References for Project Proposal

- [1] Hutchinson, G.E. (1959) Homage to santa rosalia or why are there so many kinds of animals? Am. Nat. 93, 145–159
- [2] Prates, I. et al. (2016) Inferring responses to climate dynamics from historical demography in neotropical forest lizards. Proc. Natl. Acad. Sci. U. S. A. 113, 7978–7985
- [3] Carnaval, A.C. et al. (2014) Prediction of phylogeographic endemism in an environmentally complex biome. Proc. Biol. Sci. 281
- [4] Barnosky, A.D. et al. (2011) Has the earth's sixth mass extinction already arrived? Nature 471, 51–57
- [5] Erwin, D.H. (2015) Extinction: How Life on Earth Nearly Ended 250 Million Years Ago. Princeton University Press
- [6] MacArthur, R.H. and Wilson, E.O. (1967) The theory of island biogeography. Princeton University Press
- [7] Hubbell, S.P. (2001) The unified neutral theory of biodiversity and biogeography, vol. 32. Princeton University Press
- [8] Gillespie, R. (2004) Community assembly through adaptive radiation in hawaiian spiders. Science 303, 356–359
- [9] Owens, H.L. et al. (2017) The latitudinal diversity gradient in new world swallowtail butterflies is caused by contrasting patterns of out-of- and into-the-tropics dispersal. Glob. Ecol. Biogeogr. 26, 1447–1458
- [10] Janzen, D.H. (1967) Why mountain passes are higher in the tropics. Am. Nat. 101, 233–249
- [11] Mittelbach, G.G. et al. (2007) Evolution and the latitudinal diversity gradient: speciation, extinction and biogeography. Ecol. Lett. 10, 315–331
- [12] Pianka, E.R. (1966) Latitudinal gradients in species diversity: A review of concepts. Am. Nat. 100, 33–46
- [13] Ricklefs, R.E. (2006) The unified neutral theory of biodiversity: do the numbers add up? Ecology 87, 1424–1431
- [14] Chisholm, R.A. and O'Dwyer, J.P. (2014) Species ages in neutral biodiversity models. Theor. Popul. Biol. 93, 85–94
- [15] Rosindell, J. et al. (2015) Unifying ecology and macroevolution with individual-based theory. Ecol. Lett. 18, 472–482
- [16] Rosindell, J. et al. (2012) The case for ecological neutral theory. Trends Ecol. Evol. 27, 203–208
- [17] Chisholm, R.A. and Pacala, S.W. (2010) Niche and neutral models predict asymptotically equivalent species abundance distributions in high-diversity ecological communities. *Proc.* Natl. Acad. Sci. U. S. A. 107, 15821–15825

- [18] McGill, B. (2003) Strong and weak tests of macroecological theory. Oikos 102, 679–685
- [19] McGill, B.J. et al. (2007) Species abundance distributions: moving beyond single prediction theories to integration within an ecological framework. Ecol. Lett. 10, 995–1015
- [20] Leibold, M.A. and Chase, J.M. (2017) Metacommunity Ecology. Princeton University Press
- [21] Rominger, A.J. et al. Linking evolutionary and ecological theory illuminates non-equilibrium biodiversity. *Trends Ecol. Evol.*
- [22] Etienne, R.S. (2007) A neutral sampling formula for multiple samples and an 'exact' test of neutrality. *Ecology Letters* 10, 608–618
- [23] Chesson, P. (2000) Mechanisms of maintenance of species diversity. *Annu. Rev. Ecol. Syst.* 31, 343–366
- [24] Ricklefs, R.E. and Bermingham, E. (2001) Nonequilibrium diversity dynamics of the lesser antillean avifauna. *Science* 294, 1522–1524
- [25] Qian, H. et al. (2005) Beta diversity of angiosperms in temperate floras of eastern asia and eastern north america. Ecol. Lett. 8, 15–22
- [26] Yu, X.Q. et al. (2017) Insights into the historical assembly of east asian subtropical evergreen broadleaved forests revealed by the temporal history of the tea family. New Phytol. 215, 1235–1248
- [27] Carnaval, A.C. and Moritz, C. (2008) Historical climate modelling predicts patterns of current biodiversity in the brazilian atlantic forest. *J. Biogeogr.* 35, 1187–1201
- [28] Carnaval, A.C. et al. (2009) Stability predicts genetic diversity in the brazilian atlantic forest hotspot. Science 323, 785–789
- [29] Burbrink, F.T. et al. (2016) Asynchronous demographic responses to pleistocene climate change in eastern nearctic vertebrates. Ecol. Lett. 19, 1457–1467
- [30] Barnosky, A.D. et al. (2012) Approaching a state shift in earth/'s biosphere. Nature 486, 52–58
- [31] Overcast, I. et al. An integrated model of population genetics and community ecology. Mol. Ecol.
- [32] Beaumont, M.A. (2010) Approximate bayesian computation in evolution and ecology. *Annu. Rev. Ecol. Evol. Syst.*
- [33] Rosindell, J. et al. (2010) Protracted speciation revitalizes the neutral theory of biodiversity. Ecol. Lett. 13, 716–727
- [34] Rosindell, J. and Phillimore, A.B. (2011) A unified model of island biogeography sheds light on the zone of radiation. *Ecol. Lett.* 14, 552–560
- [35] Haegeman, B. and Etienne, R.S. (2017) A general sampling formula for community structure data. *Methods Ecol. Evol.*
- [36] Grilli, J. et al. (2017) Higher-order interactions stabilize dynamics in competitive network models. Nature 548, 210–213

- [37] HilleRisLambers, J. et al. (2012) Rethinking community assembly through the lens of coexistence theory. Annual Review of
- [38] Adler, P.B. et al. (2010) Coexistence of perennial plants: an embarrassment of niches. Ecol. Lett., no-no
- [39] Jabot, F. et al. (2008) Reconciling neutral community models and environmental filtering: theory and an empirical test. Oikos 117, 1308–1320
- [40] Tuomisto, H. et al. (2003) Dispersal, environment, and floristic variation of western amazonian forests. Science 299, 241–244
- [41] Schrider, D.R. and Kern, A.D. (2018) Supervised machine learning for population genetics: A new paradigm. *Trends Genet*.
- [42] Overcast, I. et al. (2017) Strategies for improving approximate bayesian computation tests for synchronous diversification. BMC Evol. Biol. 17, 203
- [43] R Development Core, T. (2013) R: A language and environment for statistical computing. Vienna, Austria
- [44] Losos, J.B. and Schluter, D. (2000) Analysis of an evolutionary species—area relationship. Nature 408, 847
- [45] Wagner, C.E. et al. (2014) Cichlid species-area relationships are shaped by adaptive radiations that scale with area. Ecol. Lett. 17, 583–592
- [46] Ogden, R. and Thorpe, R.S. (2002) Molecular evidence for ecological speciation in tropical habitats. *Proc. Natl. Acad. Sci. U. S. A.* 99, 13612–13615
- [47] Rundle, H.D. and Nosil, P. (2005) Ecological speciation. Ecol. Lett. 8, 336–352
- [48] May, R.M. (1973) Qualitative stability in model ecosystems. Ecology 54, 638–641
- [49] Nuismer, S.L. et al. (2013) Coevolution and the architecture of mutualistic networks. Evolution 67, 338–354
- [50] Quental, T.B. and Marshall, C.R. (2013) How the red queen drives terrestrial mammals to extinction. *Science*
- [51] O'Dwyer, J.P. and Chisholm, R. (2014) A mean field model for competition: From neutral ecology to the red queen. *Ecol. Lett.* 17, 961–969
- [52] Rabosky, D.L. (2009) Ecological limits and diversification rate: alternative paradigms to explain the variation in species richness among clades and regions. *Ecol. Lett.* 12, 735–743
- [53] Rominger, A.J. et al. (2015) Community assembly on isolated islands: macroecology meets evolution. Glob. Ecol. Biogeogr.
- [54] Gillespie, R.G. and Baldwin, B.G. (2010) Island biogeography of remote archipelagoes. *The theory of island biogeography revisited*, 358–387
- [55] Guralnick, R. et al. (2017) Humboldt core toward a standardized capture of biological inventories for biodiversity monitoring, modeling and assessment. Ecography

- [56] Rominger, A.J. and Huang, E.G. (2016). hdimDB: an R package for biodiversity database management with google sheets. https://github.com/hawaiiDimensions/db/tree/master/hdimDB
- [57] RStudio, Inc (2013) Easy web applications in R
- [58] Wickham, H. and Francois, R. (2015) dplyr: A grammar of data manipulation. R package version 0. 4 3
- [59] Flemons, P. et al. (2007) A web-based GIS tool for exploring the world's biodiversity: The global biodiversity information facility mapping and analysis portal application (GBIF-MAPA). Ecol. Inform. 2, 49–60
- [60] Sherry, S.T. et al. (2001) dbSNP: the NCBI database of genetic variation. Nucleic Acids Res. 29, 308–311
- [61] Benson, D. et al. (1993) GenBank. Nucleic Acids Res. 21, 2963–2965
- [62] Hinchliff, C.E. et al. (2015) Synthesis of phylogeny and taxonomy into a comprehensive tree of life. Proc. Natl. Acad. Sci. U. S. A. 112, 12764–12769
- [63] Jetz, W. et al. (2012) Integrating biodiversity distribution knowledge: toward a global map of life. Trends Ecol. Evol. 27, 151–159
- [64] Bartomeus, I. and Molina, P.J. (2018). TraitBase. https://traitbase.info/
- [65] Poelen, J.H. et al. (2014) Global biotic interactions: An open infrastructure to share and analyze species-interaction datasets. Ecol. Inform. 24, 148–159
- [66] Chamberlain, S. et al. (2014) rgbif: Interface to the global biodiversity information facility API. R package version 0. 7 7
- [67] Winter, D.J. (2017) rentrez: An R package for the NCBI eUtils API. Tech. Rep. e3179v2, PeerJ Preprints
- [68] Michonneau, F. et al. (2016) rotl: an R package to interact with the open tree of life data. Methods Ecol. Evol. 7, 1476–1481
- [69] Molina, P.J. and Bartomeus, I. (2017). traitbaser: R package providing API access to traitbase https://www.traitbase.info. https://github.com/metadevpro/traitbaser
- [70] Poelen, J. et al. (2018). rglobi: R interface to global biotic interactions
- [71] Douglas, K. and Douglas, S. (2003) PostgreSQL: A Comprehensive Guide to Building, Programming, and Administering PostgresSQL Databases. Sams Publishing
- [72] Brown, J.H. et al. (2004) Toward a metabolic theory of ecology. Ecology 85, 1771–1789
- [73] Price, C.A. et al. (2012) Testing the metabolic theory of ecology. Ecology letters 15, 1465–1474
- [74] Elith, J. and 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

- [75] Krehenwinkel, H. et al. (2017) Estimating and mitigating amplification bias in qualitative and quantitative arthropod metabarcoding. Sci. Rep. 7, 17668
- [76] Che, J. et al. (2012) Universal coi primers for dna barcoding amphibians. Molecular Ecology Resources 12, 247–258
- [77] Bi, Y. et al. (2018) Chloroplast genomic resources for phylogeny and dna barcoding: a case study on fritillaria. Scientific reports 8, 1184
- [78] Lopez-Gonzalez, G. et al. (2011) ForestPlots.net: a web application and research tool to manage and analyse tropical forest plot data. J. Veq. Sci. 22, 610–613
- [79] ter Steege, H. and et al. (2011). Amazon tree diversity network. http://atdn.myspecies.info/
- [80] RAINFOR (2018). Amazon forest inventory network. http://www.rainfor.org/
- [81] Webb, C.O. et al. (2008) Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Bioinformatics 24
- [82] Harmon, L.J. et al. (2013) Arbor: Comparative analysis workflows for the tree of LifeCall for SubmissionsAVAToL CollectionBlog PostTwitter. PLoS Curr.
- [83] Rosindell, J. and Harmon, L.J. (2013) A unified model of species immigration, extinction and abundance on islands. J. Biogeogr. 40, 1107–1118
- [84] Felsenstein, J. (2012) A comparative method for both discrete and continuous characters using the threshold model. Am. Nat. 179, 145–156
- [85] Wilson, W.G. et al. (2003) Biodiversity and species interactions: extending Lotka-Volterra community theory. Ecol. Lett. 6, 944–952
- [86] Kendall, D.G. (1948) On some modes of population growth leading to r. a. fisher's logarithmic series distribution. *Biometrika* 35, 6–15
- [87] Waples, R.S. and Yokota, M. (2007) Temporal estimates of effective population size in species with overlapping generations. *Genetics* 175, 219–233
- [88] Rosenberg, N.A. and Nordborg, M. (2002) Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. *Nat. Rev. Genet.* 3, 380–390
- [89] Kelleher, J. et al. (2016) Efficient coalescent simulation and genealogical analysis for large sample sizes. PLoS Comput. Biol. 12, e1004842
- [90] Anderson, J. et al. (2014) The more, the merrier: the blessing of dimensionality for learning large gaussian mixtures. In *Conference on Learning Theory*. jmlr.org, pp. 1135–1164
- [91] Breiman, L. (2001) Statistical modeling: The two cultures (with comments and a rejoinder by the author). Stat. Sci. 16, 199–231
- [92] Tingley, M.W. and Beissinger, S.R. (2009) Detecting range shifts from historical species occurrences: new perspectives on old data. *Trends Ecol. Evol.* 24, 625–633
- [93] May, F. et al. (2017) mobsim: An R package for the simulation and measurement of biodiversity across spatial scales

- [94] Chao, A. et al. (2010) Phylogenetic diversity measures based on hill numbers. Philos. Trans. R. Soc. Lond. B Biol. Sci. 365, 3599–3609
- [95] Karp, D.S. et al. (2012) Intensive agriculture erodes?-diversity at large scales. Ecol. Lett. 15
- [96] Barnosky, A.D. *et al.* (2001) Temperate terrestrial vertebrate faunas in north and south america: Interplay of ecology, evolution, and geography with biodiversity. *Conserv. Biol.* 15, 658–674
- [97] do Amaral, F.R. et al. (2016) The "atlantis forest hypothesis" does not explain atlantic forest phylogeography. Proc. Natl. Acad. Sci. U. S. A. 113, E2097–E2098
- [98] Prates, I. et al. (2016) A mid-pleistocene rainforest corridor enabled synchronous invasions of the atlantic forest by amazonian anole lizards. Mol. Ecol. 25, 5174–5186
- [99] Maestri, R. et al. (2016) Predictors of intraspecific morphological variability in a tropical hotspot: comparing the influence of random and non-random factors. J. Biogeogr. 43, 2160– 2172
- [100] Zamborlini Saiter, F. et al. (2016) Environmental correlates of floristic regions and plant turnover in the atlantic forest hotspot. J. Biogeogr. 43, 2322–2331
- [101] Montade, V. et al. (2016) Pollen-based characterization of montane forest types in north-eastern brazil. Rev. Palaeobot. Palynol. 234, 147–158
- [102] Bernal, J.P. et al. (2016) High-resolution holocene south american monsoon history recorded by a speleothem from botuverá cave, brazil. Earth Planet. Sci. Lett. 450, 186–196
- [103] Bustamante, M.G. et al. (2016) Holocene changes in monsoon precipitation in the andes of NE peru based on δ 18O speleothem records. Quat. Sci. Rev. 146, 274–287
- [104] Gu, F. et al. (2017) Long-term vegetation, climate and ocean dynamics inferred from a 73,500 years old marine sediment core (GeoB2107-3) off southern brazil. Quat. Sci. Rev. 172, 55–71
- [105] Dawson, M.N. (2016) Island and island-like marine environments. Glob. Ecol. Biogeogr. 25, 831–846
- [106] Dawson, M.N. et al. (2016) Biogeography of islands, lakes, and mountaintops; evolutionary
- [107] Meyerhof, M.S. et al. (2016) Microbial community diversity, structure and assembly across oxygen gradients in meromictic marine lakes, palau. Environ. Microbiol. 18, 4907–4919
- [108] Schiebelhut, L.M. et al. (2017) A comparison of DNA extraction methods for high-throughput DNA analyses. Mol. Ecol. Resour. 17, 721–729
- [109] Swift, H.F. et al. (2016) Three routes to crypsis: Stasis, convergence, and parallelism in the mastigias species complex (scyphozoa, rhizostomeae). Mol. Phylogenet. Evol. 99, 103–115
- [110] Wilson, J. et al. (2017) Primary production, community respiration, and net community production along oxygen and nutrient gradients: Environmental controls and biogeochemical feedbacks within and across "marine lakes". Frontiers in Marine Science 4, 12
- [111] Brewer, M.S. et al. (2015) Shifting habitats, morphology, and selective pressures: developmental polyphenism in an adaptive radiation of hawaiian spiders. Evolution 69, 162–178

- [112] Brewer, M.S. et al. (2014) New sequencing technologies, the development of genomics tools, and their applications in evolutionary arachnology. J. Arachnol. 42, 1–15
- [113] Gillespie, R.G. (2013) Adaptive radiation: Convergence and non-equilibrium. Curr. Biol. 23, R71–R74
- [114] Shaw, K.L. and Gillespie, R.G. (2016) Comparative phylogeography of oceanic archipelagos: Hotspots for inferences of evolutionary process. *Proc. Natl. Acad. Sci. U. S. A.* 113, 7986–7993
- [115] Gillespie, R.G. (2016) Island time and the interplay between ecology and evolution in species diversification. *Evol. Appl.* 9, 53–73
- [116] Gillespie, R.G. and Roderick, G.K. (2014) Evolution: Geology and climate drive diversification. *Nature* 509, 297–298
- [117] Krehenwinkel, H. et al. (2017) A cost-efficient and simple protocol to enrich prey DNA from extractions of predatory arthropods for large-scale gut content analysis by illumina sequencing. Methods Ecol. Evol. 8, 126–134
- [118] Warren, B.H. et al. (2015) Islands as model systems in ecology and evolution: prospects fifty years after MacArthur-Wilson. Ecol. Lett. 18, 200–217
- [119] Yim, K.M. et al. (2014) Comparative transcriptomics of maturity-associated color change in hawaiian spiders. J. Hered. 105 Suppl 1, 771–781
- [120] Krehenwinkel, H. et al. (2018) The effect of DNA degradation bias in passive sampling devices on metabarcoding studies of arthropod communities and their associated microbiota. PLoS One 13, e0189188
- [121] Graham, N.R. et al. (2017) Island ecology and evolution: challenges in the anthropocene. Environ. Conserv. 44, 323–335
- [122] Guralnick, R.P. et al. (2007) Towards a collaborative, global infrastructure for biodiversity assessment. Ecol. Lett. 10, 663–672
- [123] Guralnick, R. et al. (2009) Sharing: lessons from natural history's success story. Nature 462, 34
- [124] Guralnick, R. and Constable, H. (2010) VertNet: Creating a data-sharing community. *Bioscience* 60, 258–259
- [125] Parr, C.S. et al. (2012) Evolutionary informatics: unifying knowledge about the diversity of life. Trends Ecol. Evol. 27, 94–103
- [126] Stucky, B.J. et al. (2014) The BiSciCol triplifier: bringing biodiversity data to the semantic web. BMC Bioinformatics 15, 257
- [127] Yilmaz, P. et al. (2011) Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIxS) specifications. Nat. Biotechnol. 29, 415
- [128] Xue, A.T. and Hickerson, M.J. (2017) MultiDICE: R package for comparative population genomic inference under hierarchical codemographic models of independent single-population size changes. *Mol. Ecol. Resour.*

- [129] Emerson, B.C. et al. (2015) Model misspecification confounds the estimation of rates and exaggerates their time dependency. Mol. Ecol. 24, 6013–6020
- [130] Myers, E.A. et al. (2016) Asynchronous diversification of snakes in the north american warm deserts. J. Biogeogr.
- [131] Boehm, J.T. et al. (2016) Urbanization shapes the demographic history of a native rodent (the white-footed mouse, peromyscus leucopus) in new york city. Biology
- [132] Joseph, T.A. et al. (2016) Demographic inference under a spatially continuous coalescent model. Heredity 117, 94–99
- [133] Burbrink, F.T. et al. (2016) Asynchronous demographic responses to pleistocene climate change in eastern nearctic vertebrates. Ecol. Lett.
- [134] Brown, J.L. et al. (2016) Predicting the genetic consequences of future climate change: The power of coupling spatial demography, the coalescent, and historical landscape changes. Am. J. Bot. 103, 153–163
- [135] Prates, I. et al. (2016) Inferring responses to climate dynamics from historical demography in neotropical forest lizards. Proceedings of the National Academy of Sciences 113, 7978–7985
- [136] Demos, T.C. et al. (2015) Comparative population genomics of african montane forest mammals support population persistence across a climatic gradient and quaternary climatic cycles. PLoS One 10, e0131800
- [137] Lipshutz, S.E. et al. (2017) Behavioural response to song and genetic divergence in two subspecies of white-crowned sparrows (zonotrichia leucophrys). Mol. Ecol. 26, 3011–3027
- [138] Harris, S.E. et al. (2016) Urbanization shapes the demographic history of a native rodent (the white-footed mouse, peromyscus leucopus) in new york city. Biol. Lett. 12
- [139] Alvarado-Serrano, D.F. and Hickerson, M.J. (2015) Spatially explicit summary statistics for historical population genetic inference. *Methods Ecol. Evol.* 7, 418–427
- [140] Xue, A.T. and Hickerson, M.J. (2015) The aggregate site frequency spectrum (aSFS) for comparative population genomic inference. *Mol. Ecol.*
- [141] Emerson, B.C. and Hickerson, M.J. (2015) Lack of support for the time-dependent molecular evolution hypothesis. *Mol. Ecol.* 24, 702–709
- [142] Boehm, J.T. et al. (2015) Population genomics reveals seahorses (hippocampus erectus) of the western Mid-Atlantic coast to be residents rather than vagrants. PLoS One 10, e0116219
- [143] Robinson, J.D. et al. (2014) Sampling strategies for frequency spectrum-based population genomic inference. BMC Evol. Biol. 14, 254
- [144] Robinson, J.D. et al. (2014) ABC inference of multipopulation divergence with admixture from unphased population genomic data. Mol. Ecol. 23, 4458–4471
- [145] Smith, B.T. et al. (2014) The drivers of tropical speciation. Nature
- [146] Chan, Y.L. et al. (2014) Detecting concerted demographic response across community assemblages using hierarchical approximate bayesian computation. Mol. Biol. Evol., msu187

- [147] Demos, T.C. et al. (2014) Uncovering cryptic diversity and refugial persistence among small mammal lineages across the eastern afromontane biodiversity hotspot. Mol. Phylogenet. Evol. 71, 41–54
- [148] Hickerson, M.J. et al. (2014) Recommendations for using msbayes to incorporate uncertainty in selecting an abc model prior: a response to oaks et al. Evolution 68, 284–294

References for Student Training Plan

- [1] Woodin, T. et al. (2010) Vision and change in biology undergraduate education, a call for action–initial responses. CBE Life Sci. Educ. 9, 71–73
- [2] Cook, J.A. et al. (2014) Natural history collections as emerging resources for innovative education. BioScience 64, 725–734
- [3] Lacey, E.A. et al. (2017) Climate change, collections and the classroom: using big data to tackle big problems. Evolution: Education and Outreach 10, 2
- [4] Goring, S.J. et al. (2014) Improving the culture of interdisciplinary collaboration in ecology by expanding measures of success. Frontiers in Ecology and the Environment 12, 39–47
- [5] Wuchty, S. et al. (2007) The increasing dominance of teams in production of knowledge. Science 316, 1036–1039
- [6] Cheruvelil, K.S. et al. (2014) Creating and maintaining high-performing collaborative research teams: the importance of diversity and interpersonal skills. Frontiers in Ecology and the Environment 12, 31–38
- [7] Jones, B.F. et al. (2008) Multi-university research teams: Shifting impact, geography, and stratification in science. Science 322, 1259–1262