Daniel S. Fisher.

Theoretical Population Biology 130: 13–49 (2019).

“Agarwala and Fisher present a creative new approach to the analysis of theoretical models of adaptive walks on fitness landscapes. The authors first introduce a class of high-dimensional random fitness landscapes. To focus on the way in which their local properties depend on evolutionary history, the authors characterize these landscapes in terms of the correlations between the fitnesses of genomes as a function of genetic distance. They then show that the long-distance statistics of epistatic interactions determine how the statistics of the local landscapes (e.g. the DFE of new mutations) depend on evolutionary history. They also consider adaptive dynamics in fitness “seascapes” in slowly varying environments. Their work brings a fresh conceptual perspective to the extensive literature on fitness landscapes. It develops a rich mathematical framework that sheds light on how we should characterize these landscapes, while also providing insight into empirical efforts to measure and analyze evolutionary dynamics across them.”

In addition to the two winning articles, the committee wished to draw attention to two other papers, Úbeda et al. (2019) and Khan and Wahl (2020), writing “The following papers deserve honorable mentions because they are beautiful examples of what theoretical population biology can contribute to science. Both develop original models to study biologically relevant and timely problems. The interesting and careful analyses suggest new solutions and yield substantial insights.”

PRDM9 and the evolution of recombination hotspots.

Francisco Úbeda, Timothy W. Russell, Vincent A. A. Jansen.

Theoretical Population Biology 126: 19–32 (2019).

Quantifying the forces that maintain prophages in bacterial genomes.

Amjad Khan, Lindi M. Wahl.

Theoretical Population Biology 133: 168–179 (2020).

We congratulate the authors and again thank Profs. Bürger, Desai, and Neuhauser for their efforts.

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