

List of publications

Siavash Mirarab

November 24, 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* (also appeared in *RECOMB 2019*), [syz063](#), 2019.
4. Maryam Rabiee and **Siavash Mirarab**. INSTRAL: Discordance-Aware Phylogenetic Placement Using Quartet Scores. *Systematic Biology*, [syz045](#), 2019.
5. Erfan Sayyari, Ban Kawas, and **Siavash Mirarab**. TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. *Bioinformatics (ISMB special issue)*, [35\(14\):i31–i40](#), 2019.

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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 (also appeared in RECOMB 2018)*, [20\(1\):34](#), 2019.
8. John Yin, Chao Zhang, and **Siavash Mirarab**. ASTRAL-MP: scaling ASTRAL to very large datasets using randomization and parallelization. *Bioinformatics*, [35\(20\):3961–3969](#), 2019.
9. Metin Balaban, Niema Moshiri, Uyen Mai, Xingfan Jia, and **Siavash Mirarab**. TreeCluster: Clustering biological sequences using phylogenetic trees. *PLOS ONE*, [14\(8\):e0221068](#), 2019.
10. Niema Moshiri, Manon Ragonnet-Cronin, Joel O Wertheim, and **Siavash Mirarab**. FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences. *Bioinformatics*, [35\(11\):1852–1861](#), 2019.
11. 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.
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-Madriral, 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, Claudio Sillero, 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*, [28\(21\):3441–3449.e5](#), 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.
 20. Erfan Sayyari, James B. Whitfield, and **Siavash Mirarab**. DiscoVista: Interpretable visualizations of gene tree discordance. *Molecular Phylogenetics and Evolution*, [122:110–115](#), 2018.

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.
22. 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.
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