

List of publications

Siavash Mirarab

August 3, 2016

1. Erfan Sayyari and **Siavash Mirarab**. Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. *BMC Genomics*, in press, 2016.
2. Erfan Sayyari and **Siavash Mirarab**. Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies. *Molecular Biology and Evolution*, 33(7):1654–1668, 2016.
3. Nam Nguyen, Michael Nute, **Siavash Mirarab**, and Tandy Warnow. HIPPI: Highly Accurate Protein Family Classification with Ensembles of HMMs. *BMC Genomics*, in press, 2016.
4. 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, 2016.
5. **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.
6. 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.

7. 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.
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9. **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.
10. Nam Nguyen, **Siavash Mirarab**, Keerthana Kumar, and Tandy Warnow. Ultra-large alignments using phylogeny-aware profiles. *Genome Biology*, 16(1):124, 2015.
11. 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.
12. (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.
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14. (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,

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 16. **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.
 17. **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.
 18. **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.
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25. **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.
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the Fourth International Conference on Autonomic and Autonomous Systems (ICAS), pages 175–181. IEEE, 2008.

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33. **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.
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