

## Publications by Nicholas Hamilton Barton

### 2018

Barton, N. H., & Etheridge, A. M.. (2018). Establishment in a new habitat by polygenic adaptation. *Theoretical Population Biology*. Academic Press.

Charlesworth, B., & Barton, N. H.. (2018). The spread of an inversion with migration and selection. *Genetics*. Genetics Society of America.

Ellis, T., Field, D. L., & Barton, N. H.. (2018). Inference from paternity and sibships accounting for uncertainty in genealogy. *Molecular Ecology Resources*. Wiley-Blackwell.

Novembre, J., & Barton, N. H.. (2018). Tread lightly interpreting polygenic tests of selection. *Genetics*. Genetics Society of America.

Payne, P., Geyrhofer, L., Barton, N. H., & Bollback, J. P.. (2018). CRISPR-based herd immunity can limit phage epidemics in bacterial populations. *eLife*. eLife Sciences Publications.

Ringbauer, H., Kolesnikov, A., Field, D., & Barton, N. H.. (2018). Estimating barriers to gene flow from distorted isolation-by-distance patterns. *Genetics*. Genetics Society of America.

### 2017

Barton, N. H.. (2017). How does epistasis influence the response to selection?. *Heredity*. Nature Publishing Group.

Barton, N. H., Etheridge, A. M., & Véber, A.. (2017). The infinitesimal model: Definition derivation and implications. *Theoretical Population Biology*. Academic Press.

Charlesworth, D., Barton, N. H., & Charlesworth, B.. (2017). The sources of adaptive evolution. *Proceedings of the Royal Society of London Series B Biological Sciences*. Royal Society, The.

Friedlander, T., Prizak, R., Barton, N. H., & Tkačik, G.. (2017). Evolution of new regulatory functions on biophysically realistic fitness landscapes. *Nature Communications*. Nature Publishing Group.

Lagator, M., Paixão, T., Barton, N. H., Bollback, J. P., & Guet, C.. (2017). On the mechanistic nature of epistasis in a canonical cis-regulatory element. *eLife*. eLife Sciences Publications.

Novak, S., & Barton, N. H.. (2017). When does frequency-independent selection maintain genetic variation?. *Genetics*. Genetics Society of America.

Ringbauer, H., Coop, G., & Barton, N. H.. (2017). Inferring recent demography from isolation by distance of long shared sequence blocks. *Genetics*. Genetics Society of America.

Sachdeva, H., & Barton, N. H.. (2017). Divergence and evolution of assortative mating in a polygenic trait model of speciation with gene flow. *Evolution; International Journal of Organic Evolution*. Wiley-Blackwell.

Schmidt, T. L., Barton, N. H., Rasic, G., Turley, A. P., Montgomery, B. L., Iturbe-Ormaetxe, I., Cook, P. E., Ryan, P. A., Ritchie, S. A., Hoffmann, A. A., O'Neill, S., & Turelli, M.. (2017). Successful local introduction and heterogeneous spatial spread of dengue-suppressing *Wolbachia* through an urban population of *Aedes aegypti*. *PLoS Biology*. Public Library of Science.

Turelli, M., & Barton, N. H.. (2017). Deploying dengue-suppressing *Wolbachia*: Robust models predict slow but effective spatial spread in *Aedes aegypti*. *Theoretical Population Biology*. Academic Press.

## 2016

Abbott, R., Barton, N. H., & Good, J. M.. (2016). Genomics of hybridization and its evolutionary consequences. *Molecular Ecology*. Wiley.

Barton, N. H.. (2016). Sewall Wright on evolution in Mendelian populations and the "Shifting Balance". *Genetics*. Genetics Society of America.

Barton, N. H.. (2016). Richard Hudson and Norman Kaplan on the coalescent process. *Genetics*. Genetics Society of America.

Bod'ová, K., Tkačik, G., & Barton, N. H.. (2016). A general approximation for the dynamics of quantitative traits. *Genetics*. Genetics Society of America.

Franssen, S. U., Barton, N. H., & Schlötterer, C.. (2016). Reconstruction of haplotype-blocks selected during experimental evolution.. *Molecular Biology and Evolution*. OUP.

Friedlander, T., Prizak, R., Guet, C. C., Barton, N. H., & Tkačik, G.. (2016). Intrinsic limits to gene regulation by global crosstalk. *Nature Communications*. Nature Publishing Group.

Kelleher, J., Etheridge, A. M., Véber, A., & Barton, N. H.. (2016). Spread of pedigree versus genetic ancestry in spatially distributed populations. *Theoretical Population Biology*. Academic Press.

Lohse, K., Chmelík, M., Martin, S. H., & Barton, N. H.. (2016). Efficient strategies for calculating blockwise likelihoods under the coalescent. *Genetics*. Genetics Society of America.

Paixão, T., & Barton, N. H.. (2016). The effect of gene interactions on the long-term response to selection. *PNAS*. National Academy of Sciences.

## 2015

Barton, N. H., & Servedio, M. R.. (2015). The interpretation of selection coefficients. *Evolution*. Wiley-Blackwell.

Paixão, T., Badkobeh, G., Barton, N. H., Çörüş, D., Dang, D., Friedrich, T., Lehre, P. K., Sudholt, D., Sutton, A. M., & Trubenová, B.. (2015). Toward a unifying framework for evolutionary processes. *Journal of Theoretical Biology*. Academic Press.

Polechová, J., & Barton, N. H.. (2015). Limits to adaptation along environmental gradients. *PNAS*. National Academy of Sciences.

Tuğrul, M., Paixão, T., Barton, N. H., & Tkačik, G.. (2015). Dynamics of transcription factor binding site evolution. *PLoS Genetics*. Public Library of Science.

## 2014

Barton, N. H., Novak, S., & Paixão, T.. (2014). Diverse forms of selection in evolution and computer science. *PNAS*. National Academy of Sciences.

Hearn, J., Stone, G. N., Bunnefeld, L., Nicholls, J. A., Barton, N. H., & Lohse, K.. (2014). Likelihood-based inference of population history from low-coverage de novo genome assemblies. *Molecular Ecology*. Wiley.

Kelleher, J., Etheridge, A. M., & Barton, N. H.. (2014). Coalescent simulation in continuous space: Algorithms for large neighbourhood size. *Theoretical Population Biology*. Academic Press.

de Vladar, H. P., & Barton, N. H.. (2014). Stability and response of polygenic traits to stabilizing selection and mutation. *Genetics*. Genetics Society of America.

## 2013

Barton, N. H.. (2013). Does hybridisation influence speciation? . *Journal of Evolutionary Biology*. Wiley-Blackwell.

Barton, N. H.. (2013). Recombination and sex. In *The Princeton Guide to Evolution* (328-333). Princeton University Press.

Barton, N. H., Etheridge, A. M., Kelleher, J., & Véber, A.. (2013). Inference in two dimensions: Allele frequencies versus lengths of shared sequence blocks. *Theoretical Population Biology*. Academic Press.

Barton, N. H., Etheridge, A. M., Kelleher, J., & Véber, A.. (2013). Genetic hitch-hiking in spatially extended populations. *Theoretical Population Biology*. Academic Press.

Barton, N. H., Etheridge, A. M., & Véber, A.. (2013). Modelling evolution in a spatial continuum. *Journal of Statistical Mechanics Theory and Experiment*. IOP Publishing Ltd..

Barton, N. H., & Paixão, T.. (2013). Can quantitative and population genetics help us understand evolutionary computation?. *GECCO: Genetic and evolutionary computation conference*. ACM.

Kelleher, J., Barton, N. H., & Etheridge, A. M.. (2013). Coalescent simulation in continuous space. *Bioinformatics*. Oxford University Press.

Paixão, T., & Barton, N. H.. (2013). A variance decomposition approach to the analysis of genetic algorithms. *GECCO: Genetic and evolutionary computation conference*. ACM.

## 2012

Lohse, K., Barton, N. H., Melika, G., & Stone, G. N.. (2012). A likelihood based comparison of population histories in a parasitoid guild. *Molecular Ecology*. Wiley.

Weissman, D. B., & Barton, N. H.. (2012). Limits to the rate of adaptive substitution in sexual populations. *PLoS Genetics*. Public Library of Science.

## 2011

Abbot, P., Abe, J., Alcock, J., Alizon, S., Alpedrinha, J. A., Andersson, M., Andre, J., van Baalen, M., Balloux, F., Balshine, S., Barton, N. H., Beukeboom, L. W., Biernaskie, J. M., Bilde, T., Borgia, G., Breed, M., Brown, S., Bshary, R., Buckling, A., Burley, N. T., Burton-Chellew, M. N., Cant, M. A., Chapuisat, M., Charnov, E. L., Clutton-Brock, T., Cockburn, A., Cole, B. J., Colegrave, N., Cosmides, L., Couzin, I. D., Coyne, J. A., Creel, S., Crespi, B., Curry, R. L., Dall, S. R., Day, T., Dickinson, J. L., Dugatkin, L. A., El Mouden, C., Emlen, S. T., Evans, J., Ferriere, R., Field, J., Foitzik, S., Foster, K., Foster, W. A., Fox, C. W., Gadau, J., Gandon, S., Gardner, A., Gardner, M. G., Getty, T., Goodisman, M. A., Grafen, A., Grosberg, R., Grozinger, C. M., Gouyon, P., Gwynne, D., Harvey, P. H., Hatchwell, B. J., Heinze, J., Helanterä, H., Helms, K. R., Hill, K., Jiricny, N., Johnstone, R. A., Kacelnik, A., Kiers, E. T., Kokko, H., Komdeur, J., Korb, J., Kronauer, D., Kümmerli, R., Lehmann, L., Linksvayer, T. A., Lion, S., Lyon, B., Marshall, J. A., McElreath, R., Michalakis, Y., Michod, R. E., Mock, D., Monnin, T., Montgomerie, R., Moore, A. J., Mueller, U. G., Noë, R., Okasha, S., Pamilo, P., Parker, G. A., Pedersen, J. S., Pen, I., Pfennig, D., Queller, D. C., Rankin, D. J., Reece, S. E., Reeve, H. K., Reuter, M., Roberts, G., Robson, S. K., Roze, D., Rousset, F., Rueppell, O., Sachs, J. L., Santorelli, L., Schmid-Hempel, P., Schwarz, M. P., Scott-Phillips, T., Shellmann-Sherman, J., Sherman, P. W., Shuker, D. M., Smith, J., Spagna, J. C., Strassmann, B., Suarez, A. V., Sundström, L., Taborisky, M., Taylor, P., Thompson, G., Tooby, J., Tsutsui, N. D., Tsuji, K., Turillazzi, S., Úbeda, F., Vargo, E. L., Voelkl, B., Wenseleers, T., West, S. A., West-Eberhard, M. J., Westneat, D. F., Wiernasz, D. C., Wild, G., Wrangham, R., Young, A. J., Zeh, D. W., Zeh, J. A., & Zink, A.. (2011). Inclusive fitness theory and eusociality. *Nature*. Nature Publishing Group.

Barton, N. H.. (2011). Estimating linkage disequilibria. *Heredity*. Nature Publishing Group.

Barton, N. H., & Etheridge, A. M.. (2011). The relation between reproductive value and genetic contribution. *Genetics*. Genetics Society of America.

Barton, N. H., & Turelli, M.. (2011). Spatial waves of advance with bistable dynamics: Cytoplasmic and genetic analogues of Allee effects. *American Naturalist*. University of Chicago Press.

Logeswaran, S., & Barton, N. H.. (2011). Mapping Mendelian traits in asexual progeny using changes in marker allele frequency. *Genetical Research*. Cambridge University Press.

Lohse, K., Harrison, R. J., & Barton, N. H.. (2011). A general method for calculating likelihoods under the coalescent process. *Genetics*. Genetics Society of America.

Polechová, J., & Barton, N. H.. (2011). Genetic drift widens the expected cline but narrows the expected cline width. *Genetics*. Genetics Society of America.

Polechová, J., Barton, N. H., & Marion, G.. (2011). Erratum: Species' range: Adaptation in space and time (*American Naturalist* 174 (E186 E204)) . *American Naturalist*. University of Chicago Press.

de Vladar, H. P., & Barton, N. H.. (2011). The statistical mechanics of a polygenic character under stabilizing selection mutation and drift. *Journal of the Royal Society Interface*. Royal Society of London.

de Vladar, H. P., & Barton, N. H.. (2011). The contribution of statistical physics to evolutionary biology. *Trends in Ecology and Evolution*. Cell Press.

## 2010

Barton, N. H.. (2010). What role does natural selection play in speciation?. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences*. Royal Society, The.

Barton, N. H.. (2010). Genetic linkage and natural selection. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences*. Royal Society, The.

Barton, N. H.. (2010). Mutation and the evolution of recombination. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences*. Royal Society, The.

Barton, N. H.. (2010). Understanding adaptation in large populations. *PLoS Genetics*. Public Library of Science.

Barton, N. H., Etheridge, A. M., & Véber, A.. (2010). A new model for evolution in a spatial continuum. *Electronic Journal of Probability*. Institute of Mathematical Statistics.

Barton, N. H., Kelleher, J., & Etheridge, A. M.. (2010). A new model for extinction and recolonization in two dimensions: Quantifying phylogeography. *Evolution*. Wiley-Blackwell.

Rosas, U., Barton, N. H., Copsey, L., Barbier de Reuille, P., & Coen, E.. (2010). Cryptic variation between species and the basis of hybrid performance. *PLoS Biology*. Public Library of Science.

Senn, H. V., Goodman, S. J., Swanson, G. M., Barton, N. H., & Pemberton, J. M.. (2010).

Investigating temporal changes in hybridisation and introgression between invasive sika (*Cervus nippon*) and native red deer (*Cervus elaphus*) on the Kintyre Peninsula, Scotland. *Molecular Ecology*. Wiley.

Senn, H. V., Swanson, G. M., Goodman, S. J., Barton, N. H., & Pemberton, J. M.. (2010). Phenotypic correlates of hybridisation between red and sika deer (genus *Cervus*). *Journal of Animal Ecology*. Wiley-Blackwell.

## 2009

Barton, N. H.. (2009). Why sex and recombination? . In *Cold Spring Harbor Symposia on Quantitative Biology* (187-195). Cold Spring Harbor Laboratory Press.

Barton, N. H., & Coe, J. B.. (2009). On the application of statistical physics to evolutionary biology. *Journal of Theoretical Biology*. Elsevier.

Barton, N. H., & De Cara, M. A.. (2009). The evolution of strong reproductive isolation. *Evolution; International Journal of Organic Evolution*. Wiley-Blackwell.

Barton, N. H., & de Vladar, H. P.. (2009). Statistical mechanics and the evolution of polygenic quantitative traits. *Genetics*. Genetics Society of America.

Davison, A., Barton, N. H., & Clarke, B.. (2009). The effect of chirality phenotype and genotype on the fecundity and viability of *Partula suturalis* and *Lymnaea stagnalis*: implications for the evolution of sinistral snails. *Journal of Evolutionary Biology*. Wiley-Blackwell.

Polechová, J., Barton, N. H., & Marion, G.. (2009). Species' range: Adaptation in space and time. *American Naturalist*. University of Chicago Press.

## 2008

Barton, N. H.. (2008). Identity and coalescence in structured populations: A commentary on 'Inbreeding coefficients and coalescence times' by Montgomery Slatkin. *Genetical Research*. Cambridge University Press.