

# List of publications

Siavash Mirarab

October 9, 2020

1. Uyen Mai and **Siavash Mirarab**. Log Transformation Improves Dating of Phylogenies. *Molecular Biology and Evolution*, [msaa222](#), 2020.
2. Chao Zhang, Celine Scornavacca, Erin K Molloy, and **Siavash Mirarab**. ASTRAL-Pro: Quartet-Based Species-Tree Inference despite Paralogy. *Molecular Biology and Evolution*, [msaa139](#), 2020.
3. Kristine Bohmann, **Siavash Mirarab**, Vineet Bafna, and M. Thomas P. Gilbert. Beyond DNA barcoding: The unrealized potential of genome skim data in sample identification. *Molecular Ecology*, [mec.15507](#), 2020.
4. Metin Balaban and **Siavash Mirarab**. Phylogenetic double placement of mixed samples. *Bioinformatics (ISMB Special issue)*, [36\(Supplement\\_1\):i335–i343](#), 2020.
5. Ekin Tilic, Erfan Sayyari, Josefin Stiller, **Siavash Mirarab**, and Greg W Rouse. More is needed Thousands of loci are required to elucidate the relationships of the flowers of the sea’ (Sabellida, Annelida). *Molecular Phylogenetics and Evolution*, [151:106892](#), 2020.
6. Francesco Asnicar, Andrew Maltez Thomas, Francesco Beghini, Claudia Mengoni, Serena Manara, Paolo Manghi, Qiyun Zhu, Mattia Bolzan, Fabio Cumbo, Uyen May, Jon G Sanders, Moreno Zolfo, Evguenia Kopylova, Edoardo Pasolli, Rob Knight, **Siavash Mirarab**, Curtis Huttenhower, and Nicola Segata. Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. *Nature Communications*, [11\(1\):2500](#), 2020.
7. Eleonora Rachtman, Metin Balaban, Vineet Bafna, and **Siavash Mirarab**. The impact of contaminants on the accuracy of genome skimming and the effectiveness of exclusion read filters. *Molecular Ecology Resources*, [1755–0998.13135](#), 2020.

8. Metin Balaban, Shahab Sarmashghi, and **Siavash Mirarab**. APPLES: Scalable Distance-Based Phylogenetic Placement with or without Alignments. *Systematic Biology*, [69\(3\):566–578](#), 2020.
9. Maryam Rabiee and **Siavash Mirarab**. INSTRAL: Discordance-Aware Phylogenetic Placement Using Quartet Scores. *Systematic Biology*, [69\(2\):384–391](#), 2020.
10. Maryam Rabiee and **Siavash Mirarab**. Forcing external constraints on tree inference using ASTRAL. *BMC Genomics*, [21\(S2\):218](#), 2020.
11. Qiyun Zhu\*, Uyen Mai\*, Wayne Pfeiffer, Stefan Janssen, Francesco Asnicar, Jon G. Sanders, Pedro Belda-Ferre, Gabriel A. Al-Ghalith, Evguenia Kopylova, Daniel McDonald, Tomasz Kosciolk, John B Yin, Shi Huang, Nimaichand Salam, Jian-yu Jiao, Zijun Wu, Zhenjiang Z. Xu, Kalen Cantrell, Yimeng Yang, Erfan Sayyari, Maryam Rabiee, James T Morton, Sheila Podell, 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*, [10\(1\):5477](#), 2019.
12. 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.
13. Erfan Sayyari, Ban Kavas, and **Siavash Mirarab**. TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. *Bioinformatics (ISMB special issue)*, [35\(14\):i31–i40](#), 2019.
14. 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

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\*co-first author

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  27. Erfan Sayyari and **Siavash Mirarab**. Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. *Genes*, [9\(3\):132](#), 2018.
  28. Erfan Sayyari, James B. Whitfield, and **Siavash Mirarab**. DiscoVista: Interpretable visualizations of gene tree discordance. *Molecular Phylogenetics and Evolution*, [122:110–115](#), 2018.
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<sup>†</sup>co-first author

<sup>‡</sup>co-first author

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