Siavash Mirarab

CONTACT INFORMATION	UC San Diego (ECE) e-mail: smirarab@ucsd.edu, phone: 858 822 6245 9500 Gilman Drive, Mail code 0407 http://eceweb.ucsd.edu/~smirarab/ La Jolla, CA 92093-0407 google scholar: http://goo.gl/gEswQ5

ACADEMIC POSITIONS

UC San Diego (UCSD), San Diego, CA, United States
Department of Electrical and Computer Engineering

Assistant Professor	**July 2015 − July 2020**
Associate Professor	**July 2020 − present**

EDUCATION

Ph.D **University of Texas at Austin**, US **Jan. 2011 − July 2015**
- Computer Science Department; Advisor: Prof. Tandy Warnow (& Keshav Pingali)

M.S **University of Waterloo**, ON, Canada **Sept. 2006 − Sept. 2008**
- Electrical and Computer Engineering; Advisor: Prof. Ladan Tahvildari

B.S **University of Tehran**, Tehran, Iran **Sept. 2001 − Dec. 2005**
- Electrical and Computer Engineering (Specialized in software engineering)

AWARDS

NSF CAREER award	**2019**
Alfred P. Sloan Research Fellow.	**2017**
Honorable Mention for the 2015 ACM Doctoral Dissertation Award.	**2016**
Bert Kay Dissertation Award, UT, Austin, Computer Science	**2016**
Howard Hughes Medical Institute International Student Fellowship.	**2012 - 2015**
National Science and Engineering Research Council of Canada (NSERC), Canada Graduate Scholarship (CGS-D) converted to PGS-D outside Canada.	**2011- 2012**

Other awards: UT, Austin, College of Natural Sci., Dean's Excellence Award (2011), Dean's Prestigious Fellowship Award (2011 − 2014), and MCD fellowship (2011)

RESEARCH FUNDING

NSF: CISE-1845967: "CAREER: Robust & scalable genome..." $549k (5 years)	2019
NSF: CISE-1815485 : "III: SMALL: New algorithms for genome ..." $500k (3 years)	2018
NSF: CISE-1565862: "CRII: III: Using genomic context to ..." $170k (2 years)	2016
NIH-CFAR: "Accuracy of HIV transmission network ..." $439K (2 years)	2016
CFAR, "Algorithms for prioritizing prevention intervention ... HIV", $50K	2019–2020
Sloan foundation fellowship, $60K (2 years)	2016–2018
Other gifts and internal grants ≈$100K	2017–2019

PHD STUDENTS

Niema Moshiri, Now: Assistant Teaching Professor, UCSD (CSE Dep.)	**2015 − 2019**
Erfan Sayyari: Now: PostDoctral Researcher, UCSD (CMI)	**2015 − 2019**
Current: Metin Balaban, Yueyu Jiang, Uyen Mai, Maryam Rabiee, Nora Rachtman, Shahab Sarmashghi (co-superviser), Chao Zhang	**2016 − now**

WORK EXPERIENCE

IBM, Vancouver, BC, Canada *IT Specialist*	**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 Angles, CA	**2019**
	Computational Genomics Summer Institute, Los Angles, 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., Workhop 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. Uyen Mai and <u>Siavash Mirarab</u>. Log Transformation Improves Dating of Phylogenies. *Molecular Biology and Evolution*, msaa222, 2020.
2. Chao Zhang, Celine Scornavacca, Erin K Molloy, and <u>Siavash Mirarab</u>. ASTRAL-Pro: Quartet-Based Species-Tree Inference despite Paralogy. *Molecular Biology and Evolution*, msaa139, 2020.
3. Kristine Bohmann, <u>Siavash Mirarab</u>, 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 <u>Siavash Mirarab</u>. Phylogenetic double placement of mixed samples. *Bioinformatics (ISMB Special issue)*, 36(Supplement_1):i335–i343, 2020.
5. Ekin Tilic, Erfan Sayyari, Josefin Stiller, <u>Siavash Mirarab</u>, and Greg W Rouse. More is neededThousands 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, <u>Siavash Mirarab</u>, 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 AS-TRAL. *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 Kosciolek, John B Yin, Shi Huang, Nimaichand Salam, Jian-yu Jiao, Zijun Wu, Zhen-jiang 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 Kawas, 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 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.

15. 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.

16. 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.

17. Metin Balaban, Niema Moshiri, Uyen Mai, Xingfan Jia, and Siavash Mirarab. TreeCluster: Clustering biological sequences using phylogenetic trees. *PLOS ONE*, 14(8):e0221068, 2019.

18. 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.

19. 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.

20. Maryam Rabiee, Erfan Sayyari, and Siavash Mirarab. Multi-allele species reconstruction using ASTRAL. *Molecular Phylogenetics and Evolution*, 130:286–296, 2019.

21. 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, 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.

22. Daniel McDonald and American Gut Consortium. American Gut: an Open Platform for Citizen Science Microbiome Research. *mSystems*, 3(3):e00031–18, 2018.

23. 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.

24. Stefan Janssen, Daniel McDonald, Antonio Gonzalez, Jose A. Navas-Molina, Lingjing Jiang, Zhenjiang Zech Xu, Kevin Winker, Deborah M. Kado, Eric Orwoll, Mark Manary, <u>Siavash Mirarab</u>, and Rob Knight. Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. *mSystems*, 3(3):e00021–18, 2018.

25. Chao Zhang, Maryam Rabiee, Erfan Sayyari, and <u>Siavash Mirarab</u>. ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. *BMC Bioinformatics*, 19(S6):153, 2018.

26. Uyen Mai and <u>Siavash Mirarab</u>. TreeShrink: fast and accurate detection of outlier long branches in collections of phylogenetic trees. *BMC Genomics*, 19(S5):272, 2018.

27. Erfan Sayyari and <u>Siavash Mirarab</u>. Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. *Genes*, 9(3):132, 2018.

28. Erfan Sayyari, James B. Whitfield, and <u>Siavash Mirarab</u>. DiscoVista: Interpretable visualizations of gene tree discordance. *Molecular Phylogenetics and Evolution*, 122:110–115, 2018.

29. Ali Akbari, Joseph J Vitti, Arya Iranmehr, Mehrdad Bakhtiari, Pardis C Sabeti, <u>Siavash Mirarab</u>, and Vineet Bafna. Identifying the favored mutation in a positive selective sweep. *Nature Methods*, 15(4):279–282, 2018.

30. Shubhanshu Shekhar, Sebastien Roch, and <u>Siavash Mirarab</u>. Species Tree Estimation Using ASTRAL: How Many Genes Are Enough? *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 15(5):1738–1747, 2018.

31. Niema Moshiri and <u>Siavash Mirarab</u>. A Two-State Model of Tree Evolution and Its Applications to Alu Retrotransposition. *Systematic Biology*, 67(3):475–489, 2018.

32. Erfan Sayyari, James B Whitfield, and <u>Siavash Mirarab</u>. Fragmentary Gene Sequences Negatively Impact Gene Tree and Species Tree Reconstruction. *Molecular Biology and Evolution*, 34(12):3279–3291, 2017.

33. 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, <u>Siavash Mirarab</u>, Zhenjiang Zech Xu, Lingjing Jiang, Mohamed F. Haroon, Jad Kanbar, Qiyun Zhu, Se Jin Song, Tomasz Kosciolek, 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.

34. Uyen Mai and <u>Siavash Mirarab</u>. 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.

35. Chao Zhang, Erfan Sayyari, and <u>Siavash Mirarab</u>. 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.

36. Uyen Mai, Erfan Sayyari, and <u>Siavash Mirarab</u>. Minimum variance rooting of phylogenetic trees and implications for species tree reconstruction. *PLOS ONE*, 12(8):e0182238, 2017.

37. <u>Siavash Mirarab</u>. Phylogenomics: Constrained gene tree inference. *Nature Ecology & Evolution*, 1:0056, 2017.

38. Erfan Sayyari and <u>Siavash Mirarab</u>. Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. *BMC Genomics*, 17(S10):101–113, 2016.

39. Erfan Sayyari and <u>Siavash Mirarab</u>. Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies. *Molecular Biology and Evolution*, 33(7):1654–1668, 2016.

40. Nam Nguyen, Michael Nute, <u>Siavash Mirarab</u>, and Tandy Warnow. HIPPI: highly accurate protein family classification with ensembles of HMMs. *BMC Genomics*, 17(S10):765, 2016.

41. James E Tarver, Mario dos Reis, <u>Siavash Mirarab</u>, 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.

42. <u>Siavash Mirarab</u>, 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.

43. Joel Cracraft, Peter Houde, Simon Y W Ho, David P Mindell, Jon Fjeldså, Bent Lindow, Scott V Edwards, Carsten Rahbek, <u>Siavash Mirarab</u>, 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.

44. Ruth Davidson, Pranjal Vachaspati, <u>Siavash Mirarab</u>, 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.

45. Jed Chou, Ashu Gupta, Shashank Yaduvanshi, Ruth Davidson, Mike Nute, <u>Siavash Mirarab</u>, and Tandy Warnow. A comparative study of SVDquartets and other coalescent-based species tree estimation methods. *BMC Genomics*, 16(Suppl 10):S2, 2015.

46. <u>Siavash Mirarab</u> 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.

47. Nam Nguyen, <u>Siavash Mirarab</u>, Keerthana Kumar, and Tandy Warnow. Ultra-large alignments using phylogeny-aware profiles. *Genome Biology*, 16(1):124, 2015.

48. Md Shamsuzzoha Bayzid, <u>Siavash Mirarab</u>, Bastien Boussau, and Tandy Warnow. Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. *PLoS ONE*, 10(6):e0129183, 2015.

49. <u>Siavash Mirarab</u>, 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.

50. Erich D Jarvis*, <u>Siavash Mirarab</u>* , 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.

51. <u>Siavash Mirarab</u>, 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.

52. Naim Matasci, Ling-Hong. Hung, Zhixiang Yan, Eric J Carpenter, Norman J Wickett, <u>Siavash Mirarab</u>, 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.

53. Norman J. Wickett*, <u>Siavash Mirarab</u>* , 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.

54. <u>Siavash Mirarab</u>, 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.

55. <u>Siavash Mirarab</u>, 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.

56. <u>Siavash Mirarab</u>, 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.

57. Nam Nguyen, <u>Siavash Mirarab</u>, Bo Liu, Mihai Pop, and Tandy Warnow. TIPP: taxonomic identification and phylogenetic profiling. *Bioinformatics*, 30(24):3548–3555, 2014.

58. Théo Zimmermann, <u>Siavash Mirarab</u>, and Tandy Warnow. BBCA: Improving the scalability of *BEAST using random binning. *BMC Genomics*, 15(Suppl 6):S11, 2014.

59. 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, <u>Siavash Mirarab</u>, 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.

60. Md. Shamsuzzoha Bayzid, <u>Siavash Mirarab</u>, and Tandy Warnow. Inferring optimal species trees under gene duplication and loss. In *Proceedings of the Pacific Symposium on Biocomputing (PSB)*, 250–61, 2013.

61. Nam Nguyen, <u>Siavash Mirarab</u>, and Tandy Warnow. MRL and SuperFine+ MRL: new supertree methods. *Algorithms for Molecular Biology*, 7(1):3, 2012.

62. <u>Siavash Mirarab</u>, Nam Nguyen, and Tandy Warnow. SEPP: SATé-Enabled Phylogenetic Placement. In *Proceedings of the Pacific Symposium on Biocomputing (PSB)*, 247–58, 2012.

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64. <u>Siavash Mirarab</u> and Tandy Warnow. FastSP: linear time calculation of alignment accuracy. *Bioinformatics*, 27:3250–8, 2011.

65. Hyunsook Do, <u>Siavash Mirarab</u>, 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.

66. <u>Siavash Mirarab</u> and Ladan Tahvildari. An empirical study on bayesian network-based approach for test case prioritization. In *Proceedings of ICST*, 278–287. IEEE, 2008.

67. <u>Siavash Mirarab</u>, 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.

68. Hyunsook Do, <u>Siavash Mirarab</u>, 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.

69. Mehdi Amoui, Mazeiar Salehie, <u>Siavash Mirarab</u>, and Ladan Tahvildari. Adaptive action selection in autonomic software using reinforcement learning. In *Proceedings of ICAS*, 175–181. IEEE, 2008.

70. <u>Siavash Mirarab</u> and Ladan Tahvildari. A prioritization approach for software test cases based on bayesian networks. In *Proceedings of FASE*, 276–290, 2007.

71. <u>Siavash Mirarab</u>, Alaa Hassouna, and Ladan Tahvildari. Using bayesian belief networks to predict change propagation in software systems. In *Proceedings of ICPC*, 177–188. IEEE, 2007.

72. Mehdi Amoui, <u>Siavash Mirarab</u>, 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://eceweb.ucsd.edu/~smirarab/software.html` for more.