- Edwards, S.V., Shultz, A.J., Campbell-Staton, S.C., 2015. Next-generation sequencing and the expanding domain of phylogeography. Folia Zoologica 64 (3), 187–206.
- Ekblom, R., Galindo, J., 2011. Applications of next generation sequencing in molecular ecology of non-model organisms. Heredity 107 (1), 1–15.
- Elith, J., Leathwick, J.R., 2009. Species distribution models: Ecological explanation and prediction across space and time. Annual Review of Ecology, Evolution, and Systematics 40, 677–697. Available at: http://www.annualreviews.org/eprint/ HWR4cusJrXYCSPZ9sUDj/full (accessed 11.01.16). doi:10.1146/annurev. ecolsys.110308.120159.
- Eme, D., Malard, F., Konecny-Dupré, L., Lefébure, T., Douady, C.J., 2013. Bayesian phylogeographic inferences reveal contrasting colonization dynamics among European groundwater isopods. Molecular Ecology 22 (22), 5685–5699.
- Estoup, A., Baird, S.J.E., Ray, N., *et al.*, 2010. Combining genetic, historical and geographical data to reconstruct the dynamics of bioinvasions: Application to the cane toad *Bufo marinus*. Molecular Ecology Resources 10 (5), 886–901.
- Excoffier, L., Dupanloup, I., Huerta-Sánchez, E., Sousa, V.C., Foll, M., 2013. Robust demographic inference from genomic and SNP data. PLOS Genetics 9 (10), e1003905
- Felsenstein, J., 1975. A pain in the torus: Some difficulties with models of isolation by distance. The American Naturalist 109 (967), 359–368.
- Ford, E.B., Simpson, G.G., Jepsen, G.L., Mayr, E., 1949. Early Stages in Allopatric Speciation. Princeton, NJ: Princeton University Press.
- Gamble, T., Bauer, A.M., Greenbaum, E., Jackman, T.R., 2008. Evidence for Gondwanan vicariance in an ancient clade of gecko lizards. Journal of Biogeography 35 (1), 88–104.
- Gavin, D.G., Fitzpatrick, M.C., Gugger, P.F., et al., 2014. Climate refugia: Joint inference from fossil records, species distribution models and phylogeography. New Phytologist 204 (1), 37–54.
- Goldberg, E.E., Lancaster, L.T., Ree, R.H., 2011. Phylogenetic inference of reciprocal effects between geographic range evolution and diversification. Systematic Biology 60 (4), 451–465.
- Hey, J., 2005. On the number of New World founders: A population genetic portrait of the peopling of the Americas. PLOS Biology 3 (6), e193.
- Hey, J., Nielsen, R., 2004. Multilocus methods for estimating population sizes, migration rates and divergence time, with applications to the divergence of *Drosophila pseudoobscura* and *D. persimilis*. Genetics 167 (2), 747–760.
- Hickerson, M.J., Gilchrist, M.A., Takebayashi, N., 2003. Calibrating a molecular clock from phylogeographic data: Moments and likelihood estimators. Evolution; International Journal of Organic Evolution 57, 2216–2225.
- Hickerson, M.J., Meyer, C., 2008. Testing comparative phylogeographic models of marine vicariance and dispersal using a hierarchical Bayesian approach. BMC Evolutionary Biology 8, 322.
- Hickerson, M.J., Stahl, E.A., Lessios, H.A., 2006. Test for simultaneous divergence using approximate Bayesian computation. Evolution; International Journal of Organic Evolution 60 (12), 2435–2453.
- Ho, S.Y.W., Tong, K.J., Foster, C.S.P., et al., 2015. Biogeographic calibrations for the molecular clock. Biology Letters 11 (9), 20150194.
- Hooker, J.D., 1853. Introductory Essay to the Flora of New Zealand. London: Lovell Reeve.
- von Humboldt, A., Bonpland, A., 1807. Essai Sur La Géographie Des Plantes. Paris: Chez Levrault, Schoell et compagnie, libraires, XIII–1805.
- Hung, C.-M., Drovetski, S.V., Zink, R.M., 2013. Recent allopatric divergence and niche evolution in a widespread Palearctic bird, the common rosefinch (*Carpodacus erythrinus*). Molecular Phylogenetics and Evolution 66 (1), 103–111.
- Ilves, K.L., Huang, W., Wares, J.P., Hickerson, M.J., 2010. Colonization and/or mitochondrial selective sweeps across the North Atlantic intertidal assemblage revealed by multi-taxa approximate Bayesian computation. Molecular Ecology 19 (20), 4505–4519.
- Jordan, D.S., 1905. The origin of species through isolation. Science 22, 545–562. Jordan, D.S., 1908. The law of geminate species. The American Naturalist 42, 73–80.
- Joseph, L., Moritz, C., Hugall, A., 1995. Molecular support for vicariance as a source of diversity in rainforest. Proceedings of the Royal Society B: Biological Sciences 260 (1358), 177–182.
- Kelleher, J., Barton, N.H., Etheridge, A.M., 2013. Coalescent simulation in continuous space. Bioinformatics. Available at: http://bioinformatics. oxfordjournals.org/content/early/2013/02/07/bioinformatics.btt067.abstract (accessed 11.01.16). doi:10.1093/bioinformatics/btt067.
- 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.

- Knowlton, N., Weigt, L.A., 1998. New dates and new rates for divergence across the Isthmus of Panama. Proceedings of the Royal Society B: Biological Sciences 265, 2257–2263
- Kühnert, D., Wu, C.-H., Drummond, A.J., 2011. Phylogenetic and epidemic modeling of rapidly evolving infectious diseases. Infection, Genetics and Evolution: Journal of Molecular Epidemiology and Evolutionary Genetics in Infectious Diseases 11 (8), 1825–1841.
- Kuzmina, N.A., Lemey, P., Kuzmin, I.V., et al., 2013. The phylogeography and spatiotemporal spread of south-central skunk rabies virus. PLOS ONE 8 (12), e82348
- Lacey Knowles, L., Alvarado-Serrano, D.F., 2010. Exploring the population genetic consequences of the colonization process with spatio-temporally explicit models: Insights from coupled ecological, demographic and genetic models in montane grasshoppers. Molecular Ecology 19 (17), 3727–3745.
- Lande, R., 1980. Genetic variation and phenotypic evolution during allopatric speciation. The American Naturalist 116 (4), 463–479.
- Landis, M.J., Matzke, N.J., Moore, B.R., Huelsenbeck, J.P., 2013. Bayesian analysis of biogeography when the number of areas is large. Systematic Biology 62 (6), 789–804.
- Lemey, P., Rambaut, A., Welch, J.J., Suchard, M.A., 2010. Phylogeography takes a relaxed random walk in continuous space and time. Molecular Biology and Evolution 27 (8), 1877–1885.
- Lessios, H.A., 1998. The first stage of speciation as seen in organisms separated by the Isthmus Panama. In: Howard, D.J., Berlocher, S. (Eds.), Endless Forms: Species and Speciation. Oxford: Oxford University Press, pp. 186–201.
- Lessios, H.A., 2008. The Great American Schism: Divergence of marine organisms after the rise of the Central American Isthmus. Annual Review of Ecology, Evolution, and Systematics 39, 63–91.
- Lessios, H.A., 2015. Appearance of an early closure of the Isthmus of Panama is the product of biased inclusion of data in the metaanalysis. Proceedings of the National Academy of Sciences of the United States of America 112 (43), E5765.
- Limic, V., Sturm, A., 2006. The spatial Λ-coalescent. Electronic Journal of Probability 11 (15), 363–393.
- Locke, D.P., Hillier, L.W., Warren, W.C., et al., 2011. Comparative and demographic analysis of orangutan genomes. Nature 469 (7331), 529–533.
- Losos, J.B., Glor, R.E., 2003. Phylogenetic comparative methods and the geography of speciation. Trends in Ecology & Evolution 18, 220–227.
- Manel, S., Schwartz, M.K., Luikart, G., Taberlet, P., 2003. Landscape genetics: Combining landscape ecology and population genetics. Trends in Ecology & Evolution 18, 189–197.
- Mann, D.H., Groves, P., Reanier, R.E., *et al.*, 2015. Life and extinction of megafauna in the ice-age Arctic. Proceedings of the National Academy of Sciences of the United States of America 112 (46), 14301–14306.
- Mao, K., Milne, R.I., Zhang, L., et al., 2012. Distribution of living Cupressaceae reflects the breakup of Pangea. Proceedings of the National Academy of Sciences of the United States of America 109 (20), 7793–7798.
- Marko, P.B., Eytan, R.I., Knowlton, N., 2015. Do large molecular sequence divergences imply an early closure of the Isthmus of Panama? Proceedings of the National Academy of Sciences of the United States of America 112 (43), E5766
- Matzke, N.J., 2014. Model selection in historical biogeography reveals that founderevent speciation is a crucial process in island clades. Systematic Biology 63 (6), 951–970
- Mayden, R.L., 1988. Vicariance biogeography, parsimony, and evolution in North American freshwater fishes. Systematic Zoology 37 (4), 329–355.
- Mayr, E., 1954. Geographic speciation in tropical echinoids. Evolution; International Journal of Organic Evolution 8, 1–18.
- McCartney, M.A., Keller, G., Lessios, H.A., 2000. Dispersal barriers in tropical oceans and speciation in Atlantic and eastern Pacific sea urchins of the genus *Echinometra*. Molecular Ecology 9 (9), 1391–1400.
- McGlone, M.S., 2005. Goodbye Gondwana. Journal of Biogeography 32 (5), 739–740.
- Meseguer, A.S., Lobo, J.M., Ree, R., Beerling, D.J., Sanmartín, I., 2015. Integrating fossils, phylogenies, and niche models into biogeography to reveal ancient evolutionary history: The case of *Hypericum* (hypericaceae). Systematic Biology 64 (2), 215–232.
- Metcalf, J.L., Prost, S., Nogués-Bravo, D., et al., 2014. Integrating multiple lines of evidence into historical biogeography hypothesis testing: A Bison bison case study. Proceedings of the Royal Society B: Biological Sciences 281 (1777), 20132782.
- Morrone, J.J., Carpenter, J.M., 1994. In search of a method for cladistic biogeography: An empirical comparison of component analysis, Brooks