

Siavash Mirarab

CONTACT INFORMATION	UC San Diego (ECE) 9500 Gilman Drive, Mail code 0407 La Jolla, CA 92093-0407	e-mail: smirarab@ucsd.edu , phone: 858 822 6245 http://eceweb.ucsd.edu/~smirarab/ google scholar: http://goo.gl/gEswQ5
ACADEMIC POSITIONS	UC San Diego (UCSD) , San Diego, CA, United States Department of Electrical and Computer Engineering <i>Assistant Professor</i> <i>Associate Professor</i>	July 2015 – July 2020 July 2020 – present
EDUCATION		
<i>Ph.D</i>	University of Texas at Austin , US • Computer Science Department; Advisor: Prof. Tandy Warnow (& Keshav Pingali)	Jan. 2011 – July 2015
<i>M.S</i>	University of Waterloo , ON, Canada • Electrical and Computer Engineering; Advisor: Prof. Ladan Tahvildari	Sept. 2006 – Sept. 2008
<i>B.S</i>	University of Tehran , Tehran, Iran • Electrical and Computer Engineering (Specialized in software engineering)	Sept. 2001 – Dec. 2005
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)	2021 2019 2017 2016 2016 2012 - 2015 2011- 2012
RESEARCH FUNDING	NIH/NIGMS: R35GM142725: “Biology-aware machine learning...” \$1.7 M (5 years) NSF: CISE-1845967: “CAREER: Robust & scalable genome...” \$549k (5 years) NSF: CISE-1815485 : “III: SMALL: New algorithms for genome ...” \$500k (3 years) NSF: CISE-1565862: “CRII: III: Using genomic context to ...” \$170k (2 years) NIH-CFAR: “Accuracy of HIV transmission network ...” \$439K (2 years) CFAR, “Algorithms for prioritizing prevention intervention ... HIV”, \$50K Sloan foundation fellowship, \$60K (2 years) Other gifts and internal grants ≈\$100K	2021 2019 2018 2016 2016 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	2015 – 2019 2015 – 2019 2016 – now
WORK EXPERIENCE	<i>IBM</i> , Vancouver, BC, Canada <i>IT Specialist</i>	Sept. 2008 – Dec. 2010

TEACHING:	Course Instructor (University of California, San Diego):	
	Graduate: Computational evolutionary biology	2016 – 2020
	Introduction to Computer Engineering	2016 – 2020
HIGHLIGHTS AND INVITED TALKS	See http://eceweb.ucsd.edu/~smirarab/presentations.html for a complete list	
	Bioinformatics Boot Camp for Ecology and Evolution, online	2020
	SysBioDiv and Zoological Society, Freiburg, Germany	2020
	QCB Colloquium, USC, Biological Sciences, Los Angeles, CA	2019
	Computational Genomics Summer Institute, Los Angeles, CA	2017, 2018, 2019
	Workshop on Microbiomics, Metagenomics, and Metabolomics, Buffalo, NY	2019
	Genome 10K & Vertebrate Genome Project, New York, NY	2019
	Avian Meetings, Beijing, China, San Diego, CA (with PAG)	2016, 2018, 2019
	Evolution meeting, Austin, TX, Portland, OR, Montpellier, France	2016, 2017, 2018
	ENABLE workshop, National Chung Hsing University, Taiwan	2018
	Institute for Pure & Applied Math, Workshops on MSA and HPC	2015, 2018
	ISMB, Invited Tutorial on comparative regulatory genomics, Chicago, IL	2018
	Simons Found., Workshop on Statistical Challenges in Microbiome, Boston, MA	2017
	University of Copenhagen, Seminar Series, Copenhagen, Denmark	2017
	Schloss Dagstuhl – Leibniz Center for Informatics, 16351, Dagstuhl, Germany	2016
	RECOMB, Highlights session, Warsaw, Poland	2015
	INFORMS, Big Biological Data, Philadelphia, PA	2015
	MolPhy-3, Moscow, Russia	2012
PROFESSIONAL SERVICES	Leadership: Vertebrate Genome Project (VGP), Council member.	2020
	UCSD: Curriculum Development Committee. “Engineering in Public Health”.	2020
	Conference organization: (IEEE BIBM) (2019), REOMB (2020)	2019-2020
	Program Committee: ISBM, ECCB, RECOMB-CG	2015, 2017–2020
	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 https://publons.com/researcher/697671/siavash-mirarab for a list.	
	Grant Panels: NSF, DOE	2018–2020
PUBLICATIONS	* indicates equal contribution	
	1. Metin Balaban, Daniel Roush, Qiyun Zhu, and <u>Siavash Mirarab</u> . APPLES-2 : Faster and More Accurate Distance-based Phylogenetic Placement using Divide and Conquer. <i>Molecular Ecology Resources</i> , in press, 2021.	
	2. Shahab Sarmashghi, Metin Balaban, Eleonora Rachtman, Behrouz Touri, <u>Siavash Mirarab</u> , and Vineet Bafna. Estimating repeat spectra and genome length from low-coverage genome skims with RESPECT. <i>PLoS Computational Biology</i> , in press, 2021.	
	3. <u>Siavash Mirarab</u> , Luay Nakhleh, and Tandy Warnow. Multispecies Coalescent: Theory and Applications in Phylogenetics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 52(1):247–268, 2021.	
	4. Eleonora Rachtman, Vineet Bafna, and <u>Siavash Mirarab</u> . CONSULT: accurate contamination removal using locality-sensitive hashing. <i>NAR Genomics and Bioinformatics</i> , 3(3):10.1101/2021.03.18.436035, 2021.	
	5. Chao Zhang, Yiming Zhao, Edward Louis Braun, and <u>Siavash Mirarab</u> . TAPER: Pinpointing errors in multiple sequence alignments despite varying rates of evolution. <i>Methods in Ecology and Evolution</i> , 2041–210X.13696, 2021.	
	6. Niema Moshiri, Davey M Smith, and <u>Siavash Mirarab</u> . HIV Care Prioritization using Phylogenetic Branch Length. <i>JAIDS Journal of Acquired Immune Deficiency Syndromes</i> , 86(5):2019.12.20.885202, dec 2021.	

7. Maryam Rabiee and [Siavash Mirarab](#). SODA: Multi-locus species delimitation using quartet frequencies. *Bioinformatics*, btaa1010, 2021.
8. Shaohong Feng, Josefin 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 Fjeldså, 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 Caramunt, 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 Jønsson, 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. Gemmill, Nicolas Dussex, Henrik Mouritsen, Nadine Thiele, Kira Delmore, Miriam Liedvogel, Andre Franke, Marc P. Hoepfner, Oliver Krone, Adam M. Fudickar, Borja Milá, Ellen D. Ketterson, Andrew Eric Fidler, Guillermo Friis, Ângela 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, 2020.
9. Uyen Mai and [Siavash Mirarab](#). Log Transformation Improves Dating of Phylogenies. *Molecular Biology and Evolution*, msaa222, 2020.
10. 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.
11. 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.
12. Metin Balaban and [Siavash Mirarab](#). Phylogenetic double placement of mixed samples. *Bioinformatics (ISMB Special issue)*, 36(Supplement_1):i335–i343, 2020.
13. 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.
14. 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, 2020.
15. 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.
16. Metin Balaban, Shahab Sarmashghi, and [Siavash Mirarab](#). APPLES: Scalable Distance-Based Phylogenetic Placement with or without Alignments. *Systematic Biology*, 69(3):566–578, 2020.
17. Maryam Rabiee and [Siavash Mirarab](#). INSTRAL: Discordance-Aware Phylogenetic Placement Using Quartet Scores. *Systematic Biology*, 69(2):384–391, 2020.
18. Maryam Rabiee and [Siavash Mirarab](#). Forcing external constraints on tree inference using ASTRAL. *BMC Genomics*, 21(S2):218, 2020.
19. 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, 2019.
20. 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.
 21. Erfan Sayyari, Ban Kawas, and Siavash Mirarab. TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. *Bioinformatics (ISMB)*, 35(14):i31–i40, 2019.
 22. 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.
 23. 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.
 24. 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.
 25. Metin Balaban, Niema Moshiri, Uyen Mai, Xingfan Jia, and Siavash Mirarab. TreeCluster: Clustering biological sequences using phylogenetic trees. *PLOS ONE*, 14(8):e0221068, 2019.
 26. 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.
 27. 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.
 28. Maryam Rabiee, Erfan Sayyari, and Siavash Mirarab. Multi-allele species reconstruction using ASTRAL. *Molecular Phylogenetics and Evolution*, 130:286–296, 2019.
 29. 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.
 30. Daniel McDonald and American Gut Consortium. American Gut: an Open Platform for Citizen Science Microbiome Research. *mSystems*, 3(3):e00031–18, 2018.
 31. 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.
 32. 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.
 33. 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.
 34. 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.
 35. Erfan Sayyari and Siavash Mirarab. Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. *Genes*, 9(3):132, 2018.

36. Erfan Sayyari, James B. Whitfield, and [Siavash Mirarab](#). DiscoVista: Interpretable visualizations of gene tree discordance. *Molecular Phylogenetics and Evolution*, 122:110–115, 2018.
37. 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.
38. 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*, 15(5):1738–1747, 2018.
39. 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.
40. 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.
41. 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 Lefler, 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):457–463, 2017.
42. Uyen Mai and [Siavash Mirarab](#). TreeShrink: Efficient Detection of Outlier Tree Leaves. In *Comparative Genomics. RECOMB-CG 2017. Lecture Notes in Computer Science*, volume 10562, 116–140. Springer, Cham, 2017.
43. Chao Zhang, Erfan Sayyari, and [Siavash Mirarab](#). ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. In *Comparative Genomics. RECOMB-CG 2017. Lecture Notes in Computer Science*, volume 10562, 53–75. Springer, Cham, 2017.
44. 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.
45. [Siavash Mirarab](#). Phylogenomics: Constrained gene tree inference. *Nature Ecology & Evolution*, 1:0056, 2017.
46. Erfan Sayyari and [Siavash Mirarab](#). Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. *BMC Genomics*, 17(S10):101–113, 2016.
47. 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.
48. Nam Nguyen, Michael Nute, [Siavash Mirarab](#), and Tandy Warnow. HIPPI: highly accurate protein family classification with ensembles of HMMs. *BMC Genomics*, 17(S10):765, 2016.
49. 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.
50. [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.
51. 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.
52. Ruth Davidson, Pranjal 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.
53. Jed Chou, Ashu Gupta, Shashank Yaduvanshi, Ruth Davidson, Mike Nute, [Siavash Mirarab](#), and Tandy Warnow. A comparative study of SVDquartets and other coalescent-based species tree estimation methods. *BMC Genomics*, 16(Suppl 10):S2, 2015.
54. [Siavash Mirarab](#) and Tandy Warnow. ASTRAL-II: coalescent-based species tree estimation with many hundreds of taxa and thousands of genes. *Bioinformatics*, 31(12):i44–i52, 2015.
55. Nam Nguyen, [Siavash Mirarab](#), Keerthana Kumar, and Tandy Warnow. Ultra-large alignments using phylogeny-aware profiles. *Genome Biology*, 16(1):124, 2015.

56. Md Shamsuzzoha Bayzid, [Siavash Mirarab](#), Bastien Boussau, and Tandy Warnow. Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. *PLoS ONE*, 10(6):e0129183, 2015.
57. Erich D Jarvis, [Siavash Mirarab](#), Andre J Aberer, Bo Li, Peter Houde, Cai Li, Simon Y W Ho, Brant C Faircloth, Benoit Nabholz, Jason T Howard, Alexander Suh, Claudia C Weber, Rute R da Fonseca, Alonzo Alfaro-Núñez, Nitish Narula, Liang Liu, Dave Burt, Hans Ellegren, Scott V Edwards, Alexandros Stamatakis, David P Mindell, Joel Cracraft, Edward L Braun, Tandy Warnow, Wang Jun, M Thomas Pius Gilbert, and Guojie Zhang. Phylogenomic analyses data of the avian phylogenomics project. *GigaScience*, 4(1):1–9, 2015.
58. [Siavash Mirarab](#), Nam Nguyen, Sheng Guo, Li-San Wang, Junhyong Kim, and Tandy Warnow. PASTA: Ultra-Large Multiple Sequence Alignment for Nucleotide and Amino-Acid Sequences. *Journal of Computational Biology*, 22(05):377–386, 2015.
59. 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.
60. [Siavash Mirarab](#), Md. Shamsuzzoha Bayzid, Bastien Boussau, and Tandy Warnow. Statistical binning enables an accurate coalescent-based estimation of the avian tree. *Science*, 346(6215):1250463, 2014.
61. Naim Matasci, Ling-Hong. Hung, Zhixiang Yan, Eric J Carpenter, Norman J Wickett, [Siavash Mirarab](#), Nam Nguyen, Tandy Warnow, 34 other authors, Jim Leebens-Mack, and Gane Ka-Shu Wong. Data access for the 1,000 Plants (1KP) project. *GigaScience*, 3(1):17, 2014.
62. Norman J Wickett*, [Siavash Mirarab*](#), Nam Nguyen, Tandy Warnow, 36 other authors, Gane Ka-Shu Wong, and James Leebens-Mack. Phylotranscriptomic analysis of the origin and early diversification of land plants. *Proceedings of the National Academy of Sciences (PNAS)*, 111(45):E4859–4868, 2014.
63. [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.
64. [Siavash Mirarab](#), Nam Nguyen, and Tandy Warnow. PASTA: ultra-large multiple sequence alignment. In *Proceedings of the 18th International Conference on Research in Computational Molecular Biology (RECOMB)*, 177–191, 2014.
65. [Siavash Mirarab](#), Rezwana Reaz, Md. Shamsuzzoha Bayzid, Théo Zimmermann, M Shel Swenson, and Tandy Warnow. ASTRAL: Genome-Scale Coalescent-Based Species Tree. *Bioinformatics (ECCB)*, 30(17):i541–i548, 2014.
66. Nam Nguyen, [Siavash Mirarab](#), Bo Liu, Mihai Pop, and Tandy Warnow. TIPP: taxonomic identification and phylogenetic profiling. *Bioinformatics*, 30(24):3548–3555, 2014.
67. Théo Zimmermann, [Siavash Mirarab](#), and Tandy Warnow. BBCA: Improving the scalability of *BEAST using random binning. *BMC Genomics*, 15(Suppl 6):S11, 2014.
68. Arlin Stoltzfus, Hilmar Lapp, Naim Matasci, Helena Deus, Brian Sidlauskas, Christian M Zmasek, Gaurav Vaidya, Enrico Pontelli, Karen Cranston, Rutger Vos, Campbell O Webb, Luke J Harmon, Megan Pirrung, Brian O’Meara, Matthew W Pennell, [Siavash Mirarab](#), Michael S Rosenberg, James P Balhoff, Holly M Bik, Tracy A Heath, Peter E Midford, Joseph W Brown, Emily Jane McTavish, Jeet Sukumaran, Mark Westneat, Michael E Alfaro, Aaron Steele, and Greg Jordan. Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. *BMC Bioinformatics*, 14(1):158, 2013.
69. Md. Shamsuzzoha Bayzid, [Siavash Mirarab](#), and Tandy Warnow. Inferring optimal species trees under gene duplication and loss. In *Proceedings of the Pacific Symposium on Biocomputing (PSB)*, 250–61, 2013.
70. Nam Nguyen, [Siavash Mirarab](#), and Tandy Warnow. MRL and SuperFine+ MRL: new supertree methods. *Algorithms for Molecular Biology*, 7(1):3, 2012.
71. [Siavash Mirarab](#), Nam Nguyen, and Tandy Warnow. SEPP: SATé-Enabled Phylogenetic Placement. In *Proceedings of the Pacific Symposium on Biocomputing (PSB)*, 247–58, 2012.
72. [Siavash Mirarab](#), Soroush Akhlaghi, and Ladan Tahvildari. Size-constrained regression test case selection using multicriteria optimization. *Software Engineering, IEEE Transactions on*, 38(4):936–956, 2012.
73. [Siavash Mirarab](#) and Tandy Warnow. FastSP: linear time calculation of alignment accuracy. *Bioinformatics*, 27:3250–8, 2011.
74. Hyunsook Do, [Siavash Mirarab](#), Ladan Tahvildari, and Gregg Rothermel. The effects of time constraints on test case prioritization: A series of controlled experiments. *Software Engineering, IEEE Transactions on*, 36:593–617, 2010.

75. [Siavash Mirarab](#) and Ladan Tahvildari. An empirical study on bayesian network-based approach for test case prioritization. In *Proceedings of ICST*, 278–287. IEEE, 2008.
76. [Siavash Mirarab](#), Afshar Ganjali, Ladan Tahvildari, Shimin Li, Weining Liu, and Mike Morrissey. A requirement-based software testing framework: An industrial practice. In *Proceedings ICSM*, 452–455. IEEE, 2008.
77. Hyunsook Do, [Siavash Mirarab](#), Ladan Tahvildari, and Gregg Rothermel. An empirical study of the effect of time constraints on the cost-benefits of regression testing. In *Proceedings of FSE*, 71–82. ACM, 2008.
78. Mehdi Amoui, Mazeiar Salehie, [Siavash Mirarab](#), and Ladan Tahvildari. Adaptive action selection in autonomic software using reinforcement learning. In *Proceedings of ICAS*, 175–181. IEEE, 2008.
79. [Siavash Mirarab](#) and Ladan Tahvildari. A prioritization approach for software test cases based on bayesian networks. In *Proceedings of FASE*, 276–290, 2007.
80. [Siavash Mirarab](#), Alaa Hassouna, and Ladan Tahvildari. Using bayesian belief networks to predict change propagation in software systems. In *Proceedings of ICPC*, 177–188. IEEE, 2007.
81. Mehdi Amoui, [Siavash Mirarab](#), Sepand Ansari, and Caro Lucas. A genetic algorithm approach to design evolution using design pattern transformation. *Journal of Information Technology and Intelligent Computing*, 1(2):235–244, 2006.

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://ecweb.ucsd.edu/~smirarab/software.html> for more.