

List of publications

Siavash Mirarab

March 15, 2019

1. Erfan Sayyari, Ban Kawas, and **Siavash Mirarab**. TADA : Phylogenetic augmentation of microbiome samples enhances phenotype classification. *Bioinformatics (ISMB special issue)*, accepted, 2019.
2. Maryam Rabiee and **Siavash Mirarab**. INSTRAL: Discordance-aware Phylogenetic Placement using Quartet Scores. *bioRxiv*, 432906, 2018.
3. Metin Balaban, Shahab Sarmashghi, and **Siavash Mirarab**. APPLES: Fast Distance-based Phylogenetic Placement. *bioRxiv (accepted for RECOMB 2019)*, 2018.
4. Shahab Sarmashghi, Kristine Bohmann, M. Thomas P. Gilbert, Vineet Bafna, and **Siavash Mirarab**. Skmer: assembly-free and alignment-free sample identification using genome skims. *Genome Biology*, 20(1):34, 2019.
5. Niema Moshiri, Manon Ragonnet-Cronin, Joel O Wertheim, and **Siavash Mirarab**. FAVITES: simultaneous simulation of transmission networks, phylogenetic trees, and sequences. *Bioinformatics*, bty921, 2018.
6. Maryam Rabiee, Erfan Sayyari, and **Siavash Mirarab**. Multi-allele species reconstruction using ASTRAL. *Molecular Phylogenetics and Evolution*, 130:286–296, 2019.
7. Daniel McDonald and American Gut Consortium. American Gut: an Open Platform for Citizen Science Microbiome Research. *mSystems*, 3(3), 2018.
8. Wolf L. Eiserhardt, Alexandre Antonelli, Dominic J. Bennett, Laura R. Botigué, J. Gordon Burleigh, Steven Dodsworth, Brian J. Enquist, Félix Forest, Jan T. Kim, Alexey M. Kozlov, Ilia J. Leitch, Brian S. Maitner, **Siavash Mirarab**, William H. Piel, Oscar A. Pérez-Escobar, Lisa Pokorny, Carsten Rahbek, Brody Sandel, Stephen A. Smith, Alexandros Stamatakis, Rutger A. Vos, Tandy Warnow,

and William J. Baker. A roadmap for global synthesis of the plant tree of life. *American Journal of Botany*, 105(3):614–622, 2018.

9. Stefan Janssen, Daniel McDonald, Antonio Gonzalez, Jose A. Navas-Molina, Lingjing Jiang, Zhenjiang Zech Xu, Kevin Winker, Deborah M. Kado, Eric Orwoll, Mark Manary, **Siavash Mirarab**, and Rob Knight. Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. *mSystems*, 3(3):e00021–18, 2018.
10. Chao Zhang, Maryam Rabiee, Erfan Sayyari, and **Siavash Mirarab**. ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. *BMC Bioinformatics*, 19(S6):153, 2018.
11. Uyen Mai and **Siavash Mirarab**. TreeShrink: fast and accurate detection of outlier long branches in collections of phylogenetic trees. *BMC Genomics*, 19(S5):272, 2018.
12. Erfan Sayyari and **Siavash Mirarab**. Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. *Genes*, 9(3):132, 2018.
13. Erfan Sayyari, James B. Whitfield, and **Siavash Mirarab**. DiscoVista: Interpretable visualizations of gene tree discordance. *Molecular Phylogenetics and Evolution*, 122:110–115, 2018.
14. Ali Akbari, Joseph J Vitti, Arya Iranmehr, Mehrdad Bakhtiari, Pardis C Sabeti, **Siavash Mirarab**, and Vineet Bafna. Identifying the favored mutation in a positive selective sweep. *Nature Methods*, 15(4):279–282, 2018.
15. Niema Moshiri and **Siavash Mirarab**. A Two-State Model of Tree Evolution and Its Applications to Alu Retrotransposition. *Systematic Biology*, 67(3):475–489, 2018.
16. Erfan Sayyari, James B Whitfield, and **Siavash Mirarab**. Fragmentary Gene Sequences Negatively Impact Gene Tree and Species Tree Reconstruction. *Molecular Biology and Evolution*, 34(12):3279–3291, 2017.
17. 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 Leffler, 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*, 551(7681), 2017.
18. Uyen Mai and **Siavash Mirarab**. TreeShrink: Efficient Detection of Outlier Tree Leaves. In *Lecture Notes in Computer Science*, volume 10562 LNBI, 116–140. 2017.
 19. Chao Zhang, Erfan Sayyari, and **Siavash Mirarab**. ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. In *Lecture Notes in Computer Science*, volume 10562 LNBI, 53–75. 2017.
 20. 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.
 21. 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.
 22. **Siavash Mirarab**. Phylogenomics: Constrained gene tree inference. *Nature Ecology & Evolution*, 1:0056, 2017.
 23. Erfan Sayyari and **Siavash Mirarab**. Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. *BMC Genomics*, 17(S10):101–113, 2016.
 24. 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.
 25. Nam-phuong Nguyen, Michael Nute, **Siavash Mirarab**, and Tandy Warnow. HIPPI: highly accurate protein family classification with ensembles of HMMs. *BMC Genomics*, 17(S10):765, 2016.

26. 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*, 8(2):330–344, 2016.
27. **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.
28. 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.
29. 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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34. Erich D Jarvis, **Siavash Mirarab**, Andre J Aberer, Bo Li, Peter Houde, Cai Li, Simon Y W Ho, Brant C Faircloth, Benoit Nabholz, and Jason T Howard.

Phylogenomic analyses data of the avian phylogenomics project. *GigaScience*, 4(1):4, 2015.

35. 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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37. Naim Matasci, Ling-Hong Hung, Zhixiang Yan, Eric J Carpenter, Norman J Wickett, **Siavash Mirarab**, Nam Nguyen, Tandy Warnow, Saravanaraj Ayyampalayam, and Michael Barker. Data access for the 1,000 Plants (1KP) project. *GigaScience*, 3(1):17, 2014.
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39. **Siavash Mirarab**, Md. Shamsuzzoha Bayzid, and Tandy Warnow. Evaluating Summary Methods for Multilocus Species Tree Estimation in the Presence of Incomplete Lineage Sorting. *Systematic Biology*, 65(3):366–380, 2014.

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