

# List of publications

Siavash Mirarab

November 20, 2017

1. Niema Moshiri and **Siavash Mirarab**. A Two-State Model of Tree Evolution and its Applications to Alu Retrotransposition. *Systematic Biology*, syx088, 2017.
2. Erfan Sayyari, James B Whitfield, and **Siavash Mirarab**. Fragmentary Gene Sequences Negatively Impact Gene Tree and Species Tree Reconstruction. *Molecular Biology and Evolution*, msx261–msx261, 2017.
3. Luke R. Thompson, Jon G. Sanders, Daniel McDonald, Amnon Amir, Joshua Ladau, Kenneth J. Locey, Robert J. Prill, Anupriya Tripathi, Sean M. Gibbons, Gail Ackermann, Jose A. Navas-Molina, Stefan Janssen, Evguenia Kopylova, Yoshiki Vázquez-Baeza, Antonio González, James T. Morton, **Siavash Mirarab**, Zhenjiang Zech Xu, Lingjing Jiang, Mohamed F. Haroon, Jad Kanbar, Qiyun Zhu, Se Jin Song, Tomasz Kosciolk, Nicholas A. Bokulich, Joshua Lefler, Colin J. Brislawn, Gregory Humphrey, Sarah M. Owens, Jarrad Hampton-Marcell, Donna Berg-Lyons, Valerie McKenzie, Noah Fierer, Jed A. Fuhrman, Aaron Clauset, Rick L. Stevens, Ashley Shade, Katherine S. Pollard, Kelly D. Goodwin, Janet K. Jansson, Jack A. Gilbert, Rob Knight, and The Earth Microbiome Project Consortium. A communal catalogue reveals Earth’s multiscale microbial diversity. *Nature*, 2017.
4. Uyen Mai and **Siavash Mirarab**. TreeShrink: Efficient Detection of Outlier Tree Leaves. In Joao Meidanis and Luay Nakhleh, editors, *Lecture Notes in Computer Science*, volume 10562 LNBI, 116–140. 2017.
5. Chao Zhang, Erfan Sayyari, and **Siavash Mirarab**. ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. In Joao Meidanis and Luay Nakhleh, editors, *Lecture Notes in Computer Science*, volume 10562 LNBI, 53–75. 2017.

6. Uyen Mai, Erfan Sayyari, and **Siavash Mirarab**. Minimum variance rooting of phylogenetic trees and implications for species tree reconstruction. *PLOS ONE*, 12(8):e0182238, 2017.
7. Shubhanshu Shekhar, Sebastien Roch, and **Siavash Mirarab**. Species tree estimation using ASTRAL: how many genes are enough? *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, PP(99):1–1, 2017.
8. **Siavash Mirarab**. Phylogenomics: Constrained gene tree inference. *Nature Ecology & Evolution*, 1:0056, 2017.
9. Erfan Sayyari and **Siavash Mirarab**. Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. *BMC Genomics*, 17(S10):101–113, 2016.
10. 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.
11. Nam Nguyen, Michael Nute, **Siavash Mirarab**, and Tandy Warnow. HIPPI: Highly Accurate Protein Family Classification with Ensembles of HMMs. *BMC Genomics*, in press, 2016.
12. 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*, evv261, 2016.
13. **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.
14. 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.

15. 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.
16. 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.
17. **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.
18. Nam Nguyen, **Siavash Mirarab**, Keerthana Kumar, and Tandy Warnow. Ultra-large alignments using phylogeny-aware profiles. *Genome Biology*, 16(1):124, 2015.
19. 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.
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21. 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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23. Naim Matasci, Ling-Hong Hung, Zhixiang Yan, Eric J Carpenter, Norman J Wickett, **Siavash Mirarab**, Nam Nguyen, Tandy Warnow, Saravanaraj Ayyampalayam, and

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31. Arlin Stoltzfus, Hilmar Lapp, Naim Matasci, Helena Deus, Brian Sidlauskas, Christian M Zmasek, Gaurav Vaidya, Enrico Pontelli, Karen Cranston, Rutger Vos, Campbell O Webb, Luke J Harmon, Megan Pirrung, Brian O’Meara, Matthew W Pennell, **Siavash Mirarab**, Michael S Rosenberg, James P Balhoff, Holly M Bik, Tracy A Heath, Peter E Midford, Joseph W Brown, Emily Jane McTavish, Jeet Sukumaran, Mark Westneat, Michael E Alfaro, Aaron Steele, and Greg Jordan. Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. *BMC bioinformatics*, 14(1):158, 2013.
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