

### 7.3 Bibliography

- Adams, K.L., & Palmer, J.D. (2003). *Evolution of mitochondrial gene content: gene loss and transfer to the nucleus*. *Molecular Phylogenetics and Evolution*, 29(3), 380-395.
- Alberts, B., Johnson, A., Lewis, J., Raff, M., Roberts, K. and Walter, P. (2007). *Molecular Biology of the Cell* (5th ed.). New York, NY.: Garland Science
- Boore, J.L. (1999). *Animal mitochondrial genomes*. *Nucleic Acids Research*, 27(8), 1767-1780.
- Boore, J.L., & Brown, W.M. (1998). *Big trees from little genomes: mitochondrial gene order as a phylogenetic tool*. *Current Opinion in Genetics & Development*, 8(6), 668-674.
- Burger, G., Gray, M.W., & Lang, B.F. (2003). *Mitochondrial genomes: anything goes*. *Trends in Genetics*, 19(12), 709-716.
- Efron, B. (1982). *The jackknife, the bootstrap, and other resampling plans*. Philadelphia, Pa.: Society for Industrial and Applied Mathematics.
- Efron, B. and Tibshirani, R. J. (1993). *An Introduction to the Bootstrap* (1st ed.). New York, NY.: Chapman and Hall/CRC
- Felsenstein, J. (1985). *Confidence-Limits on Phylogenies - an Approach Using the Bootstrap*. *Evolution*, 39(4), 783-791.
- Felsenstein, J., & Kishino, H. (1993). *Is There Something Wrong with the Bootstrap on Phylogenies - a Reply*. *Systematic Biology*, 42(2), 193-200.
- Hillis, D.M., & Bull, J.J. (1993). *An Empirical-Test of Bootstrapping as a Method for Assessing Confidence in Phylogenetic Analysis*. *Systematic Biology*, 42(2), 182-192.
- Hu, P., Geles, K.G., Paik, J.H., DePinho, R.A., & Tjian, R. (2008). *Codependent activators direct myoblast-specific MyoD transcription*. *Dev Cell*, 15(4), 534-546.
- Jameson, D., Gibson, A.P., Hudelot, C. & Higgs, P.G. (2003) *OGRe: a relational database for comparative analysis of mitochondrial genomes*. *Nucl. Acids. Res.* 31, 202-206.
- Knight, R., Maxwell, P., Birmingham, A., Carnes, J., *et. al.* (2007). *PyCogent: a toolkit for making sense from sequence*. *Genome Biology*, 8(8).
- Kumar, S., Nei, M., Dudley, J., & Tamura, K. (2008). *MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences*. *Briefings in Bioinformatics*, 9(4), 299-306.
- Maddison, W.P. (1997). *Gene trees in species trees*. *Systematic Biology*, 46(3), 523-536.
- Paradis, E., Claude, J., & Strimmer, K. (2004). *APE: Analyses of Phylogenetics and Evolution in R language*. *Bioinformatics*, 20(2), 289-290.
- Perelman, P., Johnson, W.E., Roos, C., Seuanez, H.N., Horvath, J.E., Moreira, M.A., *et. al.* (2011). *A molecular phylogeny of living primates*. *PLoS Genet*, 7(3), e1001342.

Queiroz, A. and Wimberger P. (2009). *The Usefulness of Behavior for Phylogeny Estimation : Levels of Homoplasy in Behavioral and Morphological Characters*. Society, 47(1), 46-60.

R Development Core Team (2012). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL <http://www.R-project.org/>.

Schliep, K.P. (2011). *phangorn: phylogenetic analysis in R*. Bioinformatics, 27(4), 592-593.

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., & Kumar, S. (2011). *MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods*. Molecular Biology and Evolution, 28(10), 2731-2739.

Venter, J.C., Adams, M.D., Myers, E.W., Li, P.W., *et. al.* (2001). *The sequence of the human genome*. Science, 291(5507), 1304-1351.