

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://ecweb.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>	July 2015 – present
EDUCATION	<i>Ph.D</i> University of Texas at Austin , Austin, Texas, Department of Computer Science <ul style="list-style-type: none">Advisors: Prof. Tandy Warnow, Prof. Keshav PingaliNovel scalable approaches for multiple sequence alignment and phylogenetic reconstruction <i>Master of Science (University of Waterloo, ON, Canada)</i> <ul style="list-style-type: none">Electrical and Computer Engineering, Advisors: Prof. Ladan TahvildariThesis: A Bayesian Framework for Software Regression Testing <i>Bachelor of Science (University of Tehran)</i> <ul style="list-style-type: none">Electrical and Computer Engineering (Specialized in software engineering).	Jan. 2011 – July 2015 Sept. 2006 – Sept. 2008 Sept. 2001 – Dec. 2005
MAJOR AWARDS	NSF CAREER award Alfred P. Sloan Research Fellow. Honorable Mention for the 2015 ACM Doctoral Dissertation Award. 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.	2019 2017 2016 2012 - 2015 2011- 2012
OTHER AWARDS	UT, Austin, Computer Science, Bert Kay Dissertation Award, 2015 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) 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	2019 2018 2016 2016 2019–2020 2016–2018 2017–2019
PHD STUDENTS	Niema Moshiri, Now: Assistant Teaching Professor, UCSD (CSE Dep.) Erfan Sayyari: Now: PostDoctral Researcher, UCSD (CMI) Current: Metin Balaban, Uyen Mai, Maryam Rabie, Nora Ratchman, Shahab Sar-mashghi (co-supervisor), Chao Zhang	2015 – 2019 2015 – 2019 2016 – now

1. 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.
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.
6. 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 Hvilsum, 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.

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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-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.
14. Daniel McDonald and American Gut Consortium. American Gut: an Open Platform for Citizen Science Microbiome Research. *mSystems*, 3(3):e00031–18, 2018.
15. 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.

16. 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.
17. 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.
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.
23. 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.
24. 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 Kosciółek, Nicholas A. Bokulich, Joshua Leffler, 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.

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26. 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.
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28. 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.
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30. Erfan Sayyari and **Siavash Mirarab**. Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. *BMC Genomics*, 17(S10):101–113, 2016.
31. 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.
32. 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.
33. 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.
34. **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.
35. 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.

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37. 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.
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39. Nam Nguyen, **Siavash Mirarab**, Keerthana Kumar, and Tandy Warnow. Ultra-large alignments using phylogeny-aware profiles. *Genome Biology*, 16(1):124, 2015.
40. 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.
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43. 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.
44. 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.
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46. **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.

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63. **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.
64. 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.

PROFESSIONAL EXPERIENCE	International Business Machines (IBM) , Vancouver, British Columbia, Canada <i>IT Specialist</i> Sept. 2008 – Dec. 2010
TEACHING	Course Instructor (University of California, San Diego): Graduate: Statistical learning in bioinformatics. 2016 Graduate: Computational evolutionary biology. 2017 – 2019 Introduction to Computer Engineering 2016 – 2019
OLDER:	Software Testing and Quality Assurance (TA), University of Waterloo. Winter 2007 Scientific & Technical Communication (TA), University of Tehran. Fall 2005 Ann Arbor, Michigan, Phylogenomics Symposium and Software School 2015 UT Austin, Summer school on Phylogenomics and Metagenomics Summer 2014 Evolution meetings (NC), Software School on ASTRAL and PASTA Summer 2014 UT Austin, Workshop on Phylogeny and Alignment Estimation Winter 2013
HIGHLIGHTS AND INVITED TALKS	See http://ecweb.ucsd.edu/~smirarab/presentations.html for a complete list 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. 2019 UCSD: Curriculum Development Committee. “Engineering in Public Health”. 2019 Conference organization: (IEEE BIBM) (2019), REOMB (2020) 2007-2019 Program Committee: ISBM, ECCB, RECOMB-CG 2015, 2017–2019 Paper Review: See https://publons.com/researcher/697671/siavash-mirarab for a list. Includes papers in: Nature Ecology and Evolution, Nature Communications, Systematic Biology, PLOS Genetics, Journal of the American Statistical Association, Journal of ACM, IEEE Transaction on Computational Biology and Bioinformatics, Theoretical Population Genetics, Bioinformatics, BMC Bioinformatics, Genome Biology and Evolution, GigaScience 2007-2019 Grant Panels: NSF 2018