



## Editorial

## The 2018 Marcus W. Feldman Prize in Theoretical Population Biology



We are pleased to introduce the Marcus W. Feldman Prize in Theoretical Population Biology, to be awarded biennially to up to two outstanding articles published in *Theoretical Population Biology* during a two-year period. Each prize includes an award of \$500.

Contributions to *TPB* address problems in demography, ecology, epidemiology, evolution, and genetics through a theoretical approach. They are mathematically substantial, requiring significant theoretical insight. Their results are motivated and interpreted in relation to biological phenomena, and they contribute to enhancing biological understanding (see Rosenberg, 2014, 2015). In offering a prize to outstanding articles, we seek to encourage and celebrate excellence in reporting theoretical work in population biology.

The prize honors Marcus W. Feldman, co-founder and longtime editor of the journal, and its most prolific contributor of original research throughout its history. In managing *Theoretical Population Biology* from 1972 to 2012, Marc Feldman has made an extraordinary contribution to supporting mathematical and theoretical research in population biology. His high standards for insightful theoretical work are evident in his many articles in *TPB*.

We have initiated the Feldman Prize on the occasion of Marc Feldman's 75th birthday in 2017.

### The winners of the 2018 Feldman Prize

For the inaugural award, we requested nominations from the eight editors who managed the review process for papers published in *TPB* during calendar years 2015 and 2016. Editors examined all the submissions whose review process they supervised, and from among 116 articles published in the journal in 2015 and 2016, we received nominations in support of 13 papers. A Feldman Prize committee of Eva Kisdi, Shripad Tuljapurkar (chair), and John Wakeley chose the winners, considering the nominations, the nominated papers, and the reviews received for the papers during the review process.

The committee selected one winning article:

A general condition for adaptive genetic polymorphism in temporally and spatially heterogeneous environments.

Hannes Svardal, Claus Rueffler, Joachim Hermisson  
*Theoretical Population Biology* 99: 76–97 (2015).

In choosing this paper, the committee reported:

*“How spatial and temporal variation in the environment can maintain biodiversity is a question that has intrigued theoretical biologists for decades. By investigating a general model and using the more modern tools of adaptive dynamics, Svardal, Rueffler, and Hermisson have achieved both a synthesis of many classical results and a significant extension to arbitrary patterns of spatiotemporal variation. The sheer amount of work that went into the analysis is impressive; while many papers justifiably simplify the analysis by making special assumptions that expose the bare bones, Svardal et al. strove for generality. This effort led to elegant and heuristically interpretable conditions for adaptive diversification, and in an accessible and beautifully written paper, the authors explain these conditions in clear terms. Numerical simulations not only confirm the analytical predictions but also show the limits of their validity, and experimentally clarify the precise reason why the analytical predictions break down when assumptions behind them are strongly violated. The results are relevant both for ecology (how spatiotemporal variation maintains species diversity) and for population genetics (maintenance of genetic polymorphism), main areas of focus for Theoretical Population Biology.”*

The committee also wished to acknowledge three papers as deserving of honorable mention.

Bayesian pedigree inference with small numbers of single nucleotide polymorphisms via a factor-graph representation.

Eric C Anderson, Thomas C Ng  
*Theoretical Population Biology* 107: 39–51 (2016).

Looking down in the ancestral selection graph: A probabilistic approach to the common ancestor type distribution.

Ute Lenz, Sandra Kluth, Ellen Baake, Anton Wakolbinger  
*Theoretical Population Biology* 103: 27–37 (2015).

Likelihood-based tree reconstruction on a concatenation of aligned sequence data sets can be statistically inconsistent.

Sebastien Roch, Mike Steel  
*Theoretical Population Biology* 100: 56–62 (2015).

The committee found that these three papers “provide substantial and useful new theoretical insights, are good examples of mathematical thinking applied to serious biological questions, and deserve attention from people using theoretical approaches to ecological and

evolutionary models,” and that they are “distinguished examples of high-quality theoretical work in biology.”

We thank Profs. Kisdi, Tuljapurkar, and Wakeley, editorial assistant Larry Bond, the nominating editors, and the dozens of reviewers whose comments were taken into account both during the nomination and for the final choice by the committee. We are pleased to offer our congratulations to the authors.

## References

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Available online 24 November 2017