

PUBLICATIONS

- Barton, N.H. (2013) Differentiation. In *The Princeton Guide to Evolution*, Ed. J. Losos, Princeton University Press.
- N.H. Barton, A.M. Etheridge, and A. Véber. 2013. Modelling evolution in a spatial continuum. *Journal of Statistical Physics*. doi 10.1088/1742-5468/2013/01/P01002
- Barton, N.H. (2013) Does hybridisation influence speciation? *Journal of Evolutionary Biology* 26: 267-269
- J. Kelleher, Barton, N.H., and A. M. Etheridge. 2013. Coalescent simulation in continuous space. *Bioinformatics* 29: 955-956
- N.H. Barton, A.M. Etheridge, J. Kelleher and A. Véber. 2013. Inference for the spatial lambda-Fleming-Viot process. *Theoretical Population Biology* 87: 105-119
- N.H. Barton, A.M. Etheridge, J. Kelleher and A. Véber. 2013. Genetic hitch-hiking in spatially extended populations. *Theoretical Population Biology* 87: 75-89.
- Paixão, T. and N.H. Barton (2013). A variance decomposition approach to the analysis of genetic algorithms, GECCO'13 Proceedings of the 15th Annual Conference on Genetic and Evolutionary Computation, pp. 845-852. doi: [10.1145/2463372.2463470](https://doi.org/10.1145/2463372.2463470)
- Barton, N.H. and T. Paixão (2013). Can quantitative and population genetics help us understand evolutionary computation? GECCO'13 Proceedings of the 15th Annual Conference on Genetic and Evolutionary Computation pp 1573-1580. doi: [10.1145/2463372.2463568](https://doi.org/10.1145/2463372.2463568)
- Hearn, J., Stone, G.N., Bunnefeld, L., Nicholls, J., Barton, N.H., Lohse, K. 2014. Likelihood-based inference of population history from low coverage de novo genome assemblies. *Molecular Ecology* 23: 198-211. DOI: 10.1111/mec.12578
- Barton, N.H., Novak, S., Paixão, T. 2014. Diverse forms of selection in evolution and computer science. *PNAS* doi/10.1073/pnas.1410107111. (commentary).
- Vladar, H.P., Barton, N.H. 2014. Stability and response of polygenic traits to stabilizing selection and mutation. *Genetics* 197:749-767.
- Kelleher, J., Etheridge, A.M., Barton, N.H. (2014) Coalescent simulation in continuous space: algorithms for large neighbourhood size. *Theoretical Population Biology* 95: 13-23. doi 10.1016/j.tpb.2014.05.001
- Barton, N.H. and Servedio, M.R. 2015. The interpretation of selection coefficients. *Evolution* 69: 1101-1112.
- Polechova, J., Barton, N.H. 2015. Limits to adaptation along environmental gradients. *Proc. Natl. Acad. Sci. (USA)* 112: 6401-6406.
- Paixao, T., Badkobeh, G., Barton, N.H., Dolgan, C., Dang, D.C., Friedrich, T., Lehre, P.K., Sudholt, D., Trubenova, B. 2015. Towards a unifying framework for evolutionary processes. *J. Theor. Biol.* 383: 28-43.
- Tugrul, M., Paixao, T., Barton, N.H., Tkacik, G. 2015. Dynamics of transcription factor binding site evolution. *PLoS Genetics* 11(11): e1005639. doi:10.1371/journal.pgen.1005639
- Kelleher, J., Etheridge, A.M., Veber, A., Barton, N.H. 2016. Spread of pedigree versus genetic ancestry in spatially distributed populations. *Theor. Pop. Biol.* 108: 1-12
- Lohse, K., Chmelik, M., Martin, S.H., Barton, N.H. 2016. Efficient strategies for calculating blockwise likelihoods under the coalescent. *Genetics* 202: 775-786
- Paixao, T., Barton, N.H. 2016. The effect of gene interactions on the long-term response to selection. *PNAS* doi:10.1073/pnas.1518830113
- Bodova, K., Tkacik, G., Barton, N.H. 2016. A general approximation for the dynamics of quantitative traits. *Genetics* doi: 10.1534/genetics.115.184127