

# Siavash Mirarab

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CONTACT INFORMATION	UC San Diego (ECE) 9500 Gilman Drive, Mail code 0407 La Jolla, CA 92093-0407	e-mail: <a href="mailto:smirarab@ucsd.edu">smirarab@ucsd.edu</a> , phone: 858 822 6245 <a href="http://ecweb.ucsd.edu/~smirarab/">http://ecweb.ucsd.edu/~smirarab/</a> google scholar: <a href="http://goo.gl/gEswQ5">http://goo.gl/gEswQ5</a>
ACADEMIC POSITIONS	<b>UC San Diego (UCSD)</b> , San Diego, CA, United States Department of Electrical and Computer Engineering <i>Assistant Professor</i> <i>Associate Professor</i>	<b>July 2015 – July 2020</b> <b>July 2020 – present</b>
EDUCATION		
<i>Ph.D</i>	<b>University of Texas at Austin</b> , US • Computer Science Department; Advisor: Prof. Tandy Warnow (& Keshav Pingali)	<b>Jan. 2011 – July 2015</b>
<i>M.S</i>	<b>University of Waterloo</b> , ON, Canada • Electrical and Computer Engineering; Advisor: Prof. Ladan Tahvildari	<b>Sept. 2006 – Sept. 2008</b>
<i>B.S</i>	<b>University of Tehran</b> , Tehran, Iran • Electrical and Computer Engineering (Specialized in software engineering)	<b>Sept. 2001 – Dec. 2005</b>
AWARDS	NIH-NIGMS MIRA award NSF CAREER award Alfred P. Sloan Research Fellow. Honorable Mention for the 2015 ACM Doctoral Dissertation Award. Bert Kay Dissertation Award, UT, Austin, Computer Science Howard Hughes Medical Institute International Student Fellowship. National Science and Engineering Research Council of Canada (NSERC), Canada Graduate Scholarship (CGS-D) converted to PGS-D outside Canada. Other awards: UT, Austin, College of Natural Sci., Dean's Excellence Award (2011), Dean's Prestigious Fellowship Award (2011 – 2014), and MCD fellowship (2011)	<b>2021</b> <b>2019</b> <b>2017</b> <b>2016</b> <b>2016</b> <b>2012 - 2015</b> <b>2011- 2012</b>
RESEARCH FUNDING	NIH/NIGMS: R35GM142725: "Biology-aware machine learning..." NSF: CISE-1845967: "CAREER: Robust & scalable genome..." NSF: CISE-1815485 : "III: SMALL: New algorithms for genome ..." NSF: CISE-1565862: "CRII: III: Using genomic context to ..." NIH-CFAR: "Accuracy of HIV transmission network ..." CFAR, "Algorithms for prioritizing prevention intervention ... HIV", Sloan foundation fellowship, Other gifts and internal grants	\$1.7 M (5 years) 2021 \$549k (5 years) 2019 \$500k (3 years) 2018 \$170k (2 years) 2016 \$439K (2 years) 2016 \$50K 2019–2020 2016–2018 2017–2019
PHD STUDENTS	Niema Moshiri, Now: Assistant Teaching Professor, UCSD (CSE Dep.) Erfan Sayyari: Now: PostDoctrnal Researcher, UCSD (CMI) Current: Metin Balaban, Yueyu Jiang, Uyen Mai, Maryam Rabiee, Nora Rachtman, Shahab Sarmashghi (co-superviser), Chao Zhang	<b>2015 – 2019</b> <b>2015 – 2019</b> <b>2016 – now</b>
WORK EXPERIENCE	<i>IBM</i> , Vancouver, BC, Canada <i>IT Specialist</i>	<b>Sept. 2008 – Dec. 2010</b>

TEACHING:	<b>Course Instructor (University of California, San Diego):</b>	
	Graduate: Computational evolutionary biology	<b>2016 – 2020</b>
	Introduction to Computer Engineering	<b>2016 – 2020</b>
HIGHLIGHTS AND INVITED TALKS	See <a href="http://ecweb.ucsd.edu/~smirarab/presentations.html">http://ecweb.ucsd.edu/~smirarab/presentations.html</a> for a complete list	
	Bioinformatics Boot Camp for Ecology and Evolution, online	<b>2020</b>
	SysBioDiv and Zoological Society, Freiburg, Germany	<b>2020</b>
	QCB Colloquium, USC, Biological Sciences, Los Angeles, CA	<b>2019</b>
	Computational Genomics Summer Institute, Los Angeles, CA	<b>2017, 2018, 2019</b>
	Workshop on Microbiomics, Metagenomics, and Metabolomics, Buffalo, NY	<b>2019</b>
	Genome 10K & Vertebrate Genome Project, New York, NY	<b>2019</b>
	Avian Meetings, Beijing, China, San Diego, CA (with PAG)	<b>2016, 2018, 2019</b>
	Evolution meeting, Austin, TX, Portland, OR, Montpellier, France	<b>2016, 2017, 2018</b>
	ENABLE workshop, National Chung Hsing University, Taiwan	<b>2018</b>
	Institute for Pure & Applied Math, Workshops on MSA and HPC	<b>2015, 2018</b>
	ISMB, Invited Tutorial on comparative regulatory genomics, Chicago, IL	<b>2018</b>
	Simons Found., Workshop on Statistical Challenges in Microbiome, Boston, MA	<b>2017</b>
	University of Copenhagen, Seminar Series, Copenhagen, Denmark	<b>2017</b>
	Schloss Dagstuhl – Leibniz Center for Informatics, 16351, Dagstuhl, Germany	<b>2016</b>
	RECOMB, Highlights session, Warsaw, Poland	<b>2015</b>
	INFORMS, Big Biological Data, Philadelphia, PA	<b>2015</b>
	MolPhy-3, Moscow, Russia	<b>2012</b>
PROFESSIONAL SERVICES	Leadership: Vertebrate Genome Project (VGP), Council member.	<b>2020</b>
	UCSD: Curriculum Development Committee. “Engineering in Public Health”.	<b>2020</b>
	Conference organization: (IEEE BIBM) (2019), REOMB (2020)	<b>2019-2020</b>
	Program Committee: ISBM, ECCB, RECOMB-CG	<b>2015, 2017–2020</b>
	Paper Review for journals in biology (e.g., Nature Ecology and Evolution), math (e.g., Journal of the American Statistical Association), and computer science (Journal of ACM). See <a href="https://publons.com/researcher/697671/siavash-mirarab">https://publons.com/researcher/697671/siavash-mirarab</a> for a list.	
	Grant Panels: NSF, DOE	<b>2018–2020</b>
PUBLICATIONS	* indicates equal contribution	
	<ol style="list-style-type: none"> <li>1. Metin Balaban, Yueyu Jiang, Qiyun Zhu, Daniel McDonald, Rob Knight, and <u>Siavash Mirarab</u>. Generation of accurate, expandable phylogenomic trees with uDance. <i>Nature Biotechnology</i>, Online, July 2023.</li> <li>2. Daniel McDonald, Yueyu Jiang, Metin Balaban, Kalen Cantrell, Qiyun Zhu, Antonio Gonzalez, James T. Morton, Giorgia Nicolaou, Donovan H. Parks, Søren M. Karst, Mads Albertsen, Philip Hugenholtz, Todd DeSantis, Se Jin Song, Andrew Bartko, Aki S. Havulinna, Pekka Jousilahti, Susan Cheng, Michael Inouye, Teemu Niiranen, Mohit Jain, Veikko Salomaa, Leo Lahti, <u>Siavash Mirarab</u>, and Rob Knight. Greengenes2 unifies microbial data in a single reference tree. <i>Nature Biotechnology</i>, Online, July 2023.</li> <li>3. Chao Zhang, Rasmus Nielsen, and <u>Siavash Mirarab</u>. CASTER: Direct species tree inference from whole-genome alignments. <i>bioRxiv</i>, prepress, 2023.</li> <li>4. Shayesteh Arasti, Puoya Tabaghi, Yasamin Tabatabaee, and Siavash Mirarab. Optimal Tree Metric Matching Enables Phylogenomic Branch Length Reconciliation. <i>bioRxiv</i>, 2023.11.13.566962, January 2023.</li> <li>5. Ali Osman Berk Şapcı, Eleonora Rachtman, and <u>Siavash Mirarab</u>. CONSULT-II: Taxonomic Identification Using Locality Sensitive Hashing. In Katharina Jahn and Tomáš Vinař, editors, <i>Comparative Genomics</i>, 196–214, Cham, 2023. Springer Nature Switzerland.</li> <li>6. Shayesteh Arasti and <u>Siavash Mirarab</u>. Optimal Subtree Prune and Regraft for Quartet Score in Sub-Quadratic Time. In Djamal Belazzougui and Aïda Ouangraoua, editors, <i>23rd International</i></li> </ol>	

- Workshop on Algorithms in Bioinformatics (WABI 2023)*, volume 273 of *Leibniz International Proceedings in Informatics (LIPIcs)*, 4:1–4:20, Dagstuhl, Germany, 2023. Schloss Dagstuhl – Leibniz-Zentrum für Informatik. ISSN: 1868-8969.
7. Uyen Mai, Eduardo Charvel, and [Siavash Mirarab](#). Expectation-Maximization enables Phylogenetic Dating under a Categorical Rate Model. In *RECOMB*, 2023.
  8. Yasamin Tabatabaee, Chao Zhang, Tandy Warnow, and [Siavash Mirarab](#). Phylogenomic branch length estimation using quartets. *Bioinformatics*, 39(Supplement\_1):i185–i193, June 2023.
  9. Afif Elghraoui, [Siavash Mirarab](#), Krister M Swenson, and Faramarz Valafar. Evaluating impacts of syntenic block detection strategies on rearrangement phylogeny using Mycobacterium tuberculosis isolates. *Bioinformatics*, 39(1):btad024, January 2023.
  10. Chao Zhang, Andrey V. Bzikadze, Yana Safonova, and [Siavash Mirarab](#). A scalable model for simulating multi-round antibody evolution and benchmarking of clonal tree reconstruction methods. *Frontiers in Immunology*, 13:1014439, 2022.
  11. Chao Zhang and [Siavash Mirarab](#). Weighting by Gene Tree Uncertainty Improves Accuracy of Quartet-based Species Trees. *Molecular Biology and Evolution*, 39(12):msac215, October 2022.
  12. Chao Zhang and [Siavash Mirarab](#). ASTRAL-Pro 2: ultrafast species tree reconstruction from multi-copy gene family trees. *Bioinformatics*, 38(21):4949–4950, September 2022.
  13. Metin Balaban, Nishat Anjum Bristy, Ahnaf Faisal, Md. Shamsuzzoha Bayzid, and [Siavash Mirarab](#). Genome-wide alignment-free phylogenetic distance estimation under a no strand-bias model. *Bioinformatics Advances*, 2(1):2021.11.10.468111, January 2022.
  14. Maryam Rabiee and [Siavash Mirarab](#). QuCo: quartet-based co-estimation of species trees and gene trees. *Bioinformatics*, 38(Supplement\_1):i413–i421, June 2022.
  15. Yueyu Jiang, Puoya Tabaghi, and [Siavash Mirarab](#). Learning Hyperbolic Embedding for Phylogenetic Tree Placement and Updates. *Biology*, 11(9):1256, 2022. ISBN: 2079-7737.
  16. Navid Bin Hasan, Metin Balaban, Avijit Biswas, Md. Shamsuzzoha Bayzid, and [Siavash Mirarab](#). Distance-Based Phylogenetic Placement with Statistical Support. *Biology*, 11(8):1212, August 2022. ISBN: 2079-7737.
  17. Eleonora Rachtman, Shahab Sarmashghi, Vineet Bafna, and [Siavash Mirarab](#). Quantifying the uncertainty of assembly-free genome-wide distance estimates and phylogenetic relationships using subsampling. *Cell Systems*, 13(10):817–829.e3, October 2022.
  18. Uyen Mai and [Siavash Mirarab](#). Completing gene trees without species trees in sub-quadratic time. *Bioinformatics*, 38(6):1532–1541, March 2022.
  19. Metin Balaban, Yueyu Jiang, Daniel Roush, Qiyun Zhu, and [Siavash Mirarab](#). Fast and accurate distance-based phylogenetic placement using divide and conquer. *Molecular Ecology Resources*, 22(3):1213–1227, April 2022.
  20. Shahab Sarmashghi, Metin Balaban, Eleonora Rachtman, Behrouz Touri, [Siavash Mirarab](#), and Vineet Bafna. Estimating repeat spectra and genome length from low-coverage genome skims with RESPECT. *PLOS Computational Biology*, 17(11):e1009449, November 2021.
  21. [Siavash Mirarab](#), Luay Nakhleh, and Tandy Warnow. Multispecies Coalescent: Theory and Applications in Phylogenetics. *Annual Review of Ecology, Evolution, and Systematics*, 52(1):247–268, November 2021.
  22. Eleonora Rachtman, Vineet Bafna, and [Siavash Mirarab](#). CONSULT: accurate contamination removal using locality-sensitive hashing. *NAR Genomics and Bioinformatics*, 3(3):10.1101/2021.03.18.436035, June 2021.
  23. Chao Zhang, Yiming Zhao, Edward Louis Braun, and [Siavash Mirarab](#). TAPER: Pinpointing errors in multiple sequence alignments despite varying rates of evolution. *Methods in Ecology and Evolution*, 12(11):2145–2158, November 2021.
  24. Niema Moshiri, Davey M Smith, and [Siavash Mirarab](#). HIV Care Prioritization Using Phylogenetic Branch Length. *JAIDS Journal of Acquired Immune Deficiency Syndromes*, 86(5):626–637, April 2021.
  25. Maryam Rabiee and [Siavash Mirarab](#). SODA: multi-locus species delimitation using quartet frequencies. *Bioinformatics*, 36(24):5623–5631, April 2021.
  26. Shaohong Feng, Josef Stiller, Yuan Deng, Joel Armstrong, Qi Fang, Andrew Hart Reeve, Duo Xie, Guangji Chen, Chunxue Guo, Brant C. Faircloth, Bent Petersen, Zongji Wang, Qi Zhou, Mark Diekhans, Wanjun Chen, Sergio Andreu-Sánchez, Ashot Margaryan, Jason Travis Howard, Carole Parent, George Pacheco, Mikkel-Holger S. Sinding, Lara Puetz, Emily Cavill, Ângela M. Ribeiro, Leopold Eckhart, Jon Fjeldsâ, Peter A. Hosner, Robb T. Brumfield, Les Christidis, Mads F. Bertelsen, Thomas Sicheritz-Ponten, Dieter Thomas Tietze, Bruce C. Robertson, Gang Song, Gerald Borgia, Santiago Claramunt, Irby J. Lovette, Saul J. Cowen, Peter Njoroge, John Philip Dumbacher, Oliver A. Ryder, Jérôme Fuchs, Michael Bunce, David W. Burt, Joel Cracraft, Guanliang Meng, Shannon J. Hackett, Peter G. Ryan,

- Knud Andreas Jönsson, Ian G. Jamieson, Rute R. da Fonseca, Edward L. Braun, Peter Houde, Siavash Mirarab, Alexander Suh, Bengt Hansson, Suvi Ponnikas, Hanna Sigeman, Martin Stervander, Paul B. Frandsen, Henriette van der Zwan, Rencia van der Sluis, Carina Visser, Christopher N. Balakrishnan, Andrew G. Clark, John W. Fitzpatrick, Reed Bowman, Nancy Chen, Alison Cloutier, Timothy B. Sackton, Scott V. Edwards, Dustin J. Foote, Subir B. Shakya, Frederick H. Sheldon, Alain Vignal, André E. R. Soares, Beth Shapiro, Jacob González-Solís, Joan Ferrer-Obiol, Julio Rozas, Marta Riutort, Anna Tigano, Vicki Friesen, Love Dalén, Araxi O. Urrutia, Tamás Székely, Yang Liu, Michael G. Campana, André Corvelo, Robert C. Fleischer, Kim M. Rutherford, Neil J. Gemmell, Nicolas Dussex, Henrik Mouritsen, Nadine Thiele, Kira Delmore, Miriam Liedvogel, Andre Franke, Marc P. Hoeppner, Oliver Krone, Adam M. Fudickar, Borja Milá, Ellen D. Ketterson, Andrew Eric Fidler, Guillermo Friis, Ángela M. Parody-Merino, Phil F. Battley, Murray P. Cox, Nicholas Costa Barroso Lima, Francisco Prosdocimi, Thomas Lee Parchman, Barney A. Schlinger, Bette A. Loiselle, John G. Blake, Haw Chuan Lim, Lainy B. Day, Matthew J. Fuxjager, Maude W. Baldwin, Michael J. Braun, Morgan Wirthlin, Rebecca B. Dikow, T. Brandt Ryder, Glauco Camenisch, Lukas F. Keller, Jeffrey M. DaCosta, Mark E. Hauber, Matthew I. M. Louder, Christopher C. Witt, Jimmy A. McGuire, Joann Mudge, Libby C. Megna, Matthew D. Carling, Biao Wang, Scott A. Taylor, Glaucia Del-Rio, Alexandre Aleixo, Ana Tereza Ribeiro Vasconcelos, Claudio V. Mello, Jason T. Weir, David Haussler, Qiye Li, Huanming Yang, Jian Wang, Fumin Lei, Carsten Rahbek, M. Thomas P. Gilbert, Gary R. Graves, Erich D. Jarvis, Benedict Paten, and Guojie Zhang. Dense sampling of bird diversity increases power of comparative genomics. *Nature*, 587(7833):252–257, November 2020.
27. Uyen Mai and [Siavash Mirarab](#). Log Transformation Improves Dating of Phylogenies. *Molecular Biology and Evolution*, 38(3):1151–1167, March 2021.
  28. Chao Zhang, Celine Scornavacca, Erin K Molloy, and [Siavash Mirarab](#). ASTRAL-Pro: Quartet-Based Species-Tree Inference despite Paralogy. *Molecular Biology and Evolution*, 37(11):3292–3307, November 2020.
  29. 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.
  30. Metin Balaban and [Siavash Mirarab](#). Phylogenetic double placement of mixed samples. *Bioinformatics*, 36(Supplement\_1):i335–i343, July 2020.
  31. 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, October 2020.
  32. Francesco Asnicar, Andrew Maltez Thomas, Francesco Beghini, Claudia Mengoni, Serena Manara, Paolo Manghi, Qiyun Zhu, Mattia Bolzan, Fabio Cumbo, Uyen Mai, 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, December 2020. Publisher: Springer US ISBN: 0348556977.
  33. 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*, 20(3):1755–0998.13135, May 2020.
  34. Metin Balaban, Shahab Sarmashghi, and [Siavash Mirarab](#). APPLES: Scalable Distance-Based Phylogenetic Placement with or without Alignments. *Systematic Biology*, 69(3):566–578, May 2020.
  35. Maryam Rabiee and [Siavash Mirarab](#). INSTRAL: Discordance-Aware Phylogenetic Placement Using Quartet Scores. *Systematic Biology*, 69(2):384–391, August 2020.
  36. Maryam Rabiee and [Siavash Mirarab](#). Forcing external constraints on tree inference using ASTRAL. *BMC Genomics*, 21(S2):218, April 2020. Publisher: BMC Genomics.
  37. 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 Kosciółek, 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, December 2019.
  38. 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, Dennis W Stevenson, Kristian K Ullrich, Norman J Wickett, Lisa DeGironimo, Patrick P Edger, Ingrid E Jordon-Thaden, Steve Joya, Tao Liu, Barbara Melkonian, Nicholas W Miles, Lisa Pokorny, Charlotte Quigley, Philip Thomas, Juan Carlos Villarreal, Megan M Augustin, Matthew D

- Barrett, Regina S Baucom, David J Beerling, Ruben Maximilian Benstein, Ed Biffin, Samuel F Brockington, Dylan O Burge, Jason N Burris, Kellie P Burris, Valérie Burtet-Sarramegna, Ana L Caicedo, Steven B Cannon, Zehra Çebi, Ying Chang, Caspar Chater, John M Cheeseman, Tao Chen, Neil D Clarke, Harmony Clayton, Sarah Covshoff, Barbara J Crandall-Stotler, Hugh Cross, Claude W DePamphilis, Joshua P Der, Ron Determann, Rowan C Dickson, Verónica S Di Stilio, Shona Ellis, Eva Fast, Nicole Feja, Katie J Field, Dmitry A Filatov, Patrick M Finnegan, Sandra K Floyd, Bruno Fogliani, Nicolás García, Gildas Gâteblé, Grant T Godden, Falcia (Qi Yun) Goh, Stephan Greiner, Alex Harkess, James Mike Heaney, Katherine E Helliwell, Karolina Heyduk, Julian M Hibberd, Richard G J Hodel, Peter M Hollingsworth, Marc T J Johnson, Ricarda Jost, Blake Joyce, Maxim V Kapralov, Elena Kazamia, Elizabeth A Kellogg, Marcus A Koch, Matt Von Konrat, Kálmán Könyves, Toni M Kutchan, Vivienne Lam, Anders Larsson, Andrew R Leitch, Roswitha Lentz, Fay-Wei Li, Andrew J Lowe, Martha Ludwig, Paul S Manos, Evgeny Mavrodiev, Melissa K McCormick, Michael McKain, Tracy McLellan, Joel R McNeal, Richard E Miller, Matthew N Nelson, Yanhui Peng, Paula Ralph, Daniel Real, Chance W Riggins, Markus Ruhsam, Rowan F Sage, Ann K Sakai, Moira Scascitella, Edward E Schilling, Eva-Marie Schlösser, Heike Sederoff, Stein Servick, Emily B Sessa, A Jonathan Shaw, Shane W Shaw, Erin M Sigel, Cynthia Skema, Alison G Smith, Ann Smithson, C Neal Stewart, John R Stinchcombe, Peter Szövényi, Jennifer A Tate, Helga Tiebel, Dorset Trapnell, Matthieu Villegente, Chun-Neng Wang, Stephen G Weller, Michael Wenzel, Stina Weststrand, James H Westwood, Dennis F Whigham, Shuangxiu Wu, Adrien S Wulff, Yu Yang, Dan Zhu, Cuili Zhuang, Jennifer Zuidof, Mark W Chase, J Chris Pires, Carl J Rothfels, Jun Yu, Cui Chen, Li Chen, Shifeng Cheng, Juanjuan Li, Ran Li, Xia Li, Haorong Lu, Yanxiang Ou, Xiao Sun, Xuemei Tan, Jingbo Tang, Zhijian Tian, Feng Wang, Jun Wang, Xiaofeng Wei, Xun Xu, Zhixiang Yan, Fan Yang, Xiaoni Zhong, Feiyu Zhou, Ying Zhu, Yong Zhang, Saravanaraj Ayyampalayam, Todd J Barkman, Nam-phuong Nguyen, Naim Matasci, David R Nelson, Erfan Sayyari, Eric K Wafula, Ramona L Walls, Tandy Warnow, Hong An, Nils Arrigo, Anthony E Baniaga, Sally Galuska, Stacy A Jorgensen, Thomas I Kidder, Hanghui Kong, Patricia Lu-Irving, Hannah E Marx, Xinshuai Qi, Chris R Reardon, Brittany L Sutherland, George P Tiley, Shana R Welles, Rongpei Yu, Shing Zhan, Lydia Gramzow, Günter Theißen, Gane Ka-Shu Wong, and One Thousand Plant Transcriptomes Initiative. One thousand plant transcriptomes and the phylogenomics of green plants. *Nature*, 574(7780):679–685, October 2019.
39. Erfan Sayyari, Ban Kawas, and [Siavash Mirarab](#). TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. *Bioinformatics*, 35(14):i31–i40, July 2019.
  40. 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 Siegmund, 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, June 2019.
  41. 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, December 2019.
  42. John Yin, Chao Zhang, and [Siavash Mirarab](#). ASTRAL-MP: scaling ASTRAL to very large datasets using randomization and parallelization. *Bioinformatics*, 35(20):3961–3969, October 2019.
  43. Metin Balaban, Niema Moshiri, Uyen Mai, Xingfan Jia, and [Siavash Mirarab](#). TreeCluster: Clustering biological sequences using phylogenetic trees. *PLOS ONE*, 14(8):e0221068, 2019.
  44. 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, June 2019.
  45. Peter Houde, Edward L Braun, Nitish Narula, Uriel Minjares, and [Siavash Mirarab](#). Phylogenetic Signal of Indels and the Neoavian Radiation. *Diversity*, 11(7):108, July 2019.
  46. Maryam Rabiee, Erfan Sayyari, and [Siavash Mirarab](#). Multi-allele species reconstruction using ASTRAL. *Molecular Phylogenetics and Evolution*, 130:286–296, January 2019. Publisher: Elsevier.
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SELECTED  
SOFTWARE  
(PUBLICLY  
AVAILABLE)

**ASTRAL** (<https://github.com/smirarab/ASTRAL>)

Coalescent-based species tree estimation from gene trees

**PASTA** (<https://github.com/smirarab/pasta>)

Multiple sequence alignment of ultra-large datasets (up to a million sequences)

**SEPP,TIPP,UPP** (<https://github.com/smirarab/sepp>)

Phylogenetic placement and taxonomic identification of metagenomic reads

**TreeShrink** (<https://github.com/uym2/TreeShrink>)

Finding and removing spuriously long branches

**DiscoVista** (<https://github.com/esayyari/DiscoVista>)

Visualizing phylogenetic discordances

**FAVITES** (<https://github.com/niemasd/FAVITES>)

Simulating HIV evolution

**APPLES** (<https://github.com/balabanmetin/apples>)

Phylogenetic placement using distances

**TreeCluster** (<https://github.com/niemasd/TreeCluster>)

Clustering leaves of a phylogeny in linear time with gurantees

See <http://eceweb.ucsd.edu/~smirarab/software.html> for more.