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Editorial Core elements of a *TPB* paper

The subject matter of *Theoretical Population Biology* lies at the intersection between mathematics and biology, and we seek papers that contain elements of both fields. Many ways exist to report contributions that combine math and biology; we receive submissions that span the full range from math with relatively little biology to biology with relatively little math. Beyond high-quality science and relevance to the scope of the journal, what features are we seeking for manuscripts submitted to *TPB*? To help prospective authors, this editorial describes core elements of typical *TPB* papers, as exemplified by some of the articles we published in 2013.

First, TPB papers are biologically motivated. They aspire to address problems in biology through a theoretical approach. Perhaps the effect of one biological phenomenon on another is of interest, and a study might be framed in terms of exploring the relationship conceptually and mathematically (Nilsen et al., 2013; Van Cleve and Lehmann, 2013; Wittmann et al., 2013). An empirical phenomenon observed in a specific organism or group of organisms might generate a need for a model (Della Rossa et al., 2013; Lončarić and Hackenberger, 2013; Mathias and Chesson, 2013; Turner et al., 2013). A comparison of, or analysis of the relationship between, two or more models might be of interest (Huillet and Möhle, 2013; Lambert and Stadler, 2013; Walters and Kendal, 2013). A project might seek to understand a new aspect of an important model in an established area of theory, or to extend a theoretical framework to accommodate additional biological phenomena or more general assumptions (Geoghegan and Spencer, 2013; Messinger and Ostling, 2013; Schreiber and Killingback, 2013; Sverdlov and Thompson, 2013). These scenarios all have in common that the biology drives the theory.

Second, TPB papers are mathematically substantial. A new configuration of assumptions might be used to build a model and analyze its mathematical properties (Barton et al., 2013; Huang et al., 2013), or new techniques might be presented for the analysis of model features (Bansaye and Lambert, 2013; Steinrücken et al., 2013b). Under the assumptions of a model, new theoretical results might be obtained (Good and Desai, 2013; Schraiber et al., 2013), existing results enhanced through new derivations or connections (Cohen, 2013; Tazzyman and Bonhoeffer, 2013), or new features computed numerically or by simulation (Carja et al., 2013; Fogarty et al., 2013). A statistical method for data analysis might be devised under the assumptions of a model (Slatkin, 2013; Steinrücken et al., 2013a), or the mathematical or computational properties of such a method might be evaluated (Bryc et al., 2013; Cowell, 2013). In each case, the theory or methodological insight required for the advance is nontrivial.

Third, results in *TPB* papers are formulated in relation to the biological phenomena. Ideally, the exposition—and especially abstracts, results sections, and figures—enables both theorists

and non-theorists to extract the main biological conclusions. The empirical relevance of the work is demonstrated, for example, by an illustration with data (Cowell, 2013; Matthews and Garenne, 2013), by simulation or computation using parameter values relevant to empirical scenarios (Barraquand and Yoccoz, 2013; Glass and Barnes, 2013; Sverdlov and Thompson, 2013), by centering the work around a specific empirical problem (Boni et al., 2013; Dexter and Kowalewski, 2013), or through discussion sections that comment both on the value of the work as theory and on its contributions to the biological question at hand (Bansaye and Lambert, 2013; Good and Desai, 2013; Schreiber and Killingback, 2013; Wittmann et al., 2013).

Each *TPB* paper incorporates its own distinctive mixture of these elements, and *TPB* offers authors considerable flexibility in organizing their manuscripts. Authors adopt a variety of styles of mathematical writing, with the goal of keeping papers clear, readable, and biologically grounded—for example, writing in a formal theorem—proof style (Huillet and Möhle, 2013; Steinrücken et al., 2013b), presenting derivations in a less formal but still mathematical narrative (Huang et al., 2013; Schraiber et al., 2013), or placing proofs or other math tangential to the biology in appendices (Cohen, 2013; Van Cleve and Lehmann, 2013). Irrespective of the scientific, structural, and stylistic choices that authors make, the core features of sound motivation from a biological perspective, significant mathematical contribution, and successful interpretation in relation to advancing biology represent the hallmark of the most distinguished *TPB* work.

References

- Bansaye, V., Lambert, A., 2013. New approaches to source-sink metapopulations decoupling demography and dispersal. Theor. Popul. Biol. 88, 31–46.
- Barraquand, F., Yoccoz, N.G., 2013. When can environmental variability benefit population growth? Counterintuitive effects of nonlinearities in vital rates. Theor. Popul. Biol. 89, 1–11.
- Barton, N.H., Etheridge, A.M., Kelleher, J., Véber, A., 2013. Genetic hitchhiking in spatially extended populations. Theor. Popul. Biol. 87, 75–89.
- Boni, M.F., Galvani, A.P., Wickelgren, A.L., Malani, A., 2013. Economic epidemiology of avian influenza on smallholder poultry farms. Theor. Popul. Biol. 90, 135–144.
- Bryc, K., Bryc, W., Silverstein, J.W., 2013. Separation of the largest eigenvalues in eigenanalysis of genotype data from discrete subpopulations. Theor. Popul. Biol. 89, 34–43.
- Carja, O., Liberman, U., Feldman, M.W., 2013. Evolution with stochastic fitness: a role for recombination. Theor. Popul. Biol. 86, 29–42.
- Cohen, J.E., 2013. Taylor's power law of fluctuation scaling and the growth-rate theorem. Theor. Popul. Biol. 88, 94–100.
- Cowell, R.G., 2013. A simple greedy algorithm for reconstructing pedigrees. Theor. Popul. Biol. 83, 55–63.
- Della Rossa, F., Fasani, S., Rinaldi, S., 2013. Conditions for patchiness in plankton models. Theor. Popul. Biol. 83, 95–100.
- Dexter, T.A., Kowalewski, M., 2013. Jackknife-corrected parametric bootstrap estimates of growth rates in bivalve mollusks using nearest living relatives. Theor. Popul. Biol. 90, 36–48.

- Fogarty, L., Creanza, N., Feldman, M.W., 2013. The role of cultural transmission in human demographic change: an age-structured model. Theor. Popul. Biol. 88, 68–77.
- Geoghegan, J.L., Spencer, H.G., 2013. The evolutionary potential of paramutation: a population-epigenetic model. Theor. Popul. Biol. 88, 9–19.
- Glass, K., Barnes, B., 2013. Eliminating infectious diseases of livestock: a metapopulation model of infection control. Theor. Popul. Biol. 85, 63–72.
- Good, B.H., Desai, M.M., 2013. Fluctuations in fitness distributions and the effects of weak linked selection on sequence evolution. Theor. Popul. Biol. 85, 86–102. Huang, L., Buzbas, E.O., Rosenberg, N.A., 2013. Genotype imputation in a coalescent
- model with infinitely-many-sites mutation. Theor. Popul. Biol. 87, 62–74. Huillet, T., Möhle, M., 2013. On the extended Moran model and its relation to
- Huillet, I., Mohle, M., 2013. On the extended Moran model and its relation to coalescents with multiple collisions. Theor. Popul. Biol. 87, 5–14.
- Lambert, A., Stadler, T., 2013. Birth-death models and coalescent point processes: the shape and probability of reconstructed phylogenies. Theor. Popul. Biol. 90, 113-128.
- Lončarić, Ž., Hackenberger, B.K., 2013. Stage and age structured Aedes vexans and Culex pipiens (Diptera: Culicidae) climate-dependent matrix population model. Theor. Popul. Biol. 83, 82–94.
- Mathias, A., Chesson, P., 2013. Coexistence and evolutionary dynamics mediated by seasonal environmental variation in annual plant communities. Theor. Popul. Biol. 84, 56–71.
- Matthews, A.P., Garenne, M.L., 2013. A dynamic model of the marriage market—Part 1: Matching algorithm based on age preference and availability. Theor. Popul. Biol. 88, 78–85.
- Messinger, S.M., Ostling, A., 2013. Predator attack rate evolution in space: the role of ecology mediated by complex emergent spatial structure and self-shading. Theor. Popul. Biol. 89, 55–63.
- Nilsen, E.B., Finstad, A.G., Næsje, T.F., Sverdrup-Thygeson, A., 2013. Using mass scaling of movement cost and resource encounter rate to predict animal body size–population density relationships. Theor. Popul. Biol. 86, 23–28.
- Schraiber, J.G., Griffiths, R.C., Evans, S.N., 2013. Analysis and rejection sampling of Wright-Fisher diffusion bridges. Theor. Popul. Biol. 89, 64–74.

- Schreiber, S.J., Killingback, T.P., 2013. Spatial heterogeneity promotes coexistence of rock-paper-scissors metacommunities. Theor. Popul. Biol. 86, 1–11.
- Slatkin, M., 2013. A method for estimating the effective number of loci affecting a quantitative character. Theor. Popul. Biol. 89, 44–54.
- Steinrücken, M., Paul, J.S., Song, Y.S., 2013a. A sequentially Markov conditional sampling distribution for structured populations with migration and recombination. Theor. Popul. Biol. 87, 51–61.
- Steinrücken, M., Wang, Y.X.R., Song, Y.S., 2013b. An explicit transition density for a multi-allelic Wright–Fisher diffusion with general diploid selection. Theor. Popul. Biol. 83, 1–14.
- Sverdlov, S., Thompson, E.A., 2013. Correlation between relatives given complete genotypes: from identity by descent to identity by function. Theor. Popul. Biol. 88, 57–67.
- Tazzyman, S.J., Bonhoeffer, S., 2013. Fixation probability of mobile genetic elements such as plasmids. Theor. Popul. Biol. 90, 49–55.
- Turner, M., Lenhart, S., Rosenthal, B., Zhao, X., 2013. Modeling effective transmission pathways and control of the world's most successful parasite. Theor. Popul. Biol. 86, 50–61.
- Van Cleve, J., Lehmann, L., 2013. Stochastic stability and the evolution of coordination in spatially structured populations. Theor. Popul. Biol. 89, 75–87.
- Walters, C.E., Kendal, J.R., 2013. An SIS model for cultural trait transmission with conformity bias. Theor. Popul. Biol. 90, 56–63.
- Wittmann, M.J., Hutzenthaler, M., Gabriel, W., Metzler, D., 2013. Ecological and genetic effects of introduced species on their native competitors. Theor. Popul. Biol. 84, 25–35.

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