



## Editorial

## The 2020 Feldman Prize



This year, we announce the second Marcus W. Feldman Prize in Theoretical Population Biology. The Feldman Prize is awarded to up to two outstanding articles published in *Theoretical Population Biology* during a period of two years. Each prize includes an award of \$500 from the publisher.

The journal's editors examine all the submissions that they handled, and nominate the most outstanding papers among them. A committee chooses among the nominations, evaluating the papers and the reviews received during the peer review process. Excluding editorials and commentaries, a total of 97 articles appeared in *TPB* during 2017 and 2018. This year's Feldman Prize committee consisted of Ellen Baake, Lilach Hadany (chair), and Shripad Tuljapurkar.

The committee selected two winning articles, [Barton et al. \(2017\)](#) and [Kobayashi et al. \(2018\)](#):

The infinitesimal model: Definition, derivation, and implications. N.H. Barton, A.M. Etheridge, A. Véber. *Theoretical Population Biology* 118: 50–73 (2017).

*“Barton, Etheridge, and Véber consider a particular case of the famous infinitesimal model in population genetics. The focus of this paper is to show that when individual alleles make small contributions to a phenotype, the trait distribution within families rapidly approaches a normally distributed limit. The limiting variance is shown to depend only on the variance in the ancestral population and the pedigree relating individuals in those families. The authors describe a purely phenotypic model in which the mid-point rule is used to construct offspring phenotypes. The variances between related individuals depend only on their relatedness, and the authors show how these variances can be tracked over time at the level of an individual or a population. Mutation and certain kinds of migration are shown to be readily included. All of this is clever and clear. In the careful analysis that follows, the authors assume that many alleles of ‘small’ effect, defined in a precise way, make up a phenotype, and of course alleles in an individual come from its parents. They then use modern versions of the venerable central limit theorem to show that the phenotypes of offspring within families follow a multivariate normal distribution. They use even richer limit theorems to show that the limit is robust to some kinds of epistasis. This powerful analysis shows how limit theory for sums of certain kinds of dependent random variables is valuable in genetic contexts. It provides valuable insight into the use of the breeder’s equation in artificial breeding, and the authors close with a discussion of applications to laboratory and natural populations. This paper is a great illustration of how one can use sophisticated mathematics to address changes in genes and phenotypes.”*

Genealogies and ages of cultural traits: An application of the theory of duality to the research on cultural evolution. Yutaka Kobayashi, Joe Yuichiro Wakano, Hisashi Ohtsuki. *Theoretical Population Biology* 123: 18–27 (2018).

*“Kobayashi, Wakano, and Ohtsuki introduce a coalescent theory for cultural evolution. Their work provides a significant leap on the topic of cultural inheritance, and offers a new perspective on inheritance processes with transmission from multiple sources. Building on concepts and methods from mathematical population genetics and extending them, they present a model in which multiple traits are independently transmitted from generation to generation by means of cultural learning. They then derive the corresponding ancestral process that describes the cultural genealogy of a trait carried by a sample of individuals. As an important functional of this genealogy, the age-frequency spectrum is identified, which gives the numbers of distinct cultural traits in specific age-frequency classes found in a sample. The age-frequency spectrum is shown to undergo a transition from a phase with a moderate number of young, rare traits to a phase with numerous very old, common traits when the expected number of cultural parents per individual surpasses one. The article uses nontrivial mathematical methods such as duality theory, inclusion-exclusion principles, and various limiting procedures as the population size gets large. All this is carefully worked out and explained, and the resulting paper is extremely well written and very transparent. The originality, the magnitude of the advance, and the quality of the work are all impressive.”*

We thank Profs. Baake, Hadany, and Tuljapurkar for serving on the selection committee and congratulate the authors of the winning papers.

## References

- Barton, N.H., Etheridge, A.M., Véber, A., 2017. The infinitesimal model: Definition, derivation, and implications. *Theor. Popul. Biol.* 118, 50–73.  
 Kobayashi, Y., Wakano, J.Y., Ohtsuki, H., 2018. Genealogies and ages of cultural traits: an application of the theory of duality to the research on cultural evolution. *Theor. Popul. Biol.* 123, 18–27.

Editor-in-Chief  
 Noah A. Rosenberg  
 Stanford University, United States  
 E-mail address: [noahr@stanford.edu](mailto:noahr@stanford.edu).

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