

# List of publications

Siavash Mirarab

November 14, 2019

1. Qiyun Zhu, Uyen Mai, Wayne Pfeiffer, Stefan Janssen, Francesco Asnicar, G Sanders, Jon, Pedro Belda-ferre, Gabriel A Al-ghalith, Evguenia Kopylova, Daniel Mcdonald, John B Yin, Shi Huang, Nimaichand Salam, Jian-yu Jiao, Zijun Wu, Z Xu, Kalen Cantrell, Yimeng Yang, Erfan Sayyari, Maryam Rabiee, James T Morton, Dan Knights, Wen-jun Li, Curtis Huttenhower, Nicola Segata, Larry Smarr, **Siavash Mirarab**, and Rob Knight. Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. *Nature Communications*, In press, 2019.
2. James H Leebens-Mack\*, Michael S Barker\*, Eric J Carpenter\*, Michael K Deyholos\*, Matthew A Gitzendanner\*, Sean W Graham\*, Ivo Grosse\*, Zheng\* Li, Michael Melkonian\*, **Siavash Mirarab\***, Martin Porsch\*, Marcel Quint\*, Stefan A Rensing\*, Douglas E Soltis\*, Pamela S Soltis\*, Stevenson\*, and the rest of One Thousand Plant Transcriptomes Initiative. One thousand plant transcriptomes and the phylogenomics of green plants. *Nature*, 574(7780):679–685, 2019.
3. Metin Balaban, Shahab Sarmashghi, and **Siavash Mirarab**. APPLES: Scalable Distance-based Phylogenetic Placement with or without Alignments. *Systematic Biology*, syz063, 2019.
4. Maryam Rabiee and **Siavash Mirarab**. INSTRAL: Discordance-Aware Phylogenetic Placement Using Quartet Scores. *Systematic Biology*, syz045, aug 2019.
5. Erfan Sayyari, Ban Kawas, and **Siavash Mirarab**. TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. *Bioinformatics*, 35(14):i31–i40, 2019.

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6. Lei Chen, Qiang Qiu, Yu Jiang, Kun Wang, Zeshan Lin, Zhipeng Li, Faysal Bibi, Yongzhi Yang, Jinhuan Wang, Wenhui Nie, Weiting Su, Guichun Liu, Qiye Li, Weiwei Fu, Xiangyu Pan, Chang Liu, Jie Yang, Chenzhou Zhang, Yuan Yin, Yu Wang, Yue Zhao, Chen Zhang, Zhongkai Wang, Yanli Qin, Wei Liu, Bao Wang, Yandong Ren, Ru Zhang, Yan Zeng, Rute R. da Fonseca, Bin Wei, Ran Li, Wenting Wan, Ruoping Zhao, Wenbo Zhu, Yutao Wang, Shengchang Duan, Yun Gao, Yong E. Zhang, Chunyan Chen, Christina Hvilsom, Clinton W. Epps, Leona G. Chemnick, Yang Dong, **Siavash Mirarab**, Hans Redlef Siegismund, Oliver A. Ryder, M. Thomas P. Gilbert, Harris A. Lewin, Guojie Zhang, Rasmus Heller, and Wen Wang. Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. *Science*, 364(6446):eaav6202, 2019.
7. 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.
8. Metin Balaban, Niema Moshiri, Uyen Mai, Xingfan Jia, and **Siavash Mirarab**. TreeCluster: Clustering biological sequences using phylogenetic trees. *PLOS ONE*, 14(8):e0221068, 2019.
9. Peter Houde, Edward L Braun, Nitish Narula, Uriel Minjares, and **Siavash Mirarab**. Phylogenetic Signal of Indels and the Neoavian Radiation. *Diversity*, 11(7):108, 2019.
10. Niema Moshiri, Manon Ragonnet-Cronin, Joel O Wertheim, and **Siavash Mirarab**. FAVITES: simultaneous simulation of transmission networks, phylogenetic trees, and sequences. *Bioinformatics*, bty921, 2018.
11. John Yin, Chao Zhang, and **Siavash Mirarab**. ASTRAL-MP: scaling ASTRAL to very large datasets using randomization and parallelization. *Bioinformatics*, btz211, 2019.
12. Maryam Rabiee, Erfan Sayyari, and **Siavash Mirarab**. Multi-allele species reconstruction using ASTRAL. *Molecular Phylogenetics and Evolution*, 130:286–296, 2019.
13. Shyam Gopalakrishnan, Mikkel-Holger S. Sinding, Jazmín Ramos-Madrigal, Jonas Niemann, Jose A. Samaniego Castruita, Filipe G. Vieira, Christian Carøe, Marc

- de Manuel Montero, Lukas Kuderna, Aitor Serres, Víctor Manuel González-Basallote, Yan-Hu Liu, Guo-Dong Wang, Tomas Marques-Bonet, **Siavash Mirarab**, Carlos Fernandes, Philippe Gaubert, Klaus-Peter Koepfli, Jane Budd, Eli Knispel Rueness, Mads Peter Heide-Jørgensen, Bent Petersen, Thomas Sicheritz-Ponten, Lutz Bachmann, Øystein Wiig, Anders J. Hansen, and M. Thomas P. Gilbert. Interspecific Gene Flow Shaped the Evolution of the Genus *Canis*. *Current Biology*, 2018.
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  18. 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.
  19. Erfan Sayyari and **Siavash Mirarab**. Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. *Genes*, 9(3):132, 2018.
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21. 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.
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27. 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.
28. 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.

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  42. Erich D Jarvis\*, **Siavash Mirarab**<sup>†</sup>, 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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