References

PR05 (2005). Strange bayes indeed: uniform topological prior imply non-uniform clade priors. *Molecular Phylogenetics and Evolution* 34, 203–211.

Ackerly, D. D. (2000, Oct). Taxon sampling, correlated evolution, and independent contrasts. *Evolution* 54(5), 1480–1492.

Aldous 1995 Aldous, D. (1995). Random Discrete Structures. New York: Springer.

Aldous, D. (1996). Probability distributions on cladograms. In D. Aldous and R. Pemantle (Eds.), Random Discrete Structures, Volume 75 of The IMA Volumes in Mathematics and its Applications, pp. 1–18. Springer-Verlag.

Aldous, D. (2001). Stochastic models and descriptive statistics for phylogenetic trees, from Yule to today. Statistical Science 16(1), 23–34.

Allman, E. S., J. H. Degnan, and J. A. Rhodes (2011a). Determining species tree topologies from clade probabilities under the coalescent. *Journal of Theoretical Biology* 289, 96–106.

Allman Allman, E. S., J. H. Degnan, and J. A. Rhodes (2011b). Identifying the rooted species tree from the distribution of unrooted gene trees under the coalescent.

Journal of Mathematical Biology 62, 833–862.

Andrieu2010 Andrieu, C., A. Doucet, and R. Holenstein (2010). Particle Markov chain Monte Carlo methods. Journal of the Royal Statistical Society: Series B (Statistical Methodology) 72(3), 269–342.

Andrieu 2005 Andrieu, C., A. Doucet, and V. Tadic (2005). Online EM for parameter estimation in nonlinear-non Gaussian state-space models. *Proc. IEEE CDC*.

Andrieu C. and G. O. Roberts (2009). The Pseudo-Marginal Approach for Efficient Monte Carlo Computations. The Annals of Statistics 37(2), 697–725.

Arnason, E. (2004). Mitochondrial cytochrome b variation in the high-fecundity Atlantic cod: trans-Atlantic clines and shallow gene genealogy. Genetics 166, 1871–1885.

Arulampalam, M., S. Maskell, N. Gordon, and T. Clapp (2002). A tutorial on particle filters for online nonlinear/non-gaussian bayesian tracking. Signal Processing, IEEE Transactions on 50(2), 174–188.

Backeljau, T., L. D. Bruyn, H. D. W. K. Jordaens, S. V. Dongen, and B. Winnepenninckx (1996). Multiple upgma and neighbor-joining trees and the performance of some computer packages. *Molecular Biology and Evolution* 13(2), 309–313.

- Bafna, V. and V. Bansal (2004, April). The number of recombination events in a sample history: Conflict graph and lower bounds. *IEEE/ACM Trans. Comput. Biol. Bioinformatics* 1(2), 78–90.
- Bagchi 1985 Bagchi, A. and A. K. Pal (1985). Asymptotic normality in the generalized Polya–Eggenberger urn model, with an application to computer data structures.

 SIAM Journal on Algebraic and Discrete Methods 6(3), 394–405.
- Bandelt, H.-J. and A. Dress (1986, September). Reconstructing the shape of a trea from observed dissimilarity data. Advances in Applied Mathematics 7, 309–343.
- Barthélemy, J.-P. and A. Guenoche (1991). Trees and Proximity Representations. London: Wiley.
- Beaumont, M. A., W. Zhang, and D. J. Balding (2002). Approximate bayesian computation in population genetics. *Genetics* 162, 2025–2035.
- Beckenbach, A. (1994). Mitochondrial haplotype frequencies in oysters: neutral alternatives to selection models. In B. Golding (Ed.), *Non-neutral Evolution*, pp. 188–198. New York: Chapman and Hall.
 - Benavoli 2007 Benavoli, A., L. Chisci, and A. Farina (2007). Tracking of a ballistic missile with a-priori information. Aerospace and Electronic Systems, IEEE Transactions on 43(3), 1000–1016.
 - Berti P., I. Crimaldi, L. Pratelli, and P. Rigo (2010). Central limit theorems for multicolor urns with dominated colors. Stochastic Processes and their Applications 120, 1473–1491.
- Blackwell, D. and J. B. MacQueen (1973). Ferguson distribution via Pólya Urn schemes. *The Annals of Statistics* 1(2), 353–355.
- Blum, M. G. B. and O. Francois (2005a). Minimal clade size and external branch length under the neutral coalescent. Advances in Applied Probability 37, 647–662.
- Blum2005index Blum, M. G. B. and O. Francois (2005b). On statistical tests of phylogenetic tree imbalance: The sackin and other indices revisited. *Mathematical Biosciences* 195, 141–153.
 - Blum Blum, M. G. B., O. Francois, and S. Janson (2006). The mean, variance and limiting distribution of two statistics sensitive to phylogenetic tree balance.

 The Annals of Applied Probability 16(4), 2195–2214.
- Bortolussi 2006 Bortolussi, N., E. Durand, M. Blum, and O. Francois (2006). aptreeshape: statistical analysis of phylogenetic tree shape. *Bioinformatics* 22(3), 363–364.

Bortolussi2009

Bortolussi, N., E. Durand, M. Blum, and O. Francois (2009). Analyses of phylogenetic treeshape. http://cran.r-project.org/web/packages/apTreeshape/apTreeshape.pdf, Feb 22, 2013.

Brown1994

Brown, J. K. M. (1994). Probabilities of evolutionary trees. Systematic Biology 43(1), 78–91.

Browning2013

Browning, B. L. and S. R. Browning (2013). Improving the accuracy and efficiency of identity-by-descent detection in population data. *Genetics* 194(2), 459–471.

Browning2007

Browning, S. R. and B. L. Browning (2007). Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering. *The American Journal of Human Genetics* 81(5), 1084 – 1097.

Brumfield2010

Brumfield, R. T. and M. D. Carling (2010). The influence of hybrid zones on species tree inference in manakins. In L. L. Knowles and L. S. Kubatko (Eds.), *Estimating Species Trees, Practical and Theoretical Aspects*, pp. 115–127. Hoboken, NJ: Wiley-Blackwell.

Bruno2000

Bruno, W. J., N. D. Socci, and A. L. Halpern (2000). Weighted neighbor joining: a likelihood-based approach to distance-based phylogeny reconstruction. *Molecular Biology and Evolution* 17, 189–197.

Bryant2004

Bryant, D. (2004). The splits in the neighbourhood of a tree. Annals of Combinatorics 8(1), 1–11.

Bryant2002

Bryant, D. and V. Moulton (2002). Neighbornet: an agglomerative method for the construction of planar phylogenetic networks. *Algorithms in Bioinformatics*, 375–391.

Bryant2009

Bryant, D. and M. A. Steel (2009). Computing the distribution of a tree metric. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 6(3), 420–426.

Buckley2006

Buckley, T. R., M. Cordeiro, D. C. Marshall, and C. Simon (2006). Differentiating between hypotheses of lineage sorting and introgression in New Zealand alpine cicadas (*Maoricicada Dugdale*). Systematic Biology 55(3), 411–425.

Buneman1971

Buneman, P. (1971). The Recovery of Trees from Measures of Dissimilarity. In D. Kendall and P. Tautu (Eds.), *Mathematics in the Archeological and Historical Sciences*, pp. 387–395. Edinburgh University Press.

 ${\tt Buneman1974_DM}$

Buneman, P. (1974a). A Characterisation of Rigid Circuit Graphs. *Discrete Mathematics 9*, 205–212.

Buneman1974_JCT

Buneman, P. (1974b). A Note on the Metric Properties of Trees. *Journal of Combinatorial Theory (B)* 17, 48–50.

- Burgess, R. and Z. Yang (2008). Estimation of hominoid ancestral population sizes under bayesian coalescent models incorporating mutation rate variation and sequencing errors. *Molecular Biology and Evolution* 25(9), 1979–1994.
- Cardona Cardona, G., F. Rossell, and G. Valiente (2008). Extended Newick: it is time for a standard representation of phylogenetic networks. *BMC Bioinformatics* 9(532-540).
 - Chen2001 Chen, F. C. and W. H. Li (2001). Genomic divergences between humans and other hominoids and the effective population size of the common ancestor of humans and chimpanzees. *American Journal of Human Genetics* 68, 444–456.
- Chen2009macs Chen, G. K., P. Marjoram, and J. D. Wall (2009). Fast and flexible simulation of dna sequence data. *Genome Res.* 19, 136–142.
- Colless, D. H. (1982). Review of "Phyogenetics: The theory and practice of phylogenetic systematics". Systematic Zoology 31, 100–104.
- Cummings 2008 Cummings, M. P., M. C. Neel, and K. L. Shaw (2008). A genealogical approach to quantifying lineage divergence. *Evolution* 62(9), 2411–2422.
 - Darlu, P. and G. Lecointre (2002). When does the incongruence length difference test fail? *Molecular Biology and Evolution* 19, 432–437.
 - Daubin, V. and H. Ochman (2004). Quartet mapping and the extent of lateral transfer in bacterial genomes. *Molecular Biology and Evolution* 1, 86–89.
- de Quieroz, K. (2007). Species concepts and species delimitation. Systematic Biology 56, 879–886.
- deQuieroz, K. and J. Gauthier (1990). Phylogeny as a central principle in taxonomy: phylogenetic definitions of taxon names. Systematic Zoology 39(4), 307–322.
 - Degnan, J. H. (2010). Probabilities of gene tree topologies with intraspecific sampling given a species tree. In L. L. Knowles and L. S. Kubatko (Eds.), Estimating Species Trees, Practical and Theoretical Aspects, pp. 53–77. Hoboken, NJ: Wiley-Blackwell.
 - Degnan, J. H., M. DeGiorgio, D. Bryant, and N. A. Rosenberg (2009). Properties of consensus methods for inferring species trees from gene trees. Systematic biology 58(1), 35–54.
 - Degnan, J. H. and N. A. Rosenberg (2006). Discordance of species trees with their most likely gene trees. *PLoS Genetics* 2, 762–768.
 - Degnan, J. H. and L. A. Salter (2005). Gene tree distributions under the coalescent process. *Evolution* 59, 24–37.

- Desper, R. and O. Gascuel (2004). Theoretical foundation of the balanced minimum evolution method of phylogenetic inference and its relationship to weighted least-squares tree fitting. *Molecular Biology and Evolution 21*, 587–598.
- DiltheyMHC Dilthey, A., C. Cox, Z. Iqbal, M. R. Nelson, and G. McVean (0000). Improved genome inference in the mhc using a population reference graph. $un-known \ \theta(0), 0.$
- Dilthey2013 Dilthey, A., S. Leslie, L. Moutsianas, J. Shen, C. Cox, M. R. Nelson, and G. McVean (2013, 02). Multi-population classical hla type imputation. *PLoS Comput Biol* 9(2), e1002877.
- Donnelly, P. and T. Kurtz (1999). Particle representations for measure-valued population models. *The Annals of Probability* 27(1), 166–205.
 - Doucet, A. (2007). Sequential Monte Carlo methods lectures at Machine Learning Summer School (MLSS), Tübingen 2007 . http://videolectures.net/mlss07_doucet_smcm/.
 - Doucet, A., N. de Freitas, and N. Gordon (2001). An introduction to sequential Monte Carlo methods. In A. Doucet, N. de Freitas, and N. Gordon (Eds.), Sequential Monte Carlo Methods in Practice. New York: Springer-Verlag.
 - Doucet, A., S. Godsill, and C. Andrieu (2000). On sequential monte carlo sampling methods for bayesian filtering. *Statistics and Computing* 10, 197–208.
 - Doucet, A. and A. M. Johansen (2008). A tutorial on particle filtering and smoothing: Fifteen years later. www.cs.ubc.ca/ arnaud/doucet_johansen_tutorialPF.pdf.
 - Doyle, J. J. (1997). Trees within trees: Genes and species, molecules and morphology. Systematic Biology 46(3), 537–553.
 - Dress, A., A. von Haeseler, and M. Krueger (1986). Reconstructing phylogenetic trees using variants of the "four-point condition". *Studien zur Klassi-fikation* 17, 299–305.
- Drummond2007beast Drummond, A. and A. Rambaut (2007). BEAST: Bayesian evolutionary analysis by sampling trees. BMC Evolutionary Biology 7(1), 214.
 - Drummond A. J., A. Rambaut, B. Shapiro, and O. G. Pybus (2005). Bayesian coalescent inference of past population dynamics from molecular sequences.

 *Molecular Biology and Evolution 22(5), 1185–1192.
- Drummond A. J., M. A. Suchard, D. Xie, and A. Rambaut (2012). Bayesian phylogenetics with BEAUti and the BEAST 1.7. Molecular Biology and Evolution 29(8), 1969–1973.

- Durbin, R. (2014). Efficient haplotype matching and storage using the positional BurrowsWheeler transform (PBWT). *Bioinformatics* 30(9), 12661272.
- Dutheil, J. Y., G. Ganapathy, A. Hobolth, T. Mailund, M. K. Uyenoyama, and M. H. Schierup (2009). Ancestral population genomics: the coalescent hidden Markov model approach. *Genetics* 183(1), 259–274.
- Edwards 2007 Edwards, S., L. Liu, and D. K. Pearl (2007). High-resolution species trees without concatenation. *Proceedings of the National Academy of Sciences of the United States of America* 104 (14), 5936–5941.
 - Eldon, B. (2011). Estimation of parameters in large offspring number models and ratios of coalescence times. *Theoretical Population Biology* 80, 16–28.
 - Eldon, B., M. Birkner, J. Blath, and F. Freund (2015). Can the site-frequency spectrum distinguish exponential population growth from multiple-merger coalescents? *Genetics* 199(3), 841–856.
- Eldon, B. and J. H. Degnan (2011). Concordance between species trees and gene genealogies with asynchronous multiple mergers. Slides, www.newton.ac.uk/programmes/PLG/seminars/062016301.pdf.
 - Eldon, B. and J. H. Degnan (2012). Multiple merger gene genealogies in two species: monophyly, paraphyly, and polyphyly for two examples of Lambda coalescents. *Theoretical Population Biology 82*, 117–130.
 - Eldon, B. and J. Wakeley (2006). Coalescent processes when the distribution of offspring number among individuals is highly skewed. *Genetics* 172, 2621–2633
 - Eldon, B. and J. Wakeley (2008). Linkage disequilibrium under skewed offspring distribution among individuals in a population. *Genetics* 178, 1517–1532.
 - Eriksson2009 Eriksson, A., B. Mahjani, and B. Mehlig (2009). Sequential markov coalescent algorithms for population models with demographic structure. *Theoretical Population Biology* 76(2), 84 91.
 - Ewing2006 Ewing, G. and A. Rodrigo (May 2006). Coalescent-based estimation of population parameters when the number of demes changes over time. *Molecular Biology and Evolution* 23(5), 988–996.
 - Excoffier Excoffier, L. and M. Foll (2011). fastsimcoal: A continuous-time coalescent simulator of genomic diversity under arbitrarily complex evolutionary scenarios.

 Bioinformatics 27(9), 1332–1334.
 - Excoffier 2000 Excoffier, L., J. Novembre, and S. Schneider (2000). Computer note. simcoal: a general coalescent program for the simulation of molecular data in interconnected populations with arbitrary demography. *Journal of Heredity 91*(6), 506–509.

Felsensteinlist

Felsenstein, J. Phylogeny programs. http://evolution.genetics.washington.edu/phylip/software.html.

Felsenstein1978misleading

Felsenstein, J. (1978a). Cases in which parsimony or compatibility methods will be positively misleading. Systematic Biology 27, 401–410.

Felsentein1978

Felsenstein, J. (1978b). The number of evolutionary trees. Systematic Zoology 27, 27–33.

Felsenstein1981

Felsenstein, J. (1981). Evolutionary trees from DNA sequences: a maximum likelihood approach. *Journal of Molecular Evolution* 17, 368–376.

Felsenstein1993

Felsenstein, J. (1993). *PHYLIP (PHYLogeny Inference Package) version 3.6a2*. Department of Genetics, University of Washington, Seattle: Distributed by the author.

Felsentein2004

Felsenstein, J. (2004). *Inferring Phylogenies*. Sunderland, MA: Sinauer Associates

Ferretti2013

Ferretti, L., F. Disanto, and T. Wiehe (2013). The effect of single recombination events on colaescent tree height and shape. *PLOS ONE* 8(4), e60123. doi:10.1371/journal.pone.0060123.

Fisher1930

Fisher, R. A. (1930). The genetical theory of natural selection. Oxford: Clarendon Press.

Fitch1971

Fitch, W. M. (1971). Toward defining the course of evolution: minimum change for a specific tree topology. *Systematic Zoology* 20(4), 406–416.

Galtier2004

Galtier, N. and A. Jean-marie (2004). Markov-modulated markov chains and the covarion process of molecular evolution. *Journal of Computational Biology* 11(4), 727–733.

Zhang2009

Gaoyu, Z., L. Qiongfei, L. Qing, and Z. Zhizhao (2009). High frequency financial time series forecasting via particle filtering. In *Information Management*, Innovation Management and Industrial Engineering, 2009 International Conference on, Volume 4, pp. 62–65.

Gascuel1997

Gascuel, O. (1997). BIONJ: an improved version of the NJ algorithm based on a simple model of sequence data. *Molecular Biology and Evolution* 14(7), 685-695.

Gerard2011

Gerard, D., H. L. Gibbs, and L. Kubatko (2011). Estimating hybridization in the presence of coalescence using phylogenetic intraspecific sampling. *BMC Evolutionary Biology* 11.

Gernhard2008

Gernhard, T., K. Hartmann, and M. A. Steel (2008). Stochastic properties of generalised yule models, with biodiversity applications. *Mathematical Biology* 57, 713–735.

Gordon1993

Gordon, N., D. Salmond, and A. F. M. Smith (1993). Novel approach to nonlinear/non-Gaussian Bayesian state estimation. Radar and Signal Processing, IEE Proceedings F 140(2), 107–113.

Gravel05072011

Gravel, S., B. M. Henn, R. N. Gutenkunst, A. R. Indap, G. T. Marth, A. G. Clark, F. Yu, R. A. Gibbs, T. . G. Project, and C. D. Bustamante (2011). Demographic history and rare allele sharing among human populations. Proceedings of the National Academy of Sciences.

Green2010

Green, R. E., J. Krause, A. W. Briggs, T. Maricic, U. Stenzel, M. Kircher, N. Patterson, H. Li, W. Zhai, M. H.-Y. Fritz, N. F. Hansen, E. Y. Durand, A.-S. Malaspinas, J. D. Jensen, T. Marques-Bonet, C. Alkan, K. Prfer, M. Meyer, H. A. Burbano, J. M. Good, R. Schultz, A. Aximu-Petri, A. Butthof, B. Hber, B. Hffner, M. Siegemund, A. Weihmann, C. Nusbaum, E. S. Lander, C. Russ, N. Novod, J. Affourtit, M. Egholm, C. Verna, P. Rudan, D. Brajkovic, . Kucan, I. Guic, V. B. Doronichev, L. V. Golovanova, C. Lalueza-Fox, M. de la Rasilla, J. Fortea, A. Rosas, R. W. Schmitz, P. L. F. Johnson, E. E. Eichler, D. Falush, E. Birney, J. C. Mullikin, M. Slatkin, R. Nielsen, J. Kelso, M. Lachmann, D. Reich, and S. Pbo (2010). A draft sequence of the neandertal genome. Science 328 (5979), 710–722.

Griffiths1981

Griffiths, R. C. (1981). Neutral two-locus multiple allele models with recombination. Theoretical Population Biology 19(2), 169 – 186.

Griffiths1991

Griffiths, R. C. (1991). The two-locus ancestral graph. *Lecture Notes-Monograph Series* 18, 100–117.

Griffiths1997ARG

Griffiths, R. C. and P. Marjoram (1997). An ancestral recombination graph. In *Progress in Population Genetics and Human Evolution (Minneapolis, MN*, 1994), Volume 87 of *IMA Vol. Math. Appl.*, pp. 257–270. New York: Springer.

Griffiths2003

Griffiths, R. C. and S. Tavaré (2003). The genealogy of a neutral mutation. In P. J. Green, N. L. Hjort, and S. Richardson (Eds.), *Highly Structured Stochastic Systems*, Volume 27 of *Oxford Statistical Science Series*, pp. 393–413. Oxford University Press.

Gronau2011

Gronau, I., M. J. Hubisz, B. Gulko, C. G. Danko, and A. Siepel (2011a). Nature Genetics 43, 1031-1034.

Ilan2011

Gronau, I., M. J. Hubisz, B. Gulko, C. G. Danko, and A. Siepel (2011b). Bayesian inference of ancient human demography from individual genome sequences. *Nature Genetics* 43, 10311034.

Guigo1996

Guigo, R., I. Muchnik, and T. F. Smith (1996). Reconstruction of ancient molecular phylogeny. *Molecular Phylogenetics and Evolution* 6(2), 189 – 213.

 ${\tt Guindon 2010}$

Guindon, S., J.-F. Dufayard, V. Lefort, M. Anisimova, W. Hordijk, and O. Gascuel (2010). New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Systematic Biology* 59(3), 307–321.

- Guindon Guindon, S. and O. Gascuel (2003). A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. Systematic Biology 52(5), 696–704.
 - Gusev2009 Gusev, A., J. K. Lowe, M. Stoffel, M. J. Daly, D. Altshuler, J. L. Breslow, J. M. Friedman, and I. Pe'er (2009). Whole population, genome-wide mapping of hidden relatedness. *Genome Research* 19(2), 318–326.
- Gutenkunst2009dadi Gutenkunst, R. N., R. D. Hernandez, S. H. Williamson, and C. D. Bustamante (2009). Inferring the joint demographic history of multiple populations from multidimensional SNP frequency data. *PLoS Genet* 5(10), e1000695.
 - Harding E. F. (1971). The probabilities of rooted tree-shapes generated by random bifurcation. Advances in Applied Probability 3(1), 44–77.
 - Harris 2013 Harris, K. and R. Nielsen (2013). Inferring demographic history from a spectrum of shared haplotype lengths. *PLoS Genet* 9(6), e1003521.
 - Hasegawa, M., H. Kishino, and N. Saitou (1991). On the maximum likelihood method in molecular phylogenetics. *Journal of Molecular Evolution* 32, 443–445.
 - Heard, S. B. (1992). Patterns in tree balance among cladistic. phenetic, and randomly generated phylogenetic trees. *Evolution* 46(6), 1818–1826.
 - Hedgecock, D. (1994). Does variance in reproductive success limit effective population sizes of marine organisms? In A. Beaumont (Ed.), Genetics and Evolution of Aquatic Organisms, pp. 1222–1344. London: Chapman and Hall.
 - Hedgecock, D. and A. I. Pudovkin (2011). Sweepstakes reproductive success in highly fecund marine fish and shellfish: a review and commentary. Bull Mar Sci 87, 971–1002.
 - Hedgecock, D., M. Tracey, and K. Nelson (1982). Genetics. In L. Abele (Ed.),

 The Biology of Crustacea, Volume 2, pp. 297–403. New York: Academic Press.
 - Hein 2005 Hein, J., M. H. Schierup, and C. Wiuf (2005). Gene Genealogies, Variation and Evolution: A Primer in Coalescent Theory. Oxford University Press, Oxford, UK.
 - Heled, J. and A. Drummond (2010). Bayesian inference of species trees from multilocus data. *Molecular Biology and Evolution* 27(3), 570–580.
 - Hillis, D. M. and J. P. Huelsenbeck (1992). Signal, noise, and reliability in molecular phylogenetic analyses. *Journal of Heredity* 83, 189–195.
 - Ho2011 Ho, S. Y. and B. Shapiro (2011). Skyline-plot methods for estimating demographic history from nucleotide sequences. *Molecular Ecology Resources* 11(3), 423–434.

- Hoeffding1963 Hoeffding, W. (1963). Probability inequalities for sums of bounded random variables. Journal of the American Statistical Association 58(301), 13–30.
 - Holder M. and P. O. Lweis (2003). Phylogeny estimation: traditional and bayesian approaches. *Nature reviews Genetics* 4, 275–284.
 - Holland B. and V. Moulton (2003). Consensus networks: A method for visualising incompatibilities in collections of trees. In G. Benson and R. Page (Eds.),

 Algorithms in Bioinformatics, Volume 2812 of Lecture Notes in Computer Science, pp. 165–176. Springer Berlin Heidelberg.
 - Holland, B. R., S. Benthin, P. J. Lockhart, V. Moulton, and K. T. Huber (2008).

 Using supernetworks to distinguish hybridization from lineage-sorting. *BMC Evolutionary Biology* 8, 202–213.
 - Holland, B. R., K. T. Huber, V. Moulton, and P. J. Lockhart (2004). Using consensus networks to visualize contradictory evidence for species phylogeny.

 Molecular Biology and Evolution 21(7), 1459–1461.
 - Holman, E. W. (2005). Nodes in phylogenetic trees: The relation between imbalance and number of descendent species. Systematic Biology 54(6), 895–899.
 - Huber, K. and V. Moulton (2006). Phylogenetic networks from multi-labelled trees. Journal of Mathematical Biology 52(5), 613–632.
- Hudson, R. R. (1983a). Properties of a neutral allele model with intragenic recombination. *Theoretical Population Biology* 23, 183–201.
- Hudson, R. R. (1983b). Testing the constant-rate3 neutral allele model with protein sequence data. *Evolution* 37, 203–217.
 - Hudson, R. R. (1990). Gene genealogies and the coalescent process. Oxford Surveys Evolution Biology 7, 1–44.
 - Hudson, R. R. (2002). Generating samples under a Wright-Fisher neutral model.

 Bioinformatics 18, 337–338.
 - Hudson, R. R. and J. A. Coyne (2002). Mathematical consequences of the genealogical species concept. *Evolution* 56(8), 1557–1565.
 - Hudson, R. R. and N. L. Kaplan (1985). Statistical properties of the number of recombination events in the hisotry of a sample of DNA sequences.

 Genetics 111, 147–164.
- Huelsenbeck2001mrbays Huelsenbeck, J. P. and F. Ronquist (2001). MrBayes: Bayesian inference of phylogeny. *Bioinformatics* 17, 754–755.
 - Huson, D., R. Rupp, and C. Scornavacca (2010). *Phylogenetic Networks: Concepts, Algorithms and Applications*. Cambridge, UK: Cambridge University Press.

Huson2007Splits

Huson, D. H. and D. Bryant (2007). Contents user manual for SplitsTree4 V4.8.

Huson2004

Huson, D. H., T. Dezulian, T. Klopper, and M. A. Steel (2004). Phylogenetic super-networks from partial trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 1, 151–158.

Huson2005

Huson, D. H., T. Klopper, P. J. Lockhart, and M. A. Steel (2005). Reconstruction of reticulate networks from gene trees. Research in Computational Molecular Biology 3500, 233–249.

Huson2007Dendro

Huson, D. H., D. C. Richter, C. Rausch, T. Dezulian, M. Franz, and R. Rupp (2007). Dendroscope: An interactive viewer for large phylogenetic trees. BMC Bioinformatics 8(1), 460.

Huynh2005

Huynh, T. N. D., J. Jansson, N. B. Nguyen, and W.-K. Sung (2005). Constructing a smallest refining galled phylogenetic network. Annual International Conference on Research in Computational Molecular Biology 2005, LNBI 3500, 265–280.

Degnan2012

James H. Degnan, Noah A. Rosenberg, T. S. (2012). The probability distribution of ranked gene trees on a species tree. *Mathematical Biosciences* (235), 45–55.

Jiggins2008

Jiggins, C. D., C. Salazar, M. Linares, and J. Mavarez (2008). Hybrid trait speciation and heliconius butterflies. *Philosophical Transactions of the Royal Society of London. Series B* 363, 3047–3054.

Jack2015

John D. O'Brien, Zamin Iqbal, L. A.-E. (2015). An integrative statistical model for inferring strain admixture within clinical plasmodium falciparum isolates.

Joly2009

Joly, S., P. A. McLenachan, and P. J. Lockhart (2009). A statistical approach for distinguishing hybridization and incomplete lineage sorting. The American Naturalist 174, 54–70.

Jones2011

Jones, G. R. (2011). Tree models for macroevolution and phylogenetic analysis. Systematic Biology 60(6), 735–746.

Jordan1869

Jordan, C. (1869). Sur les assemblages des lignes. Journal für die Reine und Angewandte Mathematik 70, 185–190.

JC69

Jukes, T. H. and C. R. Cantor (1969). Evolution of protein molecules. In H. N. Munro (Ed.), *Mammalian protein metabolism*, pp. 21–123. New York: Academic Press.

Kalinowski2009

Kalinowski, S. (2009). How well do evolutionary trees describe genetic relationships among populations? *Heredity* 102, 506–513.

Kang1975

Kang, A. N. C. and D. A. Ault (1975). Some properties of a centroid of a free tree. *Information Processing Letters* 4(1), 18–20.

Karr1993

Karr, A. F. (1993). Probability. New York: Springer-Verlag.

- Kerr A. M. (2013). Holothuria (semperothuria) roseomaculata n. sp. (aspidochirotida: Holothuriidae), a coral-reef inhabiting sea cucumber from the western pacific ocean. *Zootaxa 3641*(4), 384–394.
- Kim, J. (1993, Sep). Improving the accuracy of phylogenetic estimation by combining different methods. Systematic Biology 42(3), 331–340.
- Kim, J., F. J. Rohlf, and R. R. Sokal (1993, Apr). The accuracy of phylogenetic estimation using the neighbor-joining method. *Evolution* 47(2), 471–486.
- Kimura, M. (1971). Theoretical foundation of population genetics at the molecular level. *Theoretical Population Biology* 2(2), 174 208.
- Kingman, J. F. C. (1982). On the genealogy of large populations. *Journal of Applied Probability* 19, 27–43.
- Kirkpatrick, M. and M. Slatkin (1993). Searching for evolutionary patterns in the shape of a phylogenetic tree. *Evolution* 47(4), 1171–1181.
 - Kotz 2000 Kotz, S., N. Balakrishnan, and N. L. Johnson (2000). Continuous Multivariate Distributions, Volume 1, Models and Applications (2 ed.). New York: Wiley.
 - Kubatko, L. S. (2009). Identifying hybridization events in the presence of coalescence via model selection. Systematic Biology 58, 478–488.
- Kubatko2009stem Kubatko, L. S., B. C. Carstens, and L. L. Knowles (2009). STEM: species tree estimation using maximum likelihood for gene trees under coalescence.

 Bioinformatics 25 (7), 971–973.
 - Kubatko L. S. and J. Degnan (2007). Inconsistency of phylogenetic estimates from concatenated data under coalescence. Systematic Biology 56, 17–24.
 - Lapointe 2010 Lapointe, F.-J., P. Lopez, Y. Boucher, J. Koenig, and E. Bapteste (2010).

 Clanistics: a multi-level perspective for harvesting unrooted gene trees.

 Trends in Microbiology 18, 341–347.
 - Lawson, D. J., G. Hellenthal, S. Myers, and D. Falush (2012, 01). Inference of population structure using dense haplotype data. *PLoS Genet* 8(1), e1002453.
 - Leigh2008 Leigh, J. W., E. Susko, M. Baumgartner, and A. J. Roger (2008). Testing congruence in phylogenomic analysis. Systematic Biology 57(1), 104–115.
 - Li Li Li Li, A. Coghlan, J. Ruan, L. J. Coin, J.-K. Heriche, L. Osmotherly, R. Li, T. Liu, Z. Zhang, L. Bolund, G. K.-S. Wong, W. Zheng, P. Dehal, J. Wang, and R. Durbin (2006). Treefam: a curated database of phylogenetic trees of animal gene families. *Nucleic Acids Research* 34, 572–580.
 - Li, H. and R. Durbin (2011). Inference of human population history from individual whole-genome sequences. *Nature* 475, 493–496.

- Li 2003 Li, N. and M. Stephens (2003, December). Modeling Linkage Disequilibrium and Identifying Recombination Hotspots Using Single-Nucleotide Polymorphism Data. Genetics 165(4), 2213–2233.
- Li 2000 Li, S., D. K. Pearl, and H. Doss (2000). Phylogenetic tree construction using Markov Chain Monte Carlo. *Journal of the American Statistical Association* 95(450), 493–508.
- Liu, J. S., R. Chen, and W. H. Wong (1998). Rejection control and sequential importance sampling. *Journal of the American Statistical Association* 93 (443), 1022–1031.
- LiuPhD Liu, L. (2006). Reconstructing posterior distributions of a species phylogeny using estimated gene tree distributions. Ph. D. thesis, Ohio State University.
- Liu2008 Liu, L. (2008). BEST: Bayesian estimation of species trees under the coalescent model. *Bioinformatics* 24, 2542–2543.
- Liu2007 Liu, L. and D. K. Pearl (2007). Species trees from gene trees: Reconstructing bayesian posterior distributions of a species phylogeny using estimated gene tree distributions. Systematic Biology 56(3), 504–514.
- Liu Liu, L., D. K. Pearl, R. T. Brumfield, and S. V. Edwards (2008). Estimating species trees using multiple allele DNA sequence data. *Evolution* 62(8), 2080–2091.
- Liu Liu, L. and L. Yu (2010). Phybase: an R package for species tree analysis.

 Bioinformatics 26(7), 962–963.
- Liu2009review Liu, L., L. Yu, L. Kubatko, D. K. Pearl, and S. V. Edwards (2009). Coalescent methods for estimating phylogenetic trees. *Molecular Phylogenetics and Evolution* 53(1), 320–328.
 - Liu, L., L. Yu, and D. K. Pearl (2010). Maximum tree: a consistent estimator of the species tree. *Journal of Mathematical Biology* 60, 95–106.
 - Liu2009Sys Liu, L., L. Yu, D. K. Pearl, and S. V. Edwards (2009). Estimating species phylogenies using coalescence times among sequences. Systematic Biology 58(5), 468–477.
 - Locke, D. P., L. W. Hillier, W. C. Warren, K. C. Worley, L. V. Nazareth, D. M. Muzny, S.-P. Yang, Z. Wang, A. T. Chinwalla, P. Minx, M. Mitreva, L. Cook, K. D. Delehaunty, C. Fronick, H. Schmidt, L. A. Fulton, R. S. Fulton, J. O. Nelson, V. Magrini, C. Pohl, T. A. Graves, C. Markovic, A. Cree, H. H. Dinh, J. Hume, C. L. Kovar, G. R. Fowler, G. Lunter, S. Meader, A. Heger, C. P. Ponting, T. Marques-Bonet, C. Alkan, L. Chen, Z. Cheng, J. M. Kidd, E. E. Eichler, S. White, S. Searle, A. J. Vilella, Y. Chen, P. Flicek, J. Ma, B. Raney, B. Suh, R. Burhans, J. Herrero, D. Haussler, R. Faria, O. Fernando, F. Darr, D. Farr, E. Gazave, M. Oliva, A. Navarro, R. Roberto, O. Capozzi, N. Archidiacono, G. D. Valle, S. Purgato, M. Rocchi, M. K. Konkel, J. A.

Walker, B. Ullmer, M. A. Batzer, A. F. A. Smit, R. Hubley, C. Casola, D. R. Schrider, M. W. Hahn, V. Quesada, X. S. Puente, G. R. Ordoez, C. Lpez-Otn, T. Vinar, B. Brejova, A. Ratan, R. S. H. andWebb Miller, C. Kosiol, H. A. Lawson, V. Taliwal, A. L. Martins, A. Siepel, A. RoyChoudhury, X. Ma, J. Degenhardt, C. D. Bustamante, R. N. Gutenkunst, T. Mailund, J. Y. Dutheil, A. Hobolth, M. H. Schierup, O. A. Ryder, Y. Yoshinaga, P. J. de Jong, G. M. Weinstock, J. Rogers, E. R. Mardis, R. A. Gibbs, and R. K. Wilson (2011). Comparative and demographic analysis of orang-utan genomes. *Nature* 469, 529–533.

Lohmueller2009

Lohmueller, K. E., C. D. Bustamante, and A. G. Clark (2009). Methods for human demographic inference using haplotype patterns from genomewide single-nucleotide polymorphism data. *Genetics* 182(1), 217–231.

Lopes2009

Lopes, J. S., D. Balding, and M. A. Beaumont (2009). Popabc: a program to infer historical demographic parameters. *Bioinformatics* 25(20), 2747–2749.

Lunter2012SMBE

Lunter, G. (2012). A new Markovian approximation to the coalescent with recombination. Society for Molecular Biology & Evolution. http://imgpublic.mci-group.com/ie/PCO/AllAbstracts_FINAL.pdf. Aug 14, 2013.

Lunter2011

Lunter, G. and M. Goodson (2011). Stampy: A statistical algorithm for sensitive and fast mapping of illumina sequence reads. *Genome Research* 21(6), 936–939.

Ma2008

Ma, J., A. Ratan, B. J. Raney, B. B. Suh, W. Miller, and D. Haussler (2008). The infinite sites model of genome evolution. *Proceedings of the National Academy of Sciences of the United States of America* 105(38), 14254–14261.

Maddison1997nexus

Maddison, D. R., D. L. Swofford, and W. P. Maddison (1997). NEXUS: An extensible file format for systematic information. *Systematic Biology* 46(4), 590–621.

Maddison1997

Maddison, W. P. (1997). Gene trees in species trees. Systematic Biology 46(3), 523–536.

Maddison2006

Maddison, W. P. and L. L. Knowles (2006). Inferring phylogeny despite incomplete lineage sorting. *Systematic Biology* 55(1), 21–30.

Mahmoud2008

Mahmoud, H. (2008). Pólya Urn Models. Boca Raton: Chapman and Hall/CRC.

Mailund2011

Mailund, T., J. Y. Dutheil, A. Hobolth, G. Lunter, and M. H. Schierup (2011). Estimating Divergence Time and Ancestral Effective Population Size of Bornean and Sumatran Orangutan Subspecies Using a Coalescent Hidden Markov Model. *PLoS Genet* 7(3), e1001319.

Mailund2012

Mailund, T., A. E. Halager, M. Westergaard, J. Y. Dutheil, K. Munch, L. N. Andersen, G. Lunter, K. Pr'ufer, A. Scally, A. Hobolth, and M. H. Schierup. A new isolation with migration model along complete genomes infers very

different divergence processes among closely related great ape species. PLOS Genetics 8(12), doi:10.1371/journal.pgen.1003125.

Mallet2007

Mallet, J., M. Beltrán, W. Neukirchen, and M. Linares (2007). Natural hybridization in heliconiine butterflies: the species boundary as a continuum. *BMC Evolutionary Biology* 7, 28.

Margush1981

Margush, T. and F. R. Mcmorris (1981). Consensus n-trees. Bulletin of Mathematical Biology 43, 239–244.

Marjoram2006Review

Marjoram, P. and S. Tavare (2006). Modern computational approaches for analysing molecular genetic variation data. *Nature Reviews Genetics* 7(10), 759–770.

Marjoram2006

Marjoram, P. and J. Wall (2006). Fast "coalescent" simulation. *BMC Genetics* 7(1), 16.

Marshall2011

Marshall, D. C., K. B. R. Hill, J. R. Cooley, and C. Simon (2011). Hybridization, mitochondrial DNA phylogeography, and prediction of the early stages of reproductive isolation: Lessons from New Zealand cicadas (Genus Kikihia). Systematic Biology 60, 482–502.

Marshall2008

Marshall, D. C., K. Slon, J. R. Cooley, K. B. Hill, and C. Simon (2008). Steady plio-pleistocene diversification and a 2-million-year sympatry threshold in a New Zealand cicada radiation. *Molecular Phylogenetics and Evolution* 48, 1054–1066.

Mathew2013

Mathew, L. A., P. R. Staab, L. E. Rose, and D. Metzler (2013). Why to account for finite sites in population genetic studies and how to do this with jaatha 2.0. *Ecology and Evolution*, n/a-n/a.

Mathieson2014

Mathieson, I. and G. McVean (2014, 08). Demography and the age of rare variants. *PLoS Genet* 10(8), e1004528.

 ${\tt Matsumoto1998}$

Matsumoto, M. and T. Nishimura (1998). Mersenne Twister: A 623-dimensionally equidistributed uniform Pseudo-Random number generator. *ACM Transactions on Modeling and Computer Simulation* 8(1), 3–30.

Mau1999

Mau, B., M. A. Newton, and B. Larget (1999). Bayesian phylogenetic inference via markov chain monte carlo methods. *Biometrics* 55(1), 1–12.

 ${\tt McKenziethesis}$

McKenzie, A. (2000). Stochastic Speciation Models for Evolutionary Trees. Ph. D. thesis, University of Canterbury, Christchurch.

McKenzie2000

McKenzie, A. and M. A. Steel (2000). Distributions of cherries for two models of trees. *Mathematical Biosciences* 164, 81–92.

McVean2005

McVean, G. A. and N. J. Cardin (2005). Approximating the coalescent with recombination. *Philosophical Transactions of the Royal Society B: Biological Sciences* 360 (1459), 1387–1393.

mcvean_approximating_2005

McVean, G. A. T. and N. J. Cardin (2005, July). Approximating the coalescent with recombination. *Phil. Trans. R. Soc. B* 360 (1459), 1387–1393.

Meng2009

Meng, C. and L. S. Kubatko (2009). Detecting hybrid speciation in the presence of incomplete lineage sorting using gene tree incongruence: a model. *Theoretical Population Biology* 75, 35–45.

Mihaylova2004

Mihaylova, L. and R. Boel (2004). A particle filter for freeway traffic estimation. In *Decision and Control*, 2004. CDC. 43rd IEEE Conference on, Volume 2, pp. 2106–2111 Vol.2.

Miller2012

Miller, W., S. C. Schuster, A. J. Welch, A. Ratan, O. C. Bedoya-Reina, F. Zhao, H. L. Kim, R. C. Burhans, D. I. Drautz, N. E. Wittekindt, L. P. Tomsho, E. Ibarra-Laclette, L. Herrera-Estrella, E. Peacock, S. Farley, G. K. Sage, K. Rode, M. Obbard, R. Montiel, L. Bachmann, . Inglfsson, J. Aars, T. Mailund, . Wiig, S. L. Talbot, and C. Lindqvist (2012). Polar and brown bear genomes reveal ancient admixture and demographic footprints of past climate change. Proceedings of the National Academy of Sciences.

Mitchell1978

Mitchell, S. L. (1978). Another characterization of the centroid of a tree. *Discrete Mathematics* 24, 277–280.

mooers97a

Mooers, A. O. and S. B. Heard (1997). Evolutionary process from phylogenetic tree shape. *Quarterly Review of Biology* 72, 31–54.

Morgan2009

Morgan-Richards, M., R. D. Smissen, L. D. Shepherd, G. P. Wallis, J. J. Hayward, C. hang Chan, G. K. Chambers, and H. M. Chapman (2009, March). A review of genetic analyses of hybridisation in New Zealand. *Journal of the Royal Society of New Zealand* 39(1), 15–34.

Mossel2008

Mossel, E. and S. Roch (2010). Incomplete lineage sorting: consistent phylogeny estimation from multiple loci. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 7, 166–171.

Naduvilezhath2011

NADUVILEZHATH, L., L. E. ROSE, and D. METZLER (2011). Jaatha: a fast composite-likelihood approach to estimate demographic parameters. *Molecular Ecology* 20(13), 2709–2723.

Nei1987

Nei, M. (1987). *Molecular Evolutionary Genetics*. New York: Columbia University Press.

Nichols2001

Nichols, R. (2001, July). Gene trees and species trees are not the same. *Trends* in Ecology and Evolution 16(7).

Nieselt2001

Nieselt-Struwe, K. and A. von Haeseler (2001). Quartet-mapping, a generalization of the likelihood-mapping procedure. *Molecular Biology and Evolution* 7(18), 1204–1219.

nordborg98a

Nordborg, M. (1998). On the probability of neanderthal ancestry. *American Journal of Human Genetics* 63, 1237–1240.

- nordborg01a Nordborg, M. (2001). Coalescent theory. In D. J. Balding, M. Bishop, and C. Cannings (Eds.), *Handbook of Statistical Genetics*, Chapter 7, pp. 179–212. Chichester, UK: Wiley.
 - Olsen, G. (1990). Gary Olsen's interpretation of the "Newick's 8:45" tree format standard. http://evolution.genetics.washington.edu/phylip/newick_doc.html. Feb 21, 2013.
- Omeara2010 O'Meara, B. C. (2010). New heuristic methods for joint species delimitation and species tree inference. Systematic Biology 59(1), 59–73.
- Omeara2006 O'Meara, B. C. and P. C. W. Ccile An, Michael J. Sanderson (2006). Testing for different rates of continuous trait evolution using likelihood. *Evolution* 60(5), 922–933.
- Pamilo, P. and M. Nei (1988). Relationships between gene trees and species trees. *Molecular Biology and Evolution* 5, 568–583.
- Paradis, E., J. Claude, and K. Strimmer (2004). Ape: analyses of phylogenetics and evolution in R language. *Bioinformatics* 20, 289–290.
- Pinelis 2003 Pinelis, I. (2003). Evolutionary models of phylogenetic trees. *Proceedings of the Royal Society of London. Series B: Biological Sciences* 270 (1522), 1425–1431.
- Pitman1999 Pitman, J. (1999). Coalescents with multiple collisions. The Annals of Probability 27(4), 1870–1902.
 - Poe1998 Poe, S. (1998, March). Sensitivity of phylogeny estimation to taxonomic sampling. Systematic Biology 47(1), 18–31.
 - Poe1999 Poe, S. and D. L. Swofford (1999, March). Taxon sampling revisited. *Nature 398*, 299–300.
 - Pybus 2000 Pybus, O. G., A. Rambaut, and P. H. Harvey (2000). An integrated framework for the inference of viral population history from reconstructed genealogies. Genetics 155(3), 1429–1437.
 - Rmanual R Core Team (2012). R: A Language and Environment for Statistical Computing. Vienna, Austria: R Foundation for Statistical Computing. ISBN 3-900051-07-0.
- Rannala, B. and Z. Yang (1996). Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. *Journal of Molecular Evolution* 43, 304–311.
- Rannla2003 Rannala, B. and Z. Yang (2003). Bayes estimation of species divergence times and ancestral population sizes using DNA sequences from multiple loci. Genetics 164, 1645–1656.
- Ranwez, V. and O. Gascuel (2001). Quartet-based phylogenetic inference: Improvements and limits. *Molecular Biology and Evolution* 18(6), 1103–1116.

Reich2010

Reich, D., R. E. Green, M. Kircher, J. Krause, N. Patterson, E. Y. Durand, B. Viola, A. W. Briggs, U. Stenzel, P. L. F. Johnson, T. Maricic, J. M. Good, T. Marques-Bonet, C. Alkan, Q. Fu, S. Mallick, H. Li, M. Meyer, E. E. Eichler, M. Stoneking, M. Richards, S. Talamo, M. V. Shunkov, A. P. Derevianko, J.-J. Hublin, J. Kelso, M. Slatkin, and S. Pbo (2010). Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature 468, 1053–1060.

Reyer2008 Reyer, H.-U. (2008). Mating with the wrong species can be right. Trends in Ecology and Evolution 23(6), 289–292.

Robinson 1981 Robinson, D. R. and L. R. Foulds (1981). Comparison of phylogenetic trees.

Mathematical Biosciences 53, 131–1477.

Rogers, J. S. (1996). Central moments and probability distributions of three measures of phylogenetic tree imbalance. Systematic Biology 45, 99–110.

Rokas 2005 Rokas, A. and S. B. Carroll (2005). More genes or more taxa? the relative contribution of gene number and taxon number to phylogenetic accuracy.

*Molecular Biology and Evolution 22(5), 1337–1344.

Rokas 2003 Rokas, A., B. L. Williams, N. King, and S. B. Carroll (2003). Genome-scale approaches to resolving incongruence in molecular phylogenies. *Nature* 425, 798–804.

Rosen, D. E. (1978). Vicariant patterns and historical explanation in biogeography. Systematic Zoology 27(2), 159–188.

Rosenberg N. A. (2002). The probability of topological concordance of gene trees and species trees. Theoretical Population Biology 61, 225–247.

Rosenberg N. A. (2003). The shapes of neutral gene genealogies in two species: probabilities of monophyly, paraphyly and polyphyly in a coalescent model. *Evolution* 57(7), 1465–1477.

Rosenberg N. A. (2006). The mean and variance of the numbers of r-pronged nodes and r-caterpillars in yule-generated genealogical trees,. *Annals of Combinatorics* 10, 129–146.

Rosenberg2007: counting Rosenberg, N. A. (2007a). Counting coalescent histories. Journal of Computational Biology, 360–377.

Rosenberg2007:monophyly Rosenberg, N. A. (2007b). Statistical tests for taxonomic distinctiveness from observations of monophyly. *Evolution* 61(2), 317–323.

Ruan, J., H. Li, Z. Chen, A. Coghlan, L. J. M. Coin, Y. Guo, J.-K. Heriche, Y. Hu, K. Kristiansen, R. Li, T. Liu, A. Moses, J. Qin, S. Vang, A. J. Vilella, A. Ureta-Vidal, L. Bolund, J. Wang, and R. Durbin (2008). Treefam: 2008 update. *Nucleic Acids Research* 36, 735–740.

Sackin, M. J. (1972). "Good" and "bad" phenograms. Systematic Zoology 21 (2), 225–226.

Sagitov1999 Sagitov, S. (1999). The general coalescent with asynchronous mergers of ancestral lines. *Journal of Applied Probability 36*, 1116–1125.

Saitou, N. and M. Nei (1987). The Neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4(4), 406–425.

Sanderson, M. J. (1996). How many taxa must be sampled to identify the root node of a large clade? Systematic Biology 45(2), 168–173.

Sanderson, M. J., M. M. McMahon, and M. A. Steel (2011, July). Terraces on phylogenetic tree space. *Science* 333, 448–450.

Sang2000 Sang, T. and Y. Zhong (2000). Testing hybridization hypotheses based on incongruent gene trees. Systematic Biology 49, 422–434.

Sankoff Sankoff, D. D. (1975). Minimal mutation trees of sequences. SIAM Journal of Applied Mathematics 28, 35–42.

Sankoff Sankoff, D. D. and P. Rousseau (1975). Locating the vertices of a Steiner tree in arbitrary space. *Mathematical Programming 9*, 240–246.

Sargsyan, O. and J. Wakeley (2008). A coalescent process with simultaneous multiple mergers for approximating the gene genealogies of many marine organisms. *Theoretical Population Biology* 74, 104–114.

Saunders 1984 Saunders, I. W., S. Tavaré, and G. A. Watterson (1984). On the genealogy of nested subsamples from a haploid population. *Advances in Applied Probability* 16, 471–491.

Schaffner01112005 Schaffner, S. F., C. Foo, S. Gabriel, D. Reich, M. J. Daly, and D. Altshuler (2005). Calibrating a coalescent simulation of human genome sequence variation. Genome Research 15(11), 1576–1583.

Schliep2011 Schliep, K. and E. Paradis (2011). phangorn: phylogenetic analysis in r. *Bioinformatics* 27(4), 592–593.

Schmidt 2002 Schmidt, H. A., K. Strimmer, M. Vingron, and A. von Haeseler (2002). TREE-PUZZLE: maximum likelihood phylogenetic analysis using quartets and parallel computing. *Bioinformatics* 18(3), 502–504.

Schoniger1995 Schoniger, M. and A. von Haeseler (1995, Dec). Performance of the maximum likelihood, neighbor joining, and maximum parsimony methods when sequences sites are not independent. Systematic Biology 44 (4), 533–547.

Schweinsberg 2003 Schweinsberg, J. (2003). Coalescent processes obtained from supercritical Galton-Watson processes. Stochastic Processes and their Applications 106, 107–139.

Semple, C. and M. A. Steel (2003). *Phylogenetics*. Oxford, UK: Oxford University Press.

Sergio2012 Sergio, L. and J. Hey (2012). Demographic inference using spectral methods on snp data, with an analysis of the human out-of-africa expansion. *Genetics* 192(2).

Shapiro B., A. J. Drummond, A. Rambaut, M. C. Wilson, P. E. Matheus, A. V. Sher, O. G. Pybus, M. T. P. Gilbert, I. Barnes, J. Binladen, E. Willerslev, A. J. Hansen, G. F. Baryshnikov, J. A. Burns, S. Davydov, J. C. Driver, D. G. Froese, C. R. Harington, G. Keddie, P. Kosintsev, M. L. Kunz, L. D. Martin, R. O. Stephenson, J. Storer, R. Tedford, S. Zimov, and A. Cooper (2004). Rise and Fall of the Beringian Steppe Bison. Science 306 (5701), 1561–1565.

Sharkey 2001 Sharkey, M. J. and J. W. Leathers (2001). Majority does not rule: The trouble with majority-rule consensus trees. *Cladistics* 17, 282–284.

Shaw1998 Shaw, K. L. (1998). Species and the diversity of natural groups. In D. J. Howard and S. H. Berlocher (Eds.), *Endless Forms: Species and Speciation.*, pp. 44–56. Oxford, UK: Oxford University Press.

Sheehan, S., K. Harris, and Y. S. Song (2013). Estimating variable effective population sizes from multiple genomes: A sequentially markov conditional sampling distribution approach. *Genetics* 194(3), 647–662.

Shlyakhter 2014 Shlyakhter, I., P. C. Sabeti, and S. F. Schaffner (2014). Cosi2: an efficient simulator of exact and approximate coalescent with selection. *Bioinformatics* 30(23), 3427–3429.

Simon C., T. R. Buckley, F. Frati, J. B. Stewart, and A. T. Beckenbach (2006). Incorporating molecular evolution into phylogenetic analysis, and a new compilation of conserved polymerase chain reaction primers for animal mitochondrial DNA. Annual Review of Ecology Evolution and Systematics 37, 545–579.

Simon, C., F. Frati, A. Beckenbach, B. Crespi, H. Liu, and P. Flook (1994). Evolution, weighting, and phylogenetic utility of mitochondrial gene sequences and a compilation of conserved polymerase chain reaction primers. *Annals of the Entomological Society of America* 87(6), 651–701.

Skouras, K. (1998). Absolute continuity of markov chains. *Journal of Statistical Planning and Inference* 75, 1–8.

Slowinski, J. B. (1990). Probabilities of n-trees under two models: a demonstration that asymmetrical interior nodes are not improbable. Systematic Zoology 39(1), 89–94.

Smith, C. I. (2007). Historical biogeography: The new synthesis. Current Biology 17, 598–600.

Smythe, R. T. (1996). Central limit theorems for urn models. Stochastic Processes and their Applications 65, 115–137.

Sokal, R. and C. Michener (1958). A statistical method for evaluating systematic relationships. *University of Kansas Science Bulletin* 38 (22), 1409–1438.

Song 2005 Song, Y. S. and J. Hein (2005, March). Constructing minimal ancestral recombination graphs. *Journal of Computational Biology* 12(2), 147–169.

Staab2015scrm Staab, P. R., S. Zhu, D. Metzler, and G. Lunter (2015). scrm: efficiently simulating long sequences using the approximated coalescent with recombination.

Bioinformatics 31(10), 1680–1682.

Steel, M. and K. M. Pickett (2006). On the impossibility of uniform priors on clades. *Molecular Phylogenetics and Evolution* 39, 585–586.

Steel, M. A. (1993). Distributions on bicoloured binary trees arising from the principle of parsimony. *Discrete Applied Mathematics* 43, 245–261.

Steel2012 Steel, M. A. (2012). Root location in random trees: A polarity property of all sampling consistent phylogenetic models except one. *Molecular Phylogenetics* and Evolution 65(1), 345 – 348.

Steel Steel, M. A. and A. McKenzie (2001). Properties of phylogenetic trees generated by yule-type speciation models. *Mathematical Biosciences* 170, 91–112.

Steel, M. A. and D. Penny (1993). Distributions of tree comparison metrics – some new results. Systematic Biology 42(2), 126–141.

Steel Steel, M. A. and A. Rodrigo (2008, Apr). Maximum likelihood supertrees.

Systematic Biology 57(2), 243–250.

Sage 2011 Stein, W. et al. (2011). Sage Mathematics Software (Version 4.7). The Sage Development Team. http://www.sagemath.org.

Strimmer, K., N. Goldman, and A. von Haeseler (1997). Bayesian probabilities and quartet puzzling. *Molecular Biology and Evolution* 2(14), 210–211.

Strimmer1996nj Strimmer, K. and A. von Haeseler (1996a, Dec). Accuracy of neighbor joining for n-taxon trees. Systematic Biology 45(4), 516–523.

Strimmer1996 Strimmer, K. and A. von Haeseler (1996b). Quartet puzzling: a quartet maximum-likelihood method for reconstructing tree topologies. *Molecular Biology and Evolution* 13(7), 964–969.

Tajima, F. (1983). Evolutionary relationship of DNA sequences in finite populations. *Genetics* 105, 437–460.

Takacs1991 Takács, L. (1991). A bernoulli excursion and its various applications. Advances in Applied Probability 23(3), 557–585.

Takahata, N. and M. Nei (1985). Gene genealogy and variance of interpopulational nucleotide differences. *Genetics* 110, 325–344.

Tallmon, D. A., G. Luikart, and M. A. Beaumont (2004). Comparative evaluation of a new effective population size estimator based on approximate Bayesian computation. *Genetics* 167(2), 977–988.

Tavaré, S. (1984). Line-of-descent and genealogical processes and their applications in population genetics models. *Theoretical Population Biology* 26(2), 119–164.

Tellier14 Tellier, A. and C. Lemaire (2014). Coalescence 2.0: a multiple branching of recent theoretical developments and their applications. *Mol Ecol* 23, 2637–2652.

Than C. and L. Nakhleh (2009). Species tree inference by minimizing deep coalescences. *PLoS Computational Biology* 5(9), 12.

Than 2008 Than, C., D. Ruths, and L. Nakhleh (2008). PhyloNet: A software package for analyzing and reconstructing reticulate evolutionary relationships. *BMC Bioinformatics* 9, 322.

Valiente 2002 algorithms Valiente, G. (2002). Algorithms on Trees and Graphs. Berlin, Germany: Springer.

van Iersel, L., J. Keijsper, S. Kelk, L. Stougie, F. Hagen, and T. Boekhout (2008). Constructing level-2 phylogenetic networks from triplets. *Annual International Conference on Research in Computational Molecular Biology* 2008. LNCS 4955, 450–462.

Verdu2013 Verdu, P., N. S. Becker, A. Froment, M. Georges, V. Grugni, L. Quintana-Murci, J.-M. Hombert, L. Van der Veen, S. Le Bomin, S. Bahuchet, E. Heyer, and F. Austerlitz (2013). Sociocultural behavior, sex-biased admixture, and effective population sizes in central African Pygmies and Non-Pygmies. *Molecular Biology and Evolution* 30(4), 918–937.

Vinh, L. S., A. Fuehrer, and A. von Haeseler (2011). Random tree-puzzle leads to the Yule–Harding distribution. *Molecular Biology and Evolution* 28(2), 873–877.

Wakeley, J. (2008). Coalescent theory: An Introduction. Greenwood Village, CO: Roberts and Co.

Wakeley, J. and J. Hey (1997). Estimating ancestral population parameters.

Genetics 145, 847–855.

Watterson, G. (1975). On the number of segregating sites in genetical models without recombination. Theoretical Population Biology 7(2), 256 – 276.

Watterson, G. A. (1984). Lines of descent and the coalescent. Theoretical Population Biology (26), 77–92.

Wegmann, D. and L. Excoffier (2010). Bayesian inference of the demographic history of chimpanzees. *Molecular Biology and Evolution* 27(6), 1425–1435.

- Wheeler, W. C. and K. M. Pickett (2008). Topology-bayes versus clade-bayes in phylogenetic analysis. *Molecular Biology and Evolution* 25(2), 447–453.
 - Wiens, J. J. and M. R. Servedio (2000, Apr). Species delimitation in systematics: inferring diagnostic differences between species. *The Royal society Biological Science* 267(1444), 631–636.
- Wilkinson, M., J. O. McInerney, R. P. Hirt, P. G. Foster, and T. M. Embley (2007). Of clades and clans: terms for phylogenetic relationships in unrooted trees. *Trends in Ecology and Evolution* 22(3), 114–115.
 - Wiuf, C. and J. Hein (1997). On the number of ancestors to a DNA sequence.

 Genetics 147, 1459–1468.
 - Wiuf 1999 Wiuf, C. and J. Hein (1999). Recombination as a point process along sequences.

 Theoretical Population Biology 55(3), 248–259.
 - Wright, S. (1931). Evolution in mendelian populations. Genetics 16, 97–159.
 - Wu, Y. (2012). Coalescent-based species tree inference from gene tree topologies under incomplete lineage sorting by maximum likelihood. *Evolution* 66(3), 763–775.
 - Xifara, D. K., I. Mathieson, and G. McVean (0000). The detection, structure and uses of extended haplotype identity in population genetic data. $unknown \ \theta(0)$, 0.
 - Yang Z. (2006). Computational Molecular Evolution. Oxford: Oxford University Press.
 - Yang Yang, Z. (2010). A likelihood ratio test of speciation with gene flow using genomic sequence data. Genome Biology and Evolution 2, 200–211.
 - Yang Z. and B. Rannala (2010). Bayesian species delimitation using multilocus sequence data. *Proceedings of the National Academy of Sciences of* U.S.A 107(20), 9264–9269.
 - Yu. Y., J. H. Degnan, and L. Nakhleh (2012). The probability of a gene tree topology within a phylogenetic network with applications to hybridization detection. *PLoS Genet.* 8, e1002660.
 - Yu, Y., C. Than, J. H. Degnan, and L. Nakhleh (2011). Coalescent histories on phylogenetic networks and detection of hybridization despite incomplete lineage sorting. Systematic Biology 60(2), 138–149.
 - Yule, G. U. (1925). A mathematical theory of evolution. based on the conclusions of Dr. J.C. Willis, F.R.S. In *Philosophical Transactions of the Royal Society of London. Series B, Containing Papers of a Biological Character*, Volume 213, pp. 21–87. The Royal Society.

Zhang2011

Zhang, C., D. Zhang, T. Zhu, and Z. Yang (2011). Evaluation of a bayesian coalescent method of species delimitation. *Systematic Biology* 60, 747–761.

Zhu2013phd

Zhu, S. (2013). Stochastic tree models and probabilistic modelling of gene trees of given species networks. Ph. D. thesis, Department of Mathematics, University of Canterbury, Christchurch, New Zealand.

Zhu2010poster

Zhu, S. and J. H. Degnan (2010). Effect of taxon sampling on constructing species tree from gene trees. Poster, http://www.math.canterbury.ac.nz/s.zhu/my_files/taxon.pdf.

Zhu2013sim

Zhu, S., J. H. Degnan, and B. Eldon. Hybrid-lambda: simulation of multiple merger and kingman gene genealogies in species networks and species trees. arxiv.org/abs/1303.0673.

Zhu2015HybridLambda

Zhu, S., J. H. Degnan, S. J. Goldstien, and B. Eldon (2015). Hybrid-lambda: simulation of multiple merger and kingman gene genealogies in species networks and species trees. *BMC Bioinformatics* 16 (292). doi:10.1186/s12859-015-0721-y.

Zhu2011clade

Zhu, S., J. H. Degnan, and M. A. Steel (2011a). Clades, clans and reciprocal monophyly under neutral evolutionary models. *Theoretical Population Biology* 79, 220–227.

Zhu2011poster

Zhu, S., J. H. Degnan, and M. A. Steel (2011b). Probabilistic modeling of gene trees given species networks. Poster, http://www.newton.ac.uk/programmes/PLG/Zhu.pdf. Feb 21, 2013.

Zhu2013tp

Zhu, S. and M. A. Steel (2013). Does random tree puzzle produce Yule–Harding trees in the many-taxon limit? *Mathematical Biosciences* 243(1), 109–116.

Zhu2014pda

Zhu, S., C. Than, and T. Wu (2014). Clades and clans: a comparison study of two evolutionary models. *Journal of Mathematical Biology*, 1–26.

Zhu2012MBE

Zhu, T. and Z. Yang (2012). Maximum likelihood implementation of an isolation-with-migration model with three species for testing speciation with gene flow. *Molecular Biology and Evolution*.

Zilversmit2013

Zilversmit, M., E. Chase, D. Chen, P. Awadalla, K. Day, and G. McVean (2013). Hypervariable antigen genes in malaria have ancient roots. BMC Evolutionary Biology 13(1), 110.

Zwickl2002

Zwickl, D. J. and D. M. Hills (2002, Aug). Increased taxon sampling greatly reduces phylogenetic error. *Systematic Biology* 51(4), 588–598.