

- 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.
- Eklom, 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.
- Erme, D., Malard, F., Konecny-Dupré, L., Lefebvre, 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 of 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.L., 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 founder-event 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.
- Metcalfe, 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