

Molecular Evolution Reading List

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Books

- HMPG = Hahn MW (2018). *Molecular Population Genetics*. Sinauer Series. Oxford University Press (physical copy on reserve at ZSR)
- DL = Durbin R, Eddy SR, Krogh A, and Mitchison G (1998). *Biological sequence analysis: probabilistic models of proteins and nucleic acids*. Cambridge University Press. URL <https://ebookcentral.proquest.com/lib/wfu/detail.action?docID=320915> (full-text digital through ZSR Library)
- MEPA = Page RDM and Holmes EC (1991). *Molecular evolution : a phylogenetic approach*. John Wiley & Sons, Incorporated, Oxford, UNITED KINGDOM. URL <http://ebookcentral.proquest.com/lib/wfu/detail.action?docID=454344> (full-text digital through ZSR Library)

1. INTRODUCTION: GENETICS, EVOLUTION, PHYLOGENY

- 1.1. ► HMPG: Chapter 1
- 1.2. ► MEPA: Chapter 3
- 1.3. ► Gregory TR (2008). Understanding evolutionary trees. *Evolution: Education and Outreach*, 1(2):121–137. URL <http://dx.doi.org/10.1007/s12052-008-0035-x>
- 1.4. Omland KE, Cook LG, and Crisp MD (2008). Tree thinking for all biology: the problem with reading phylogenies as ladders of progress. *BioEssays*, 30(9):854–867. URL <http://dx.doi.org/10.1002/bies.20794>

2. HOMOLOGY

- 2.1. ► Fitch WM (2000). Homology: a personal view on some of the problems. *Trends in Genetics*, 16(5):227–231. URL [http://dx.doi.org/10.1016/s0168-9525\(00\)02005-9](http://dx.doi.org/10.1016/s0168-9525(00)02005-9)
- 2.2. ► Thornton JW and DeSalle R (2000). Gene family evolution and homology: genomics meets phylogenetics. *Annual Review of Genomics and Human Genetics*, 1(1):41–73. URL <http://dx.doi.org/10.1146/annurev.genom.1.1.41>
- 2.3. Koonin EV (2005). Orthologs, paralogs, and evolutionary genomics. *Annual Review of Genetics*, 39(1):309–338. URL <http://dx.doi.org/10.1146/annurev.genet.39.073003.114725>
- 2.4. Phillips AJ (2006). Homology assessment and molecular sequence alignment. *Journal of Biomedical Informatics*, 39(1):18–33. URL <http://dx.doi.org/10.1016/j.jbi.2005.11.005>

3. SEQUENCE ALIGNMENT

- 3.1. ► Morrison DA, Morgan MJ, and Kelchner SA (2015). Molecular homology and multiple-sequence alignment: an analysis of concepts and practice. *Australian Systematic Botany*, 28(1):46. URL <http://dx.doi.org/10.1071/sb15001>
- 3.2. ► Altschul SF, Gish W, Miller W, Myers EW, and Lipman DJ (1990). Basic local alignment search tool. *Journal of Molecular Biology*, 215(3):403–410
- 3.3. DL: Chapters 2 and 6
- 3.4. Morrison DA (2015). Is sequence alignment an art or a science? *Systematic Botany*, 40(1):14–26. URL <http://dx.doi.org/10.1600/036364415x686305>
- 3.5. Kumar S and Filipski A (2007). Multiple sequence alignment: in pursuit of homologous DNA positions. *Genome Research*, 17(2):127–135. URL <http://dx.doi.org/10.1101/gr.5232407>

4. MOLECULAR POPULATION GENETICS

- 4.1. ► Casillas S and Barbadilla A (2017). Molecular population genetics. *Genetics*, 205(3):1003–1035. URL <http://dx.doi.org/10.1534/genetics.116.196493>
- 4.2. ► Ellegren H and Galtier N (2016). Determinants of genetic diversity. *Nature Reviews Genetics*, 17(7):422–433. URL <http://dx.doi.org/10.1038/nrg.2016.58>
- 4.3. HMPG Chapter 3
- 4.4. Charlesworth B and Charlesworth D (2016). Population genetics from 1966 to 2016. *Heredity*, 118(1):2–9. URL <http://dx.doi.org/10.1038/hdy.2016.55>
- 4.5. Orr HA (2009). Fitness and its role in evolutionary genetics. *Nature Reviews Genetics*, 10(8):531–539. URL <http://dx.doi.org/10.1038/nrg2603>

5. PHYLOGENETICS: DISTANCE METHODS, PARSIMONY, AND MAXIMUM LIKELIHOOD

- 5.1. ► Yang Z and Rannala B (2012). Molecular phylogenetics: principles and practice. *Nature Reviews Genetics*, 13(5):303–314. URL <http://dx.doi.org/10.1038/nrg3186>
- 5.2. Holder M and Lewis PO (2003). Phylogeny estimation: traditional and Bayesian approaches. *Nature Reviews Genetics*, 4(4):275–284. URL <http://dx.doi.org/10.1038/nrg1044>
- 5.3. Felsenstein J (1981). Evolutionary trees from DNA sequences: A maximum likelihood approach. *Journal of Molecular Evolution*, 17(6):368–376. URL <http://dx.doi.org/10.1007/bf01734359>

6. PHYLOGENETICS: BAYESIAN

- 6.1. ► Huelsenbeck JP, Ronquist F, Nielsen R, and Bollback JP (2001a). Bayesian inference of phylogeny and its impact on evolutionary biology. *Science*, 294(5550):2310–2314. URL <http://dx.doi.org/10.1126/science.1065889>
- 6.2. ► Huelsenbeck JP, Ronquist F, Nielsen R, and Bollback JP (2001b). Supplementary information to: Bayesian inference of phylogeny and its impact on evolutionary biology. *Science*, 294(5550):2310–2314. URL <http://science.sciencemag.org/content/suppl/2001/12/13/294.5550.2310.DC1>
- 6.3. Nascimento FF, dos Reis M, and Yang Z (2017). A biologist’s guide to Bayesian phylogenetic analysis. *Nature Ecology & Evolution*, 1(10):1446–1454. URL <http://dx.doi.org/10.1038/s41559-017-0280-x>
- 6.4. Alfaro ME and Holder MT (2006). The posterior and the prior in Bayesian phylogenetics. *Annual Review of Ecology, Evolution, and Systematics*, 37(1):19–42. URL <http://dx.doi.org/10.1146/annurev.ecolsys.37.091305.110021>

7. TESTS OF SELECTION

- 7.1. ► McDonald JH and Kreitman M (1991). Adaptive protein evolution at the *Adh* locus in *Drosophila*. *Nature*, 351(6328):652. URL <http://dx.doi.org/10.1038/351652a0>
- 7.2. ► Frost SDW, Günthard HF, Wong JK, Havlir D, Richman DD, and Brown AJL (2001). Evidence for positive selection driving the evolution of HIV-1 *env* under potent antiviral therapy. *Virology*, 284(2):250–258. URL <http://dx.doi.org/10.1006/viro.2000.0887>
- 7.3. Vitti JJ, Grossman SR, and Sabeti PC (2013). Detecting natural selection in genomic data. *Annual Review of Genetics*, 47(1):97–120. URL <http://dx.doi.org/10.1146/annurev-genet-111212-133526>
- 7.4. Yang Z and Bielawski JP (2000). Statistical methods for detecting molecular adaptation. *Trends in Ecology & Evolution*, 15(12):496–503. URL [http://dx.doi.org/10.1016/s0169-5347\(00\)01994-7](http://dx.doi.org/10.1016/s0169-5347(00)01994-7)
- 7.5. HMPG Chapter 7
- 7.6. Nielsen R (2005). Molecular signatures of natural selection. *Annual Review of Genetics*, 39(1):197–218. URL <http://dx.doi.org/10.1146/annurev.genet.39.073003.112420>

8. PHYLOGENOMICS

- 8.1. ► Fontaine MC, Pease JB, Steele A, Waterhouse RM, Neafsey DE, Sharakhov IV, Jiang X, Hall AB, Catteruccia F, Kakani E, *et al.* (2015). Extensive introgression in a malaria vector species complex revealed by phylogenomics. *Science*, 347(6217):1258524–1258524. URL <http://dx.doi.org/10.1126/science.1258524>
- 8.2. Supplementary Materials:
<http://science.sciencemag.org/content/suppl/2014/11/25/science.1258524.DC1>
- 8.3. Bravo GA, Antonelli A, Bacon CD, Bartoszek K, Blom MPK, Huynh S, Jones G, Knowles LL, Lamichaney S, Marcussen T, *et al.* (2019). Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. *PeerJ*, 7:e6399. URL <http://dx.doi.org/10.7717/peerj.6399>

9. STUDENT CHOICE PAPERS

- 9.1. Pedersen CET, Lohmueller KE, Grarup N, Bjerregaard P, Hansen T, Siegismund HR, Moltke I, and Albrechtsen A (2016). The effect of an extreme and prolonged population bottleneck on patterns of deleterious variation: insights from the Greenlandic Inuit. *Genetics*, 205(2):787–801. URL <http://dx.doi.org/10.1534/genetics.116.193821>
- 9.2. Casas-Marce M, Marmesat E, Soriano L, Martínez-Cruz B, Lucena-Perez M, Nocete F, Rodríguez-Hidalgo A, Canals A, Nadal J, Detry C, *et al.* (2017). Spatiotemporal dynamics of genetic variation in the Iberian Lynx along its path to extinction reconstructed with ancient DNA. *Molecular Biology and Evolution*, 34(11):2893–2907. URL <http://dx.doi.org/10.1093/molbev/msx222>
- 9.3. Tarver JE, dos Reis M, Mirarab S, Moran RJ, Parker S, O'Reilly JE, King BL, O'Connell MJ, Asher RJ, Warnow T, *et al.* (2016). The interrelationships of placental mammals and the limits of phylogenetic inference. *Genome Biology and Evolution*, 8(2):330–344. URL <http://dx.doi.org/10.1093/gbe/evv261>
- 9.4. Troupin C, Dacheux L, Tanguy M, Sabeta C, Blanc H, Bouchier C, Vignuzzi M, Duchene S, Holmes EC, and Bourhy H (2016). Large-scale phylogenomic analysis reveals the complex evolutionary history of rabies virus in multiple carnivore hosts. *PLoS Pathogens*, 12(12):e1006041. URL <http://dx.doi.org/10.1371/journal.ppat.1006041>
- 9.5. Morley VJ and Turner PE (2017). Dynamics of molecular evolution in RNA virus populations depend on sudden versus gradual environmental change. *Evolution*, 71(4):872–883. URL <http://dx.doi.org/10.1111/evo.13193>
- 9.6. Safavi-Hemami H, Lu A, Li Q, Fedosov AE, Biggs J, Corneli PS, Seger J, Yandell M, and Olivera BM (2016). Venom insulins of cone snails diversify rapidly and track prey taxa. *Molecular Biology and Evolution*, 33(11):2924–2934. URL <http://dx.doi.org/10.1093/molbev/msw174>

- 9.7. Li G, Davis BW, Eizirik E, and Murphy WJ (2015). Phylogenomic evidence for ancient hybridization in the genomes of living cats (Felidae). *Genome Research*, 26(1):1–11. URL <http://dx.doi.org/10.1101/gr.186668.114>
- 9.8. Suarez-Gonzalez A, Hefer CA, Christe C, Corea O, Lexer C, Cronk QCB, and Douglas CJ (2016). Genomic and functional approaches reveal a case of adaptive introgression from *Populus balsamifera* (balsam poplar) in *P. trichocarpa* (black cottonwood). *Molecular Ecology*, 25(11):2427–2442. URL <http://dx.doi.org/10.1111/mec.13539>
- 9.9. Kursel LE and Malik HS (2017). Recurrent gene duplication leads to diverse repertoires of centromeric histones in *Drosophila* species. *Molecular Biology and Evolution*, 34(6):1445–1462. URL <http://dx.doi.org/10.1093/molbev/msx091>
- 9.10. Chuong EB, Elde NC, and Feschotte C (2016). Regulatory evolution of innate immunity through co-option of endogenous retroviruses. *Science*, 351(6277):1083–1087. URL <http://dx.doi.org/10.1126/science.aad5497>