References

[1] Darwin, C. *On the Origin of Species* (Oxford University Press, 1859). ISBN 978-0-19-921922-3.

[2] Huxley, J., Pigliucci, M., Müller, G. B. *Evolution: The Modern Synthesis*. The Definitive Edition (MIT Press, 2010).

[3] Griffiths, A. J. F., Wessler, S. R., Carroll, S. B., *et al. Introduction to Genetic Analysis* (Macmillan Higher Education, 2010).

[4] Miko, I. Gregor Mendel and the principles of inheritance. *Nature Education Knowledge*, 1(1), 2008.

[5] Polderman, T. J. C., Benyamin, B., de Leeuw, C. A., *et al.* Meta-analysis of the heritability of human traits based on fifty years of twin studies. *Nature genetics*, 47(7):pp. 702–709, July 2015.

[6] Kimball, J. W. Germline vs. Soma. `http://biology-pages.info`. Accessed 20th August 2015.

[7] O'Connor, C., Miko, I. Developing the chromosome theory. *Nature Education*, 1(1), 2008.

[8] Avery, O. T., Macleod, C. M., McCarty, M. Studies on the chemical nature of the substance inducing transformation of pneumococcal types : induction of transformation by a desoxyribonucleic acid fraction isolated from pneumococcus type III. *The Journal of experimental medicine*, 79(2):pp. 137–158, February 1944.

[9] Hershey, A. D., Chase, M. Independent functions of viral protein and nucleic acid in growth of bacteriophage. *The Journal of general physiology*, 36(1):pp. 39–56, May 1952.

[10] Sabour, D., Schöler, H. R. Reprogramming and the mammalian germline: the Weismann barrier revisited. *Current opinion in cell biology*, 24(6):pp. 716–723, December 2012.

[11] Buckley, B. A., Burkhart, K. B., Gu, S. G., *et al.* A nuclear Argonaute promotes multigenerational epigenetic inheritance and germline immortality. *Nature*, 489(7416):pp. 447–451, September 2012.

[12] Heard, E., Martienssen, R. A. Transgenerational epigenetic inheritance: myths and mechanisms. *Cell*, 157(1):pp. 95–109, March 2014.

[13] Devanapally, S., Ravikumar, S., Jose, A. M. Double-stranded RNA made in C. elegans neurons can enter the germline and cause transgenerational gene silencing. *Proceedings of the National Academy of Sciences of the United States of America*, 112(7):pp. 2133–2138, February 2015.

[14] Scally, A., Durbin, R. Revising the human mutation rate: implications for understanding human evolution. *Nature reviews. Genetics*, 2012.

[15] Ségurel, L., Wyman, M. J., Przeworski, M. Determinants of mutation rate variation in the human germline. *Annual review of genomics and human genetics*, 15:pp. 47–70, 2014.

[16] Gregory, R. T. Animal Genome Size Database. , 2015.

[17] Flicek, P., Amode, M. R., Barrell, D., *et al.* Ensembl 2014. *Nucleic acids research*, 42(D1):pp. D749–D755, December 2013.

[18] Gregory, T. R. Synergy between sequence and size in large-scale genomics. *Nature reviews. Genetics*, 6(9):pp. 699–708, September 2005.

[19] Lander, E. S. Initial impact of the sequencing of the human genome. *Nature*, 470(7333):pp. 187–197, February 2011.

[20] Mikkelsen, T. S., Wakefield, M. J., Aken, B., *et al.* Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. *Nature*, 447(7141):pp. 167–177, May 2007.

[21] Berezikov, E. Evolution of microRNA diversity and regulation in animals. *Nature reviews. Genetics*, 12(12):pp. 846–860, December 2011.

[22] Sayed, D., Abdellatif, M. MicroRNAs in Development and Disease. *Physiological Reviews*, 91(3):pp. 827–887, January 2011.

[23] Weick, E.-M., Miska, E. A. piRNAs: from biogenesis to function. *Development (Cambridge, England)*, 141(18):pp. 3458–3471, September 2014.

[24] ENCODE Project Consortium, Bernstein, B. E., Birney, E., *et al.* An integrated encyclopedia of DNA elements in the human genome. *Nature*, 489(7414):pp. 57–74, September 2012.

[25] Graur, D., Zheng, Y., Price, N., *et al.* On the immortality of television sets: "function" in the human genome according to the evolution-free gospel of ENCODE. *Genome biology and evolution*, 5(3):pp. 578–590, 2013.

[26] Siepel, A., Bejerano, G., Pedersen, J. S., *et al.* Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. *Genome research*, 15(8):pp. 1034–1050, August 2005.

[27] Zuckerkandl, E., Pauling, L. Evolutionary divergence and convergence in proteins. *Evolving genes and proteins*, 1965.

[28] The Nobel Prize in Physiology or Medicine 1968. `http://www.nobelprize.org/nobel_prizes/medicine/laureates/1968/index.html`, 2014. Accessed 18th August 2015.

[29] Kimura, M. Preponderance of synonymous changes as evidence for the neutral theory of molecular evolution. *Nature*, 267(5608):pp. 275–276, May 1977.

[30] Hedrick, P. W. *Genetics of Populations* (Jones & Bartlett Publishers, 2011).

[31] Wakeley, J. *Coalescent Theory.* An Introduction (Roberts Publishers, 2009).

[32] Maynard Smith, J., Haigh, J. The hitch-hiking effect of a favourable gene. *Genetical research*, 23(1):pp. 23–35, February 1974.

[33] Charlesworth, B., Morgan, M. T., Charlesworth, D. The effect of deleterious mutations on neutral molecular variation. *Genetics*, 134(4):pp. 1289–1303, July 1993.

[34] Stephan, W. Genetic hitchhiking versus background selection: the controversy and its implications. *Philosophical Transactions of the Royal Society of London B: Biological Sciences*, 365(1544):pp. 1245–1253, April 2010.

[35] Coyne, J. A., Orr, H. A. *Speciation* (SINAUER ASSOCIATES, 2004). ISBN 978-0-87893-089-0.

[36] Mayr, E. What is a species, and what is not? *Philosophy of Science*, 1996.

[37] Safran, R. J., Nosil, P. Speciation: The Origin of New Species. *Nature Education Knowledge*, 3(10), 2012.

[38] Nosil, P. *Ecological Speciation* (OUP Oxford, 2012).

[39] Darwin, C. *On the Origin of Species* (OUP Oxford, 2008).

[40] Fitzpatrick, B. M., Fordyce, J. A., Gavrilets, S. What, if anything, is sympatric speciation? *Journal of evolutionary biology*, 21(6):pp. 1452–1459, November 2008.

[41] Mayr, E. *Animal Species and Evolution* (Belknap Press, 1963).

[42] Adams, J. DNA sequencing technologies. *Nature Education*, 2008.

[43] Metzker, M. L. Sequencing technologies - the next generation. *Nature reviews. Genetics*, 11(1):pp. 31–46, January 2010.

[44] Sanger, F., Air, G. M., Barrell, B. G., *et al.* Nucleotide sequence of bacteriophage phi X174 DNA. *Nature*, 265(5596):pp. 687–695, February 1977.

[45] Sanger, F., Nicklen, S., Coulson, A. R. DNA sequencing with chain-terminating inhibitors. *Proceedings of the National Academy of Sciences of the United States of America*, 74(12):pp. 5463–5467, December 1977.

[46] ENA. Statistics. `http://www.ebi.ac.uk/ena/about/statistics`, 2015. European Nucleotide Archive, Accessed 15th August 2015.

[47] Wetterstrand, K. A. DNA Sequencing Costs: Data from the NHGRI Genome Sequencing Program (GSP). `http://www.genome.gov/sequencingcosts`. Accessed 15th August 2015.

[48] Baker, M. De novo genome assembly: what every biologist should know. *Nature methods*, 9(4):pp. 333–337, January 2012.

[49] Nielsen, R., Paul, J. S., Albrechtsen, A., *et al.* Genotype and SNP calling from next-generation sequencing data. *Nature reviews. Genetics*, 12(6):pp. 443–451, June 2011.

[50] Ingram, V. M. Gene mutations in human haemoglobin: the chemical difference between normal and sickle cell haemoglobin. *Nature*, 180(4581):pp. 326–328, August 1957.

[51] McDonald, J. H., Kreitman, M. Adaptive protein evolution at the Adh locus in Drosophila. *Nature*, 351(6328):pp. 652–654, June 1991.

[52] Atrian, S., Sánchez-Pulido, L., Gonzàlez-Duarte, R., *et al.* Shaping of Drosophila alcohol dehydrogenase through evolution: relationship with enzyme functionality. *Journal of molecular evolution*, 47(2):pp. 211–221, August 1998.

[53] Smith, N. G. C., Eyre-Walker, A. Adaptive protein evolution in Drosophila. *Nature*, 415(6875):pp. 1022–1024, February 2002.

[54] Mouse Genome Sequencing Consortium, Waterston, R. H., Lindblad-Toh, K., *et al.* Initial sequencing and comparative analysis of the mouse genome. *Nature*, 420(6915):pp. 520–562, December 2002.

[55] Del Punta, K., Leinders-Zufall, T., Rodriguez, I., *et al.* Deficient pheromone responses in mice lacking a cluster of vomeronasal receptor genes. *Nature*, 419(6902):pp. 70–74, September 2002.

[56] Chimpanzee Sequencing and Analysis Consortium. Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature*, 437(7055):pp. 69–87, September 2005.

[57] Pollard, K. S., Salama, S. R., Lambert, N., *et al.* An RNA gene expressed during cortical development evolved rapidly in humans. *Nature*, 443(7108):pp. 167–172, September 2006.

[58] Vitti, J. J., Grossman, S. R., Sabeti, P. C. Detecting Natural Selection in Genomic Data. *Annual review of genetics*, 47:pp. 97–120, August 2013.

[59] Fay, J. C., Wu, C. I. Hitchhiking under positive Darwinian selection. *Genetics*, 155(3):pp. 1405–1413, July 2000.

[60] Tajima, F. Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics*, 123(3):pp. 585–595, November 1989.

[61] Balding, D. J., Bishop, M., Cannings, C. *Handbook of statistical genetics* (John Wiley and Sons, 2007). ISBN 978-0-470-05830-5.

[62] Seehausen, O., Butlin, R. K., Keller, I., *et al.* Genomics and the origin of species. *Nature reviews. Genetics*, 15(3):pp. 176–192, February 2014.

[63] Saether, S. A., Saetre, G.-P., Borge, T., *et al.* Sex chromosome-linked species recognition and evolution of reproductive isolation in flycatchers. *Science (New York, N.Y.)*, 318(5847):pp. 95–97, October 2007.

[64] Kitano, J., Ross, J. A., Mori, S., *et al.* A role for a neo-sex chromosome in stickleback speciation. *Nature*, 461(7267):pp. 1079–1083, October 2009.

[65] Felsenstein, J. Skepticism Towards Santa Rosalia, or Why are There so Few Kinds of Animals? *Evolution; international journal of organic evolution*, 35(1):p. 124, January 1981.

[66] Cruickshank, T. E., Hahn, M. W. Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow. *Molecular Ecology*, 23(13):pp. 3133–3157, June 2014.

[67] Turner, T. L., Hahn, M. W., Nuzhdin, S. V. Genomic islands of speciation in Anopheles gambiae. *PLoS biology*, 3(9):p. e285, September 2005.

[68] Savolainen, V., Anstett, M.-C., Lexer, C., *et al.* Sympatric speciation in palms on an oceanic island. *Nature*, 441(7090):pp. 210–213, May 2006.

[69] Nadeau, N. J., Whibley, A., Jones, R. T., *et al.* Genomic islands of divergence in hybridizing Heliconius butterflies identified by large-scale targeted sequencing. *Philosophical Transactions of the Royal Society of London B: Biological Sciences*, 367(1587):pp. 343–353, February 2012.

[70] Ellegren, H., Smeds, L., Burri, R., *et al.* The genomic landscape of species divergence in Ficedula flycatchers. *Nature*, 491(7426):pp. 756–760, November 2012.

[71] Feder, J. L., Egan, S. P., Nosil, P. The genomics of speciation-with-gene-flow. *Trends in Genetics*, 28(7):pp. 342–350, July 2012.

[72] Via, S. Divergence hitchhiking and the spread of genomic isolation during ecological speciation-with-gene-flow. *Philosophical Transactions of the Royal Society of London B: Biological Sciences*, 367(1587):pp. 451–460, February 2012.

[73] Noor, M., Bennett, S. M. Islands of speciation or mirages in the desert? Examining the role of restricted recombination in maintaining species. *Heredity*, 2009.

[74] Turner, T. L., Hahn, M. W. Genomic islands of speciation or genomic islands and speciation? *Molecular Ecology*, 19(5):pp. 848–850, March 2010.

[75] Charlesworth, B. Measures of divergence between populations and the effect of forces that reduce variability. *Molecular biology and evolution*, 15(5):pp. 538–543, April 1998.

[76] Pennisi, E. Disputed islands. *Science (New York, N.Y.)*, 345(6197):pp. 611–613, August 2014.

[77] Poelstra, J. W., Vijay, N., Bossu, C. M., *et al.* The genomic landscape underlying phenotypic integrity in the face of gene flow in crows. *Science (New York, N.Y.)*, 344(6190):pp. 1410–1414, June 2014.

[78] Barlow, G. W. *The Cichlid Fishes.* Nature's Grand Experiment in Evolution (Basic Books, 2002).

[79] Zardoya, R., Vollmer, D. M., Craddock, C., *et al.* Evolutionary conservation of microsatellite flanking regions and their use in resolving the phylogeny of cichlid fishes (Pisces: Perciformes). *Proceedings. Biological sciences / The Royal Society*, 263(1376):pp. 1589–1598, November 1996.

[80] Streelman, J. T., Karl, S. A. Reconstructing labroid evolution with single-copy nuclear DNA. *Proceedings. Biological sciences / The Royal Society*, 264(1384):pp. 1011–1020, July 1997.

[81] Meyer, A. Phylogenetic relationships and evolutionary processes in East African cichlid fishes. *Trends in ecology & evolution*, 8(8):pp. 279–284, August 1993.

[82] Wagner, C. E., Harmon, L. J., Seehausen, O. Ecological opportunity and sexual selection together predict adaptive radiation. *Nature*, 487(7407):pp. 366–369, July 2012.

[83] Kocher, T. D. Adaptive evolution and explosive speciation: the cichlid fish model. *Nature reviews. Genetics*, 5(4):pp. 288–298, April 2004.

[84] Salzburger, W., Meyer, A., Baric, S., *et al.* Phylogeny of the Lake Tanganyika cichlid species flock and its relationship to the Central and East African haplochromine cichlid fish faunas. *Systematic biology*, 51(1):pp. 113–135, February 2002.

[85] Salzburger, W., Mack, T., Verheyen, E., *et al.* Out of Tanganyika: genesis, explosive speciation, key-innovations and phylogeography of the haplochromine cichlid fishes. *BMC evolutionary biology*, 5:p. 17, 2005.

[86] Joyce, D. A., Lunt, D. H., Genner, M. J., *et al.* Repeated colonization and hybridization in Lake Malawi cichlids. *Current biology : CB*, 21(3):pp. R108–9, February 2011.

[87] Snoeks, J., Konings, A. *The cichlid diversity of Lake Malawi/Nyasa/Niassa* (Cichlid Press, 2004).

[88] Elmer, K. R., Reggio, C., Wirth, T., *et al.* Pleistocene desiccation in East Africa bottlenecked but did not extirpate the adaptive radiation of Lake Victoria haplochromine cichlid fishes. *Proceedings of the National Academy of Sciences of the United States of America*, 106(32):pp. 13404–13409, August 2009.

[89] Seehausen, O., Terai, Y., Magalhaes, I. S., *et al.* Speciation through sensory drive in cichlid fish. *Nature*, 455(7213):pp. 620–626, October 2008.

[90] Kocher, T. D., Conroy, J. A., McKaye, K. R., *et al.* Similar morphologies of cichlid fish in Lakes Tanganyika and Malawi are due to convergence. *Molecular phylogenetics and evolution*, 2(2):pp. 158–165, June 1993.

[91] Muschick, M., Indermaur, A., Salzburger, W. Convergent evolution within an adaptive radiation of cichlid fishes. *Current biology : CB*, 22(24):pp. 2362–2368, December 2012.

[92] Laland, K., Uller, T., Feldman, M., *et al.* Does evolutionary theory need a rethink? *Nature*, 514(7521):pp. 161–164, October 2014.

[93] Brawand, D., Wagner, C. E., Li, Y. I., *et al.* The genomic substrate for adaptive radiation in African cichlid fish. *Nature*, 513(7518):pp. 375–381, September 2014.

[94] Carthew, R. W., Sontheimer, E. J. Origins and Mechanisms of miRNAs and siRNAs. *Cell*, 136(4):pp. 642–655, February 2009.

[95] Krol, J., Loedige, I., Filipowicz, W. The widespread regulation of microRNA biogenesis, function and decay. *Nature reviews. Genetics*, 11(9):pp. 597–610, September 2010.

[96] Bartel, D. P. MicroRNAs: target recognition and regulatory functions. *Cell*, 136(2):pp. 215–233, January 2009.

[97] Gunter, C., Dhand, R. The chimpanzee genome. *Nature*, 437:p. 47, 2005.

[98] Carroll, S. B. Evo-devo and an expanding evolutionary synthesis: a genetic theory of morphological evolution. *Cell*, 134(1):pp. 25–36, July 2008.

[99] Lee, R. C., Feinbaum, R. L., Ambros, V. The C. elegans heterochronic gene lin-4 encodes small RNAs with antisense complementarity to lin-14. *Cell*, 75(5):pp. 843–854, December 1993.

[100] Reinhart, B. J., Slack, F. J., Basson, M., *et al.* The 21-nucleotide let-7 RNA regulates developmental timing in Caenorhabditis elegans. *Nature*, 403(6772):pp. 901–906, February 2000.

[101] Lund, A. H. miR-10 in development and cancer. *Cell Death & Differentiation*, 17(2):pp. 209–214, May 2009.

[102] Bissels, U., Bosio, A., Wagner, W. MicroRNAs are shaping the hematopoietic landscape. *Haematologica*, 97(2):pp. 160–167, February 2012.

[103] Stark, A., Brennecke, J., Bushati, N., *et al.* Animal MicroRNAs confer robustness to gene expression and have a significant impact on 3? UTR evolution. *Cell*, 2005.

[104] Li, Y., Wang, F., Lee, J.-A., *et al.* MicroRNA-9a ensures the precise specification of sensory organ precursors in Drosophila. *Genes & development*, 20(20):pp. 2793–2805, October 2006.

[105] Li, X., Cassidy, J. J., Reinke, C. A., *et al.* A microRNA imparts robustness against environmental fluctuation during development. *Audio and Electroacoustics Newsletter, IEEE*, 137(2):pp. 273–282, April 2009.

[106] Christodoulou, F., Raible, F., Tomer, R., *et al.* Ancient animal microRNAs and the evolution of tissue identity. *Nature*, 463(7284):pp. 1084–1088, February 2010.

[107] Fujimura, K., Okada, N. Development of the embryo, larva and early juvenile of Nile tilapia Oreochromis niloticus (Pisces: Cichlidae). Developmental staging system. *Development, growth & differentiation*, 49(4):pp. 301–324, May 2007.

[108] Martin, M. Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet journal*, 2011.

[109] Friedländer, M. R., Mackowiak, S. D., Li, N., *et al.* miRDeep2 accurately identifies known and hundreds of novel microRNA genes in seven animal clades. *Nucleic acids research*, 40(1):pp. 37–52, January 2012.

[110] Langmead, B., Trapnell, C., Pop, M., *et al.* Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome biology*, 10(3):p. R25, 2009.

[111] Lorenz, R., Bernhart, S. H., Höner Zu Siederdissen, C., *et al.* ViennaRNA Package 2.0. *Algorithms for molecular biology : AMB*, 6:p. 26, 2011.

[112] Griffiths-Jones, S., Grocock, R. J., van Dongen, S., *et al.* miRBase: microRNA sequences, targets and gene nomenclature. *Nucleic acids research*, 34(Database issue):pp. D140–4, January 2006.

[113] Ro, S., Park, C., Young, D., *et al.* Tissue-dependent paired expression of miRNAs. *Nucleic acids research*, 35(17):pp. 5944–5953, 2007.

[114] Lu, J., Shen, Y., Wu, Q., *et al.* The birth and death of microRNA genes in Drosophila. *Nature genetics*, 40(3):pp. 351–355, February 2008.

[115] Rehmsmeier, M., Steffen, P., Hochsmann, M., *et al.* Fast and effective prediction of microRNA/target duplexes. *RNA (New York, N.Y.)*, 10(10):pp. 1507–1517, October 2004.

[116] Kapsimali, M., Kloosterman, W. P., de Bruijn, E., *et al.* MicroRNAs show a wide diversity of expression profiles in the developing and mature central nervous system. *Genome biology*, 8(8):p. R173, 2007.

[117] Marín, R. M., Vanícek, J. Efficient use of accessibility in microRNA target prediction. *Nucleic acids research*, 39(1):pp. 19–29, January 2011.

[118] Ko, C.-Y., Tsai, M.-Y., Tseng, W.-F., *et al.* Integration of CNS survival and differentiation by HIF2α. *Cell Death & Differentiation*, 18(11):pp. 1757–1770, November 2011.

[119] Long, J. M., Lahiri, D. K. Advances in microRNA experimental approaches to study physiological regulation of gene products implicated in CNS disorders. *Experimental neurology*, 235(2):pp. 402–418, June 2012.

[120] Loh, Y. H. E., Yi, S. V., Streelman, J. T. Evolution of MicroRNAs and the Diversification of Species. *Genome Biology and Evolution*, 3(0):pp. 55–65, January 2011.

[121] Kocher, T. D., Streelman, T., Seehausen, O., *et al.* Genetic Basis of Vertebrate Diversity: the Cichlid Fish Model. Technical report, March 2006. http://www.genome.gov/pages/research/sequencing/seqproposals/cichlidgenomeseq.pdf.

[122] Saunders, M. A., Liang, H., Li, W. H. Human polymorphism at microRNAs and microRNA target sites. *Proceedings of the National Academy of Sciences of the United States of America*, 2007.

[123] Marín, R. M., Voellmy, F., von Erlach, T., *et al.* Analysis of the accessibility of CLIP bound sites reveals that nucleation of the miRNA: mRNA pairing occurs preferentially at the 3?-end of the seed match. *RNA (New York, N.Y.)*, 2012.

[124] Ribbink, A. J., Marsh, B. A., Marsh, A. C., *et al.* A preliminary survey of the cichlid fishes of rocky habitats in Lake Malawi. *S. Afr. J. Zool.*, 18:pp. 149–310, August 1983.

[125] Konings, A. *Malaŵi Cichlids in Their Natural Habitat* (Cichlid Press, 2007).

[126] Trewavas, E. Nouvel examen des genres et sous-genres du complexe Pseudotropheus-Melanochromis du lac Malawi (Pisces, Perciformes, Cichlidae). *Revue française d'Aquariologie*, 10(4):pp. 97–106, 1983.

[127] Stauffer, J. R., Jr, Bowers, N. J., Kellogg, K. A. A revision of the blue-black Pseudotropheus zebra (Teleostei: Cichlidae) complex from Lake Malaŵi, Africa, with a description of a new genus and ten new species. In *Proceedings of the Academy of Natural Sciences of Philadelphia* (1997).

[128] Genner, M. J., Nichols, P., Carvalho, G. R., *et al.* Reproductive isolation among deep-water cichlid fishes of Lake Malawi differing in monochromatic male breeding dress. *Molecular Ecology*, 16(3):pp. 651–662, February 2007.

[129] Eccles, D. H., Trewavas, E. *Malawian Cichlid Fishes* (1989).

[130] Joyce, D. A., Lunt, D. H., Bills, R., *et al.* An extant cichlid fish radiation emerged in an extinct Pleistocene lake. *Nature*, 435(7038):pp. 90–95, May 2005.

[131] Genner, M. J., Ngatunga, B. P., Mzighani, S., *et al.* Geographical ancestry of Lake Malawi's cichlid fish diversity: Figure 1. *Biology Letters*, 11(6):p. 20150232, June 2015.

[132] Li, H. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. *arXiv.org*, March 2013.

[133] DePristo, M. A. M., Banks, E. E., Poplin, R. R., *et al.* A framework for variation discovery and genotyping using next-generation DNA sequencing data. *Nature genetics*, 43(5):pp. 491–498, April 2011.

[134] McKenna, A., Hanna, M., Banks, E., *et al.* The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. *Genome research*, 20(9):pp. 1297–1303, August 2010.

[135] Li, H. A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data. *Bioinformatics (Oxford, England)*, 27(21):pp. 2987–2993, November 2011.

[136] Browning, S. R., Browning, B. L. Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering. *American journal of human genetics*, 81(5):pp. 1084–1097, November 2007.

[137] Jun, G., Flickinger, M., Hetrick, K. N., *et al.* Detecting and estimating contamination of human DNA samples in sequencing and array-based genotype data. *American journal of human genetics*, 91(5):pp. 839–848, November 2012.

[138] Miller, W., Rosenbloom, K., Hardison, R. C., *et al.* 28-way vertebrate alignment and conservation track in the UCSC Genome Browser. *Genome research*, 17(12):pp. 1797–1808, December 2007.

[139] Harris, R. S. *Improved pairwise alignment of genomic DNA*. Ph.D. thesis, The Pennsylvania State University, 2007.

[140] Blanchette, M., Kent, W. J., Riemer, C., *et al.* Aligning multiple genomic sequences with the threaded blockset aligner. *Genome research*, 14(4):pp. 708–715, April 2004.

[141] Thorvaldsdóttir, H., Robinson, J. T., Mesirov, J. P. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. *Briefings in bioinformatics*, 14(2):pp. 178–192, March 2013.

[142] Birney, E., Bateman, A., Clamp, M. E., *et al.* Mining the draft human genome. *Nature*, 409(6822):pp. 827–828, February 2001.

[143] Rosenbloom, K. R., Armstrong, J., Barber, G. P., *et al.* The UCSC Genome Browser database: 2015 update. *Nucleic acids research*, 43(Database issue):pp. D670–81, January 2015.

[144] Thorvaldsdóttir, H., Robinson, J. T., Mesirov, J. P. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. *Briefings in bioinformatics*, 14(2):pp. 178–192, March 2013.

[145] Kent, W. J., Sugnet, C. W., Furey, T. S., *et al.* The human genome browser at UCSC. *Genome research*, 12(6):pp. 996–1006, June 2002.

[146] Kent, W. J. BLAT–the BLAST-like alignment tool. *Genome research*, 12(4):pp. 656–664, April 2002.

[147] Pendleton, M., Sebra, R., Pang, A. W. C., *et al.* Assembly and diploid architecture of an individual human genome via single-molecule technologies. *Nature methods*, 12(8):pp. 780–786, August 2015.

[148] Earl, D., Bradnam, K., St John, J., *et al.* Assemblathon 1: a competitive assessment of de novo short read assembly methods. *Genome research*, 21(12):pp. 2224–2241, December 2011.

[149] Simpson, J. T., Durbin, R. Efficient de novo assembly of large genomes using compressed data structures. *Genome research*, 22(3):pp. 549–556, March 2012.

[150] Simpson, J. T., Durbin, R. Efficient construction of an assembly string graph using the FM-index. *Bioinformatics (Oxford, England)*, 26(12):pp. i367–73, June 2010.

[151] Ferragina, P., Manzini, G. Opportunistic data structures with applications. *Foundations of Computer Science*, 2000.

[152] C. elegans Sequencing Consortium. Genome sequence of the nematode C. elegans: a platform for investigating biology. *Science (New York, N.Y.)*, 282(5396):pp. 2012–2018, December 1998.

[153] Adams, M. D., Celniker, S. E., Holt, R. A., *et al.* The genome sequence of Drosophila melanogaster. *Science (New York, N.Y.)*, 287(5461):pp. 2185–2195, March 2000.

[154] Potato Genome Sequencing Consortium, Xu, X., Pan, S., *et al.* Genome sequence and analysis of the tuber crop potato. *Nature*, 475(7355):pp. 189–195, July 2011.

[155] Charlesworth, D., Willis, J. H. The genetics of inbreeding depression. *Nature reviews. Genetics*, 10(11):pp. 783–796, November 2009.

[156] Zhang, G., Fang, X., Guo, X., *et al.* The oyster genome reveals stress adaptation and complexity of shell formation. *Nature*, 490(7418):pp. 49–54, October 2012.

[157] Vinson, J. P. J., Jaffe, D. B. D., O'Neill, K. K., *et al.* Assembly of polymorphic genomes: algorithms and application to Ciona savignyi. *Genes & development*, 15(8):pp. 1127–1135, July 2005.

[158] Donmez, N., Brudno, M. Hapsembler: An Assembler for Highly Polymorphic Genomes. In *Research in Computational Molecular Biology*, pp. 38–52 (Springer Berlin Heidelberg, Berlin, Heidelberg, 2011).

[159] Genome 10K Community of Scientists. Genome 10K: a proposal to obtain whole-genome sequence for 10,000 vertebrate species. *The Journal of heredity*, 100(6):pp. 659–674, November 2009.

[160] i5K Consortium. The i5K Initiative: advancing arthropod genomics for knowledge, human health, agriculture, and the environment. *The Journal of heredity*, 104(5):pp. 595–600, September 2013.

[161] GIGA Community of Scientists, Bracken-Grissom, H., Collins, A. G., *et al.* The Global Invertebrate Genomics Alliance (GIGA): developing community resources to study diverse invertebrate genomes. *The Journal of heredity*, 105(1):pp. 1–18, January 2014.

[162] Li, R. R., Zhu, H. H., Ruan, J. J., *et al.* De novo assembly of human genomes with massively parallel short read sequencing. *Genes & development*, 20(2):pp. 265–272, February 2010.

[163] Heliconius Genome Consortium. Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature*, 487(7405):pp. 94–98, July 2012.

[164] Charlesworth, B. Fundamental concepts in genetics: Effective population size and patterns of molecular evolution and variation. *Nature reviews. Genetics*, 10(3):pp. 195–205, March 2009.

[165] Keightley, P. D., Pinharanda, A., Ness, R. W., *et al.* Estimation of the spontaneous mutation rate in Heliconius melpomene. *Molecular biology and evolution*, 32(1):pp. 239–243, January 2015.

[166] Simpson, J. T. Exploring genome characteristics and sequence quality without a reference. *Bioinformatics (Oxford, England)*, 30(9):pp. 1228–1235, May 2014.

[167] Jiggins, C. D., Mavarez, J., Beltrán, M., *et al.* A genetic linkage map of the mimetic butterfly Heliconius melpomene. *Genetics*, 171(2):pp. 557–570, October 2005.

[168] Hardin, G. The competitive exclusion principle. *Science (New York, N.Y.)*, 131(3409):pp. 1292–1297, April 1960.

[169] Zaret, T. M., Rand, A. S. Competition in tropical stream fishes: support for the competitive exclusion principle. *Ecology*, 1971.

[170] Turner, G. F., Burrows, M. T. A Model of Sympatric Speciation by Sexual Selection. *Proceedings of the Royal Society B: Biological Sciences*, 260(1359):pp. 287–292, June 1995.

[171] Weissing, F. J., Edelaar, P., van Doorn, G. S. Adaptive speciation theory: a conceptual review. *Behavioral ecology and sociobiology*, 65(3):pp. 461–480, March 2011.

[172] M'Gonigle, L. K., Mazzucco, R., Otto, S. P., *et al.* Sexual selection enables long-term coexistence despite ecological equivalence. *Nature*, 484(7395):pp. 506–509, April 2012.

[173] Wang, J. Estimation of effective population sizes from data on genetic markers. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 360(1459):pp. 1395–1409, July 2005.

[174] Whiteley, A. R., Bhat, A., Martins, E. P., *et al.* Population genomics of wild and laboratory zebrafish (Danio rerio). *Molecular Ecology*, 20(20):pp. 4259–4276, October 2011.

[175] R Core Team. *R: A Language and Environment for Statistical Computing.* R Foundation for Statistical Computing, Vienna, Austria, 2015. `http://www.R-project.org/`.

[176] Genner, M. J., Turner, G. F. Ancient hybridization and phenotypic novelty within Lake Malawi's cichlid fish radiation. *Molecular biology and evolution*, 29(1):pp. 195–206, January 2012.

[177] Vos, P., Hogers, R., Bleeker, M., *et al.* AFLP: a new technique for DNA fingerprinting. *Nucleic acids research*, 23(21):pp. 4407–4414, November 1995.

[178] Albertson, R. C., Markert, J. A., Danley, P. D., *et al.* Phylogeny of a rapidly evolving clade: the cichlid fishes of Lake Malawi, East Africa. *Proceedings of the National Academy of Sciences of the United States of America*, 96(9):pp. 5107–5110, April 1999.

[179] Allender, C. J., Seehausen, O., Knight, M. E., *et al.* Divergent selection during speciation of Lake Malawi cichlid fishes inferred from parallel radiations in nuptial coloration. *Proceedings of the National Academy of Sciences of the United States of America*, 100(24):pp. 14074–14079, November 2003.

[180] Bouckaert, R., Heled, J. DensiTree 2: Seeing Trees Through the Forest. *bioRxiv*, 2014.

[181] Saitou, N., Nei, M. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular biology and evolution*, 4(4):pp. 406–425, July 1987.

[182] Robinson, D. F., Foulds, L. R. Comparison of phylogenetic trees. *Mathematical Biosciences*, 1981.

[183] Schliep, K. P. phangorn: phylogenetic analysis in R. *Bioinformatics (Oxford, England)*, 27(4):pp. 592–593, February 2011.

[184] Ballard, J. W. O., Whitlock, M. C. The incomplete natural history of mitochondria. *Molecular Ecology*, 13(4):pp. 729–744, April 2004.

[185] Wilson, C. C., Bernatchez, L. The ghost of hybrids past: fixation of arctic charr (Salvelinus alpinus) mitochondrial DNA in an introgressed population of lake trout (S. namaycush). *Molecular Ecology*, 1998.

[186] Zieliński, P., Nadachowska-Brzyska, K., Wielstra, B., *et al.* No evidence for nuclear introgression despite complete mtDNA replacement in the Carpathian newt (Lissotriton montandoni). *Molecular Ecology*, 22(7):pp. 1884–1903, April 2013.

[187] Pons, J.-M., Sonsthagen, S., Dove, C., *et al.* Extensive mitochondrial introgression in North American Great Black-backed Gulls (Larus marinus) from the American Herring Gull (Larus smithsonianus) with little nuclear DNA impact. *Heredity*, 112(3):pp. 226–239, March 2014.

[188] Good, J. M., Vanderpool, D., Keeble, S., *et al.* Negligible nuclear introgression despite complete mitochondrial capture between two species of chipmunks. *Evolution; international journal of organic evolution*, 69(8):pp. 1961–1972, August 2015.

[189] Bachtrog, D., Thornton, K., Clark, A., *et al.* Extensive introgression of mitochondrial DNA relative to nuclear genes in the Drosophila yakuba species group. *Evolution; international journal of organic evolution*, 60(2):pp. 292–302, February 2006.

[190] Green, R. E., Krause, J., Briggs, A. W., *et al.* A draft sequence of the Neandertal genome. *Science (New York, N.Y.)*, 328(5979):pp. 710–722, May 2010.

[191] Durand, E. Y., Patterson, N., Reich, D., *et al.* Testing for ancient admixture between closely related populations. *Molecular biology and evolution*, 28(8):pp. 2239–2252, August 2011.

[192] Martin, S. H., Davey, J. W., Jiggins, C. D. Evaluating the use of ABBA-BABA statistics to locate introgressed loci. *Molecular biology and evolution*, 32(1):pp. 244–257, January 2015.

[193] Lawson, D. J., Hellenthal, G., Myers, S., *et al.* Inference of population structure using dense haplotype data. *PLoS genetics*, 2012.

[194] Purcell, S., Neale, B., Todd-Brown, K., *et al.* PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses. *The American Journal of Human Genetics*, 81(3):pp. 559–575, September 2007.

[195] Patterson, N., Price, A. L., Reich, D. Population structure and eigenanalysis. *PLoS genetics*, 2(12):pp. e190–e190, December 2006.

[196] Ligges, U., Mächler, M. Scatterplot3d - an R Package for Visualizing Multivariate Data. *Journal of Statistical Software*, 8(11):pp. 1–20, 2003. `http://www.jstatsoft.org`.

[197] Bhatia, G., Patterson, N., Sankararaman, S., *et al.* Estimating and interpreting FST: The impact of rare variants. *Genome research*, 23(9):pp. 1514–1521, September 2013.

[198] Stamatakis, A. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics (Oxford, England)*, 22(21):pp. 2688–2690, November 2006.

[199] Stamatakis, A., Hoover, P., Rougemont, J. A rapid bootstrap algorithm for the RAxML Web servers. *Systematic biology*, 57(5):pp. 758–771, October 2008.

[200] Malinsky, M., Challis, R. J., Tyers, A. M., *et al.* Genomic islands of speciation separate cichlid ecomorphs in an East African crater lake. *Science (New York, N.Y.)*, 350(6267):pp. 1493–1498, December 2015.

[201] Ricardo, C. K. The fishes of Lake Rukwa. *Journal of the Linnean Society of London*, 1939.

[202] Delalande, M. Hydrologie et géochimie isotopique du lac Masoko et de lacs volcaniques de la province active du Rungwe (Sud-Ouest Tanzanie). *www.theses.fr*, May 2008.

[203] Barker, Williamson, Gasse, *et al.* Climatic and volcanic forcing revealed in a 50,000-year diatom record from Lake Massoko, Tanzania. *Quaternary Research*, 60(3):pp. 9–9, November 2003.

[204] Davey, J. W., Blaxter, M. L. RADSeq: next-generation population genetics. *Briefings in Functional Genomics*, 2010.

[205] Schliewen, U. K., Tautz, D., Pääbo, S. Sympatric speciation suggested by monophyly of crater lake cichlids. *Nature*, 368(6472):pp. 629–632, April 1994.

[206] Barluenga, M., Stölting, K. N., Salzburger, W., *et al.* Sympatric speciation in Nicaraguan crater lake cichlid fish. *Nature*, 439(7077):pp. 719–723, February 2006.

[207] Alexander, D. H., Novembre, J., Lange, K. Fast model-based estimation of ancestry in unrelated individuals. *Genes & development*, 19(9):pp. 1655–1664, August 2009.

[208] Martin, C. H., Cutler, J. S., Friel, J. P., *et al.* Complex histories of repeated gene flow in Cameroon crater lake cichlids cast doubt on one of the clearest examples of sympatric speciation. *Evolution; international journal of organic evolution*, May 2015.

[209] Schiffels, S., Durbin, R. Inferring human population size and separation history from multiple genome sequences. *Nature genetics*, 46(8):pp. 919–925, August 2014.

[210] Tenesa, A., Navarro, P., Hayes, B. J., *et al.* Recent human effective population size estimated from linkage disequilibrium. *Genome research*, 17(4):pp. 520–526, April 2007.

[211] Hudson, R. R. R. Generating samples under a Wright-Fisher neutral model of genetic variation. *Bioinformatics (Oxford, England)*, 18(2):pp. 337–338, February 2002.

[212] Sousa, V., Hey, J. Understanding the origin of species with genome-scale data: modelling gene flow. *Nature reviews. Genetics*, 14(6):pp. 404–414, June 2013.

[213] Beaumont, M. A. Adaptation and speciation: what can F(st) tell us? *Trends in ecology & evolution*, 20(8):pp. 435–440, August 2005.

[214] O Quin, C. T., Drilea, A. C., Conte, M. A., *et al.* Mapping of pigmentation QTL on an anchored genome assembly of the cichlid fish, Metriaclima zebra. *BMC genomics*, 14(1):p. 287, April 2013.

[215] Price, T. D., Bouvier, M. M. The evolution of F1 postzygotic incompatibilities in birds. *Evolution; international journal of organic evolution*, 56(10):pp. 2083–2089, October 2002.

[216] Stelkens, R. B., Young, K. A., Seehausen, O. The accumulation of reproductive incompatibilities in African cichlid fish. *Evolution; international journal of organic evolution*, 64(3):pp. 617–633, March 2010.

[217] Van Der Sluijs, I., Van Dooren, T. J. M., Seehausen, O., *et al.* A test of fitness consequences of hybridization in sibling species of Lake Victoria cichlid fish. *Journal of evolutionary biology*, 21(2):pp. 480–491, March 2008.

[218] Kaneshiro, K. Y. Sexual Isolation, Speciation and the Direction of Evolution. *Evolution; international journal of organic evolution*, 34(3):p. 437, May 1980.

[219] Ashburner, M., Ball, C. A., Blake, J. A., *et al.* Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nature genetics*, 25(1):pp. 25–29, May 2000.

[220] Merico, D., Isserlin, R., Stueker, O., *et al.* Enrichment map: a network-based method for gene-set enrichment visualization and interpretation. *PloS one*, 5(11):p. e13984, 2010.

[221] Sugawara, T., Terai, Y., Imai, H., *et al.* Parallelism of amino acid changes at the RH1 affecting spectral sensitivity among deep-water cichlids from Lakes Tanganyika and Malawi. *Proceedings of the National Academy of Sciences of the United States of America*, 102(15):pp. 5448–5453, April 2005.

[222] Morris, J. H., Apeltsin, L., Newman, A. M., *et al.* clusterMaker: a multi-algorithm clustering plugin for Cytoscape. *BMC bioinformatics*, 12:p. 436, 2011.

[223] Oesper, L., Merico, D., Isserlin, R., *et al.* WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. *Source code for biology and medicine*, 6:p. 7, 2011.

[224] Duester, G. Families of retinoid dehydrogenases regulating vitamin A function: production of visual pigment and retinoic acid. *European journal of biochemistry / FEBS*, 267(14):pp. 4315–4324, July 2000.

[225] Yamashita, T., Liu, J., Gao, J., *et al.* Essential and synergistic roles of RP1 and RP1L1 in rod photoreceptor axoneme and retinitis pigmentosa. *The Journal of neuroscience : the official journal of the Society for Neuroscience*, 29(31):pp. 9748–9760, August 2009.

[226] Jing, X., Malicki, J. Zebrafish ale oko, an essential determinant of sensory neuron survival and the polarity of retinal radial glia, encodes the p50 subunit of dynactin. *Development (Cambridge, England)*, 136(17):pp. 2955–2964, September 2009.

[227] Sayer, J. A., Otto, E. A., O'Toole, J. F., *et al.* The centrosomal protein nephrocystin-6 is mutated in Joubert syndrome and activates transcription factor ATF4. *Nature genetics*, 38(6):pp. 674–681, June 2006.

[228] Esterberg, R., Fritz, A. dlx3b/4b are required for the formation of the preplacodal region and otic placode through local modulation of BMP activity. *Developmental biology*, 325(1):pp. 189–199, January 2009.

[229] Kwon, H.-J., Riley, B. B. Mesendodermal signals required for otic induction: Bmp-antagonists cooperate with Fgf and can facilitate formation of ectopic otic tissue. *Developmental dynamics : an official publication of the American Association of Anatomists*, 238(6):pp. 1582–1594, June 2009.

[230] Fay, R. R., Popper, A. N. Evolution of hearing in vertebrates: the inner ears and processing. *Hearing research*, 149(1-2):pp. 1–10, November 2000.

[231] Popper, A. N., Ramcharitar, J., Campana, S. E. Why otoliths? Insights from inner ear physiology and fisheries biology. *Marine and freshwater Research*, 56(5):p. 497, 2005.

[232] Soria-Carrasco, V., Gompert, Z., Comeault, A. A., *et al.* Stick insect genomes reveal natural selection's role in parallel speciation. *Science (New York, N.Y.)*, 344(6185):pp. 738–742, May 2014.

[233] Arnegard, M. E., McGee, M. D., Matthews, B., *et al.* Genetics of ecological divergence during speciation. *Nature*, 511(7509):pp. 307–311, July 2014.

[234] Andrew, R. L., Rieseberg, L. H. Divergence is focused on few genomic regions early in speciation: incipient speciation of sunflower ecotypes. *Evolution; international journal of organic evolution*, 67(9):pp. 2468–2482, September 2013.

[235] Catchen, J. M., Amores, A., Hohenlohe, P., *et al.* Stacks: building and genotyping Loci de novo from short-read sequences. *G3 (Bethesda, Md.)*, 1(3):pp. 171–182, August 2011.

[236] Keane, T. M., Creevey, C. J., Pentony, M. M., *et al.* Assessment of methods for amino acid matrix selection and their use on empirical data shows that ad hoc assumptions for choice of matrix are not justified. *BMC evolutionary biology*, 6:p. 29, 2006.

[237] Delaneau, O., Marchini, J., Zagury, J.-F. A linear complexity phasing method for thousands of genomes. *Nature methods*, 9(2):pp. 179–181, February 2012.

[238] Delaneau, O., Howie, B., Cox, A. J., *et al.* Haplotype estimation using sequencing reads. *American journal of human genetics*, 93(4):pp. 687–696, October 2013.

[239] Quinlan, A. R., Hall, I. M. BEDTools: a flexible suite of utilities for comparing genomic features. *Bioinformatics (Oxford, England)*, 26(6):pp. 841–842, March 2010.

[240] Wakeley, J. Distinguishing migration from isolation using the variance of pairwise differences. *Theoretical population biology*, 49(3):pp. 369–386, June 1996.

[241] Alexa, A., Rahnenfuhrer, J. *topGO: topGO: Enrichment analysis for Gene Ontology*, 2010. R package version 2.20.0.

[242] Huber, W., Carey, *et al.* Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods*, 12(2):pp. 115–121, 2015. `http://www.nature.com/nmeth/journal/v12/n2/full/nmeth.3252.html`.

[243] Carlson, M. *GO.db: A set of annotation maps describing the entire Gene Ontology*, 2015. R package version 3.1.2.

[244] Carlson, M. *org.Dr.eg.db: Genome wide annotation for Zebrafish*, 2015. R package version 3.1.2.

[245] Turner, G. F., Seehausen, O., Knight, M. E., *et al.* How many species of cichlid fishes are there in African lakes? *Molecular Ecology*, 10(3):pp. 793–806, March 2001.

[246] Taylor, M. I., Meardon, F., Turner, G., *et al.* Characterization of tetranucleotide microsatellite loci in a Lake Victorian, haplochromine cichlid fish: a Pundamilia pundamilia x Pundamilia nyererei hybrid. *Molecular Ecology Notes*, 2(4):pp. 443–445, December 2002.

[247] Gabriel, S., Ziaugra, L., Tabbaa, D. SNP genotyping using the Sequenom MassARRAY iPLEX platform. *Current protocols in human genetics / editorial board, Jonathan L. Haines ... [et al.]*, Chapter 2:p. Unit 2.12, January 2009.

[248] Huber, W., Carey, V. J., Gentleman, R., *et al.* Orchestrating high-throughput genomic analysis with Bioconductor. *Nature methods*, 12(2):pp. 115–121, February 2015.

[249] Zheng, X., Levine, D., Shen, J., *et al.* A high-performance computing toolset for relatedness and principal component analysis of SNP data. *Bioinformatics*, 2012.

[250] Ueyama, H., Kuwayama, S., Imai, H., *et al.* Novel missense mutations in red/green opsin genes in congenital color-vision deficiencies. *Biochemical and biophysical research communications*, 294(2):pp. 205–209, June 2002.

[251] Conte, G. L., Arnegard, M. E., Peichel, C. L., *et al.* The probability of genetic parallelism and convergence in natural populations. *Proceedings of the Royal Society B: Biological Sciences*, 279(1749):pp. 5039–5047, December 2012.

[252] Stern, D. L. The genetic causes of convergent evolution. *Nature reviews. Genetics*, 2013.

[253] Hudson, R. R. Gene genealogies and the coalescent process. *Oxford surveys in evolutionary biology*, 1990.