

List of publications

Siavash Mirarab

February 22, 2016

1. Erfan Sayyari and **Siavash Mirarab**. Fast coalescent-based computation of local branch support from quartet frequencies. *arXiv (sub. to MBE)*, 1601.07019, 2016.
2. Erfan Sayyari and **Siavash Mirarab**. Anchored distances for quartet-based estimation of phylogenetic trees under coalescent model. *In prep.*, 2016.
3. James E Tarver, Mario Dos Reis, **Siavash Mirarab**, Raymond J Moran, Sean Parker, Joseph E O'Reilly, Benjamin L King, Mary J O'Connell, Robert J Asher, Tandy Warnow, Kevin J Peterson, Philip C J Donoghue, and Davide Pisani. The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. *Genome biology and evolution*, page evv261, jan 2016.
4. **Siavash Mirarab**, Md. Shamsuzzoha Bayzid, Bastien Boussau, and Tandy Warnow. Response to Comment on “Statistical binning enables an accurate coalescent-based estimation of the avian tree”. *Science*, 350(6257):171, 2015.
5. Joel Cracraft, Peter Houde, Simon Y W Ho, David P Mindell, Jon Fjeldså, Bent Lindow, Scott V Edwards, Carsten Rahbek, **Siavash Mirarab**, Tandy Warnow, M Thomas P Gilbert, Guojie Zhang, Edward L Braun, and Erich D Jarvis. Response to Comment on “Whole-genome analyses resolve early branches in the tree of life of modern birds”. *Science*, 349(6255):1460, 2015.
6. Ruth Davidson, Pranjali Vachaspati, **Siavash Mirarab**, and Tandy Warnow. Phylogenomic species tree estimation in the presence of incomplete lineage sorting and horizontal gene transfer. *BMC Genomics*, 16(Suppl 10):S1, 2015.
7. Jed Chou, Ashu Gupta, Shashank Yaduvanshi, Ruth Davidson, Mike Nute, **Siavash Mirarab**, and Tandy Warnow. A comparative study of SVDquartets and other

- coalescent-based species tree estimation methods. *BMC Genomics*, 16(Suppl 10):S2, 2015.
8. **Siavash Mirarab** and Tandy Warnow. ASTRAL-II: coalescent-based species tree estimation with many hundreds of taxa and thousands of genes. *Bioinformatics*, 31(12):i44–i52, 2015.
 9. Nam Nguyen, **Siavash Mirarab**, Keerthana Kumar, and Tandy Warnow. Ultra-large alignments using phylogeny-aware profiles. *Genome Biology*, 16(1):124, 2015.
 10. Md Shamsuzzoha Bayzid, **Siavash Mirarab**, Bastien Boussau, and Tandy Warnow. Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. *PLoS ONE*, 10(6):e0129183, 2015.
 11. (Erich D Jarvis, **Siavash Mirarab**)*, 100 other authors, Edward L Braun, Tandy Warnow, Wang Jun, M Thomas P Gilbert, and Guojie Zhang. Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science*, 346(6215):1320–1331, 2014.
 12. **Siavash Mirarab**, Md. Shamsuzzoha Bayzid, Bastien Boussau, and Tandy Warnow. Statistical binning enables an accurate coalescent-based estimation of the avian tree. *Science*, 346(6215):1250463, 2014.
 13. (Norman J. Wickett, **Siavash Mirarab**)*, Nam Nguyen, Tandy Warnow, Eric Carpenter, Naim Matasci, Saravanaraj Ayyampalayam, Michael Barker, J. Gordon Burleigh, Matthew A. Gitzendanner, Brad R. Ruhfel, Eric Wafula, Joshua P. Der, Sean W. Graham, Sarah Mathews, Michael Melkonian, Douglas E. Soltish, Pamela S. Soltish, Nicholas W. Miles, Carl J. Rothfels, Lisa Pokorny, A. Jonathan Shaw, Lisa DeGironimo, Dennis W. Stevenson, Barbara Surek, Juan Carlos Villarreal, Béatrice Rourev, Hervé Philippe, Claude W. dePamphilis, Tao Chen, Michael K. Deyholos, Regina S. Baucom, Toni M. Kutchan, Megan M. Augustin, Jun Wang, Yong Zhang, Zhijian Tian, Zhixiang Yan, Xiaolei Wu, Xiao Sun, Gane Ka-Shu Wong, and James Leebens-Mack. Phylotranscriptomic analysis of the origin and early diversification of land plants. *Proceedings of the National Academy of Sciences (PNAS)*, 111(45):E4859–4868, 2014.

14. **Siavash Mirarab**, Md. Shamsuzzoha Bayzid, and Tandy Warnow. Evaluating summary methods for multi-locus species tree estimation in the presence of incomplete lineage sorting. *Systematic Biology*, doi: 10.1093/sysbio/syu063, 2014.
15. **Siavash Mirarab**, Nam Nguyen, Sheng Guo, Li-San Wang, Junhyong Kim, and Tandy Warnow. PASTA: Ultra-Large Multiple Sequence Alignment for Nucleotide and Amino-Acid Sequences. *Journal of Computational Biology*, 22(05):377–386, 2015.
16. **Siavash Mirarab**, Nam Nguyen, and Tandy Warnow. PASTA: ultra-large multiple sequence alignment. In *Proceedings of the 18th International Conference on Research in Computational Molecular Biology (RECOMB)*, pages 177–191, 2014.
17. **Siavash Mirarab**, Rezwana Reaz, Md. Shamsuzzoha Bayzid, Théo Zimmermann, M Shel Swenson, and Tandy Warnow. ASTRAL: Genome-Scale Coalescent-Based Species Tree. *Bioinformatics - ECCB Special Issue*, 30(17):i541–i548, 2014.
18. Nam Nguyen, **Siavash Mirarab**, Bo Liu, Mihai Pop, and Tandy Warnow. TIPP: Taxonomic identification and phylogenetic profiling. *Bioinformatics*, doi: 10.1093/bioinformatics/btu721(24), 2014.
19. Théo Zimmermann, **Siavash Mirarab**, and Tandy Warnow. BBKA: improving the scalability of *BEAST using random binning. *BMC Genomics*, 15(Suppl 6):S11, 2014.
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23. **Siavash Mirarab**, Nam Nguyen, and Tandy Warnow. SEPP: SATé-Enabled Phylogenetic Placement. In *Proceedings of the Pacific Symposium on Biocomputing (PSB)*, pages 247–58, 2012.
24. **Siavash Mirarab**, Soroush Akhlaghi, and Ladan Tahvildari. Size-constrained regression test case selection using multicriteria optimization. *IEEE Transactions on Software Engineering*, 38(4):936–956, 2012.
25. **Siavash Mirarab** and Tandy Warnow. FastSP: linear time calculation of alignment accuracy. *Bioinformatics*, 27:3250–8, 2011.
26. Hyunsook Do, **Siavash Mirarab**, Ladan Tahvildari, and Gregg Rothermel. The effects of time constraints on test case prioritization: A series of controlled experiments. *IEEE Transactions on Software Engineering*, 36(5):593–617, 2010.
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29. Hyunsook Do, **Siavash Mirarab**, Ladan Tahvildari, and Gregg Rothermel. An empirical study of the effect of time constraints on the cost-benefits of regression testing. In *Proceedings of the 16th ACM SIGSOFT International Symposium on Foundations of Software Engineering (FSE)*, pages 71–82. ACM, 2008.
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32. **Siavash Mirarab**, Alaa Hassouna, and Ladan Tahvildari. Using bayesian belief networks to predict change propagation in software systems. In *Proceedings of the 15th International Conference on Program Comprehension (ICPC)*, pages 177–188. IEEE, 2007.
33. Mehdi Amoui, **Siavash Mirarab**, Sepand Ansari, and Caro Lucas. A genetic algorithm approach to design evolution using design pattern transformation. *Journal of Information Technology and Intelligent Computing*, 1(2):235–244, 2006.