Siavash Mirarab

CONTACT INFORMATION	UC San Diego (ECE) e-mail: `smirarab@ucsd.edu`, phone: 858 822 6245
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	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 – present**

EDUCATION

Ph.D **Jan. 2011 – July 2015**
University of Texas at Austin, Austin, Texas, Department of Computer Science
- Advisors: Prof. Tandy Warnow, Prof. Keshav Pingali
- Novel scalable approaches for multiple sequence alignment and phylogenetic reconstruction

Master of Science (University of Waterloo, ON, Canada) **Sept. 2006 – Sept. 2008**
- Electrical and Computer Engineering, Advisors: Prof. Ladan Tahvildari
- Thesis: A Bayesian Framework for Software Regression Testing

Bachelor of Science (University of Tehran) **Sept. 2001 – Dec. 2005**
- Electrical and Computer Engineering (Specialized in software engineering).

MAJOR AWARDS

NSF CAREER award	**2019**
Alfred P. Sloan Research Fellow.	**2017**
Honorable Mention for the 2015 ACM Doctoral Dissertation Award.	**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, Computer Science, Bert Kay Dissertation Award, 2015
UT, Austin, College of Natural Sci., Dean's Excellence Award, 2011
UT, Austin, Graduate Dean's Prestigious Fellowship Award, 2011, 2012, 2013, 2014
University of Texas at Austin, MCD fellowship

RESEARCH FUNDING

NSF: III-1845967: "CAREER: Robust & scalable genome..." $549k (5 years)	2019
NSF-1815485 : "III: SMALL: New algorithms for genome ..." $500k (3 years)	2018
NSF-1565862: "CRII: III: Using genomic context to ..." $170k (2 years)	2016
NIH-CFAR: "Accuracy of HIV transmission network ..." $439K (2 years)	2016
Sloan foundation fellowship $60K (2 years)	2016–2018
Other gifts and grants ≈$145K	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, Uyen Mai, Maryam Rabie, Nora Ratchman, Shahab Sarmashghi (co-superviser), Chao Zhang	**2016 – now**

PUBLICATIONS   1. Qiyun Zhu, Uyen Mai, Wayne Pfeiffer, Stefan Janssen, Francesco Asnicar, G Sanders, Jon, Pedro Belda-ferre, Gabriel A Al-ghalith, Evguenia Kopylova, Daniel Mcdonald, John B Yin, Shi Huang, Nimaichand Salam, Jian-yu Jiao, Zijun Wu, Z Xu, Kalen Cantrell, Yimeng Yang, Erfan Sayyari, Maryam Rabiee, James T Morton, 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*, In press, 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 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.

7. Shahab Sarmashghi, Kristine Bohmann, M. Thomas P. Gilbert, Vineet Bafna, and **Siavash Mirarab**. Skmer: assembly-free and alignment-free sample identi-

*Equal contributions

fication using genome skims. *Genome Biology (also appeared in RECOMB 2018)*, 20(1):34, 2019.

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), 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 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), 2017.

25. Uyen Mai and **Siavash Mirarab**. TreeShrink: Efficient Detection of Outlier Tree Leaves. In *Lecture Notes in Computer Science*, volume 10562 LNBI, 116–140. 2017.

26. Chao Zhang, Erfan Sayyari, and **Siavash Mirarab**. ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. In *Lecture Notes in Computer Science*, volume 10562 LNBI, 53–75. 2017.

27. 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.

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 (also appeared in RECOMB 2017)*, PP(99):1–1, 2017.

29. **Siavash Mirarab**. Phylogenomics: Constrained gene tree inference. *Nature Ecology & Evolution*, 1:0056, 2017.

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-phuong 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.

36. 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.

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.

38. **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.

39. N.-P.D. Nam-phuong D. 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.

41. 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.

42. **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.

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.

45. **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.

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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*Equal contributions
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47. **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.

48. **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.

49. Nam Nguyen, **Siavash Mirarab**, Bo Liu, Mihai Pop, and Tandy Warnow. TIPP: Taxonomic Identification and Phylogenetic Profiling. *Bioinformatics*, 30(24):3548–3555, 2014.

50. Théo Zimmermann, **Siavash Mirarab**, and Tandy Warnow. BBCA: Improving the scalability of *BEAST using random binning. *BMC genomics*, 15(Suppl 6):S11, 2014.

51. 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.

52. 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.

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

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

55. **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.

56. **Siavash Mirarab** and Tandy Warnow. FastSP: linear time calculation of alignment accuracy. *Bioinformatics*, 27:3250–8, 2011.

57. 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.

58. **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.

59. **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.

60. 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.

61. 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.

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

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://eceweb.ucsd.edu/~smirarab/software.html for more.

PROFESSIONAL EXPERIENCE	**International Business Machines (IBM)**, Vancouver, British Columbia, Canada
	IT Specialist **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 onPhylogeny and Alignment Estimation	**Winter 2013**

HIGHLIGHTS AND INVITED TALKS — See `http://eceweb.ucsd.edu/~smirarab/presentations.html` for a complete list

CGSI, UCLA, LA, CA	**2017, 2018, 2019**
MMM workshop, Buffalo, NY	**2019**
Bird 10K, Beijing, San Diego (PAG), New York (VGP)	**2016, 2018, 2019**
Evolution meetings, Austin, Portland, Montpellier (France)	**2016, 2017, 2018**
ENABLE, National Chung Hsing University, Taiwan	**2018**
IPAM, UCLA, LA, CA	**2015, 2018**
ISMB, invited Tutorial, Chicago, IL	**2018**
Broad Inst., Boston, MA	**2017**
University of Copenhagen, Copenhagen, Denmark	**2017**
Dagsthul, Germany	**2016**
RECOMB, highlights session, Warsaw, Poland	**2015**
INFORMS, Philadelphia, PA	**2015**
MolPhy-3, Moscow, Russia	**2012**

PROFESSIONAL SERVICES

Leadership: Vertebrate Genome Project (VGP), Council member.	**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**