

References cited

- Chindelevitch L, Li Z, Blais E, Blanchette M. 2006. On the inference of parsimonious evolutionary scenarios. *J Bioinform Comput Biol.* 4:721-744.
- Diallo AB, Makarenkov V, Blanchette M. 2007. Exact and heuristic algorithms for the indel maximum likelihood problem. *J Comput Biol.* 14:446-461.
- Ezawa K. 2016a. Characterization of multiple sequence alignment errors using complete-likelihood score and position-shift map. *BMC Bioinformatics.* 17:133.
- Ezawa K. (unpublished A) 2016b. General continuous-time Markov model of sequence evolution via insertions/deletions: Are alignment probabilities factorable? *BMC Bioinformatics.* 17:304; Erratum, 17:457.
- Ezawa K. (unpublished B) 2016c. General continuous-time Markov model of sequence evolution via insertions/deletions: Local alignment probability computation. *BMC Bioinformatics* 17:397.
- Ezawa, Graur and Landan. (Part I). Perturbative formulation of general continuous-time Markov model of sequence evolution via insertions/deletions, Part I: Theoretical basis. *bioRxiv.* 2015. doi:10.1101/023598. Accessed 4 Aug 2015.
- Ezawa, Graur and Landan. (Part II). Perturbative formulation of general continuous-time Markov model of sequence evolution via insertions/deletions, Part II: Perturbation analyses. *bioRxiv.* 2015. doi:10.1101/023606. Accessed 4 Aug 2015.
- Ezawa, Graur and Landan. (Part III). Perturbative formulation of general continuous-time Markov model of sequence evolution via insertions/deletions, Part III: Algorithm for first approximation. *bioRxiv.* 2015. doi:10.1101/023614. Accessed 4 Aug 2015.
- Farris JS. 1977. Phylogenetic analysis under Dollo's law. *Syst Zool.* 26:77-88
- Felsenstein J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. *J Mol Evol.* 17:368-376.
- Felsenstein J. 2004. *Inferring Phylogenies.* Sunderland (MA): Sinauer Associates.
- Gotoh O. 1996. Significant improvement in accuracy of multiple protein sequence alignments by iterative refinement as assessed by reference to structural alignments. *J Mol Biol.* 264:823-838.
- Holmes I, Bruno WJ. 2001. Evolutionary HMMs: a Bayesian approach to multiple sequence alignment. *Bioinformatics* 17:803-820.
- Landan G, Graur D. 2009. Characterization of pairwise and multiple sequence alignment errors. *Gene* 441:141-147.
- Lunter G. 2007. Probabilistic whole-genome alignments reveal high indel rates in the human and mouse genomes. *Bioinformatics* 23:i289-i296.
- Novák Á, Miklós I, Lyngsø R, Hein J. 2008. StatAlign: an extendable software package for joint Bayesian estimation of alignments and evolutionary trees. *Bioinformatics* 24:2403-2404.

Suchard MA, Redelings BD. 2006. BAli-Phy: simultaneous Bayesian inference of alignment and phylogeny. *Bioinformatics* 22:2047-2048.

Yang Z. 2006. Computational Molecular Evolution. New York (NY): Oxford University Press.

Yang Z. 2007. PAML: a program package for phylogenetic analysis by maximum likelihood. *Mol Biol Evol.* 24:1586-1591.