- Gavranovic, H., Tannier, E., 2010. Guided genome halving: Provably optimal solutions provide good insights into the preduplication ancestral genome of *Saccharomyces cerevisiae*. Pacific Symposium on Biocomputing 15, 21–30.
- Groussin, M., Boussau, B., Gouy, M., 2013. A branch-heterogeneous model of protein evolution for efficient inference of ancestral sequences. Systematic Biology 62, 523–538.
- Groussin, M., Hobbs, J.K., Szollosi, G.J., et al., 2015. Toward more accurate ancestral protein genotype—phenotype reconstructions with the use of species tree-aware gene trees. Molecular Biology and Evolution 32 (1), 13–22.
- Gueguen, L., Gaillard, S., Boussau, B., *et al.*, 2013. Bio++: Efficient extensible libraries and tools for computational molecular evolution. Molecular Biology and Evolution 30, 1745–1750.
- Gorecki, P., Tiuryn, J., 2006. DLS-trees: A model of evolutionary scenarios. Theoretical Computer Science 359, 378–399.
- Harmon, L.J., Losos, J.B., Davies, J., et al., 2010. Early bursts of body size and shape evolution are rare in comparative data. Evolution 64, 2385–2396.
- Huelsenbeck, J.P., Larget, B., Miller, R.E., Ronquist, F., 2002. Potential applications and pitfalls of Bayesian inference of phylogeny. Systematic Biology 51 (5), 673–688.
- Jaillon, O., Aury, J.-M., Brunet, F., et al., 2004. Genome duplication in the teleost fish *Tetraodon nigroviridis* reveals the early vertebrate proto-karyotype. Nature 431, 946–957.
- Kohn, M., Hogel, J., Vogel, W., et al., 2006. Reconstruction of a 450-My-old ancestral vertebrate protokaryotype. Trends in Genetics 22, 203–210.
- Lafond, M., Semeria, M., Swenson, K.M., Tannier, E., El-Mabrouk, N., 2013. Gene tree correction guided by orthology. BMC Bioinformatics 14 (Suppl. 15), S5.
- Larget, B., Kadane, J.B., Simon, D.L., 2005. A Bayesian approach to the estimation of ancestral genome arrangements. Molecular Phylogenetics and Evolution 36 (2), 214–223.
- Liberles, D.A., 2007. Ancestral Sequence Reconstruction. Oxford: Oxford University Press
- Louis, A., Muffato, M., Roest Crollius, H., 2013. Genomicus: Five genome browsers for comparative genomics in eukaryota. Nucleic Acids Research 41, D700–D705 (Database issue).
- Loytynoja, A., Goldman, N., 2008. Phylogeny-aware gap placement prevents errors in sequence alignment and evolutionary analysis. Science 320 (5883), 1632–1635.
- Lunter, G., Mikloos, I., Drummond, A., Jensen, J.L., Hein, J., 2005. Bayesian coestimation of phylogeny and sequence alignment. BMC Bioinformatics 6, 83.
- Ma, J., Zhang, L., Suh, B., et al., 2006. Reconstructing contiguous regions of an ancestral genome. Genome Research 16, 1557–1565.
- Ma, J., Ratan, A., Raney, B., et al., 2008. DUPCAR: Reconstructing contiguous ancestral regions with duplications. Journal of Computational Biology 15, 1007–1027.
- Maddison, W.P., 1997. Gene trees in species trees. Systematic Biology 46 (3), 523–536.
- Maddison, W.P., Midford, P.E., Otto, S.P., 2007. Estimating a binary character's effect on speciation and extinction. Systematic Biology 56, 701–710.
- Martins, E.P., 1994. Estimating the rate of phenotypic evolution from comparative data. The American Naturalist 144, 193–209.
- Martins, E.P., 1999. Estimation of ancestral states of continuous characters: A computer simulation study. Systematic Biology 48, 642–650.
- Martins, E.P., Hansen, T.F., 1997. Phylogenies and the comparative method: A general approach to incorporating phylogenetic information into the analysis of interspecific data. American Naturalist 149, 646–667.
- Manuch, J., Patterson, M., Wittler, R., Chauve, C., Tannier, E., 2012. Linearization of ancestral multichromosomal genomes. BMC Bioinformatics 13 (Suppl. 19), S11.
- Mikloos, I., Kiss, S.Z., Tannier, E., 2014. Counting and sampling SCJ small parsimony solutions. Theoretical Computer Science 552, 83–98.
- Nakatani, Y., Takeda, H., Morishita, S., 2007. Reconstruction of the vertebrate ancestral genome reveals dynamic genome reorganization in early vertebrates. Genome Research 17, 1254–1265.
- Nakhleh, L., Ruths, D., Wang, L.-S., 2005. RL4TA-HGT: A Fast and Accurate Heuristic for Reconstructing Horizontal Gene Transfer. Berlin Heidelberg: Springer-Verlag.
- Naruse, K., Tanaka, M., Mita, K., et al., 2004. A medaka gene map: The trace of ancestral vertebrate proto-chromosomes revealed by comparative gene mapping. Genome Research 14, 820–828.
- Pagel, M., 1994. Detecting correlated evolution on phylogenies: A general method for the comparative analysis of discrete characters. Proceedings of the Royal Society of London. Series B, Biological Sciences 255, 37–45.
- Pagel, M., Meade, A., Barker, D., 2004. Bayesian estimation of ancestral character states on phylogenies. Systematic Biology 53 (5), 673–684.
- Paradis, E., Claude, J., Strimmer, K., 2004. Ape: Analyses of phylogenetics and evolution in R language. Bioinformatics 20, 289–290.

- Patterson, M., Szollosi, G., Daubin, V., Tannier, E., 2013. Lateral gene transfer, rearrangement, reconciliation. BMC Bioinformatics 14 (Suppl. 15), S4.
- Pauling, L., Zuckerkandl, E., 1963. Chemical paleogenetics, molecular restoration studies of extinct forms of life. Acta Chemica Scandinavica 17, S9–S16.
- Pupko, T., Pe'er, I., Hasegawa, M., Graur, D., Friedman, N., 2002. A branch-and-bound algorithm for the inference of ancestral amino-acid sequences when the replacement rate varies among sites: Application to the evolution of five gene families. Bioinformatics 18 (8), 1116–1123.
- Putnam, N., Butts, T., Ferrier, D., *et al.*, 2008. The amphioxus genome and the evolution of the chordate karyotype. Nature 453, 1064–1071.
- Putnam, N.H., Srivastava, M., Hellsten, U., et al., 2007. Sea anemone genome reveals ancestral eumetazoan gene repertoire and genomic organization. Science 317, 86–94
- Rajaraman, A., Tannier, E., Chauve, C., 2013. FPSAC: Fast phylogenetic scaffolding of ancient contigs. Bioinformatics 29 (23), 2987–2994.
- Sankoff, D., 1975. Minimal mutation trees of sequences. SIAM Journal on Applied Mathematics 28 (1), 35–42.
- Sankoff, D., El-Mabrouk, N., 2000. Duplication, rearrangement and reconciliation. In: Sankoff, D., Nadeau, J.H. (Eds.), Comparative Genomics: Empirical and Analytical Approaches to Gene Order Dynamics, Map alignment and the Evolution of Gene Families, vol. 1. Dordrecht: Kluwer Academic Publishers, pp. 537–550.
- Sankoff, D., Zheng, C., Wall, P.K., et al., 2009. Towards improved reconstruction of ancestral gene order in angiosperm phylogeny. Journal of Computational Biology 16 (10), 1353–1367.
- Schluter, D., Price, T., Mooers, A.O., Ludwig, D., 1997. Likelihood of ancestor states in adaptive radiation. Evolution 51, 1699–1711.
- Sjostrand, J., Tofigh, A., Daubin, V., *et al.*, 2014. A Bayesian method for analyzing lateral gene transfer. Systematic Biology 63 (3), 409–420.
- Sturtevant, A., Tan, C., 1937. The comparative genetics of *Drosophila pseudoobscura* and *D. melanogaster*. Journal of Genetics 34 (3), 415–432.
- Suchard, M.A., Redelings, B.D., 2006. BAli-Phy: Simultaneous Bayesian inference of alignment and phylogeny. Bioinformatics 22 (16), 2047–2048.
- Svartman, M., Stone, G., Stanyon, R., 2006. The ancestral eutherian karyotype is present in xenarthra. PLoS Genetics 2, e109.
- Szollosi, G.J., Daubin, V., 2012. Modeling gene family evolution and reconciling phylogenetic discord. In: Anisimova, M. (Ed.), Evolutionary Genomics, vol. 856. New York, NY: Humana Press, pp. 29–51.
- Szollosi, G.J., Boussau, B., Abby, S.S., Tannier, E., Daubin, V., 2012. Phylogenetic modeling of lateral gene transfer reconstructs the pattern and relative timing of speciations. Proceedings of the National Academy of Sciences 109 (43), 17513–17518.
- Szollosi, G.J., Tannier, E., Lartillot, N., Daubin, V., 2013. Lateral gene transfer from the dead. Systematic Biology 62 (3), 386–397.
- Tamura, K., Peterson, D., Peterson, N., et al., 2011. MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Molecular Biology and Evolution 28 (10), 2731–2739.
- Than, C., Nakhleh, L., 2008. SPR-based tree reconciliation: Non-binary trees and multiple solutions. Proceedings of the 6th Asia-Pacific Bioinformatics Conference, Kyoto, Japan: APBC 2008.
- Tofigh, A., 2009. Using trees to capture reticulate evolution. PhD Thesis, KTH School of Computer Science and Communication.
- Wang, Y., Li, W., Zhang, T., *et al.*, 2006. Reconstruction of ancient genome and gene order from complete microbial genome sequences. Journal of Theoretical Biology 239 (4), 494–498.
- Woods, I., Wilson, C., Friedlander, B., *et al.*, 2005. The zebrafish gene map defines ancestral vertebrates chromosomes. Genome Research 15, 1307–1314.
- Xia, X., 2013. DAMBE5: A comprehensive software package for data analysis in molecular biology and evolution. Molecular Biology and Evolution 30 (7), 1720–1728.
- Yancopoulos, S., Attie, O., Friedberg, R., 2005. Efficient sorting of genomic permutations by translocation, inversion and block interchange. Bioinformatics 21 (16), 3340–3346.
- Yang, Z., 2006. Computational Molecular Evolution. Oxford: Oxford University Press. vol. 284.
- Yang, Z., 2007. PAML4: Phylogenetic analysis by maximum likelihood. Molecular Biology and Evolution 24 (8), 1586–1591.
- Yang, Z., Kumar, S., Nei, M., 1995. A new method of inference of ancestral nucleotide and amino acid sequences. Genetics 141 (4), 1641–1650.
- Zhang, J., Nei, M., 1997. Accuracies of ancestral amino acid sequences inferred by the parsimony, likelihood, and distance methods. Journal of Molecular Evolution 44 (1), S139–S146.
- Zheng, C., Sankoff, D., 2013. Practical aliquoting of flowering plant genomes. BMC Bioinformatics 14 (Suppl. 15), S8.