

Siavash Mirarab (Mir arabbaygi)

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| 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> <i>Associate Professor</i> <i>Full Professor</i> | July 2015 – July 2020 July 2020 – July 2025 July 2025 – 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 | Clarivate Highly Cited Researcher Best paper awards for SSB and RECOMB-CG, Best student award runnerup for MBE 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) | 2022 – 2024 2023 2021 2021 2019 2017 2016 2016 2012 - 2015 2011- 2012 |
| RESEARCH FUNDING | Minderoo Found.: “Enabling the measurement of marine...” NIH: 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 | \$726 K (2 years) 2022 \$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 \$60K (2 years) 2016–2018 ≈\$300K 2017–2024 |
| WORK EXPERIENCE | IBM , Vancouver, BC, Canada <i>IT Specialist</i> | Sept. 2008 – Dec. 2010 |

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| TEACHING: | Course Instructor (University of California, San Diego): | |
| | Graduate: Computational evolutionary biology (ECE 208) | 2016 – 2025 |
| | Introduction to Computer Engineering (ECE 30) | 2016 – 2025 |
| HIGHLIGHTS AND INVITED TALKS | See http://eceweb.ucsd.edu/~smirarab/presentations.html for a complete list | |
| | Institute for Mathematical and Statistical Innovation (IMSI), Chicago, IL | 2025 |
| | Computational Genomics Summer Institute (CGSI), Los Angeles, CA | 2017 – 2025 |
| | Evolution Meeting, Athens, GA, Albuquerque, NM | 2023, 2025 |
| | Institute for Comp. and Exp. Research in Mathematics (ICERM), Rhode Island | 2024 |
| | SMBE, Puerto Vallarta, AI in genomics, | 2024 |
| | Mathematics of Evolution, Singapore, | 2023 |
| | RECOMB-seq, San Diego, keynote speaker, | 2022 |
| | Asilomar Conference on Signals, Systems, and Computers, Monterey, | 2022 |
| | OH-Know!, Norway (online), | 2021 |
| | Phyloseminars, online, | 2021 |
| | Grainger Bioinformatics Center Symposium, online, | 2020 |
| | SysBioDiv and Zoological Society, Freiburg, Germany | 2020 |
| | QCB Colloquium, USC, Biological Sciences, Los Angeles, CA | 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–present |
| | UCSD: Curriculum Development Committee. “Engineering in Public Health”. | 2020 |
| | Conference organization: (IEEE BIBM) (2019), REOMB (2021) | 2019-2020 |
| | Program Committee: ISBM, ECCB, RECOMB-CG, RECOMB | 2015, 2017–2024 |
| | Paper Review for journals of wide readership (e.g., Science, Nature methods), in biology (e.g., Nature Ecology and Evolution), in math (e.g., Journal of the American Statistical Association), and in computer science (Journal of ACM). | |
| | Grant Panels: NSF, DOE, NIH | 2018–2023 |
| PUBLICATIONS | * indicates equal contribution | |
| | 1. Chao Zhang, Rasmus Nielsen and <u>Siavash Mirarab</u> . ASTER: A Package for Large-scale Phylogenomic Reconstructions. <i>Molecular Biology and Evolution</i> , msaf172 2025. | |
| | 2. Anshu Gupta, <u>Siavash Mirarab</u> and Yatish Turakhia. Accurate, scalable, and fully automated inference of species trees from raw genome assemblies using ROADIES. <i>Proceedings of the National Academy of Sciences</i> , 122(19):e2500553122, 2025. | |

3. Chao Zhang, Rasmus Nielsen and [Siavash Mirarab](#). CASTER: Direct species tree inference from whole-genome alignments. *Science*, eadk9688 2025.
4. Puoya Tabaghi, Michael Khanzadeh, Yusu Wang and [Siavash Mirarab](#). Principal Component Analysis in Space Forms. *IEEE Transactions on Signal Processing*, 72:4428–4443, 2024.
5. Ali Osman Berk Sapci and [Siavash Mirarab](#). Memory-bound k -mer selection for large and evolutionary diverse reference libraries. *Genome Research*, 34:1455–1467 2024.
6. Uyen Mai, Eduardo Charvel and [Siavash Mirarab](#). Expectation-Maximization enables Phylogenetic Dating under a Categorical Rate Model. *Systematic Biology*, 73(5):823–838 2024.
7. Josefin Stiller, Shaohong Feng, Al-Aabid Chowdhury et al. Complexity of avian evolution revealed by family-level genomes. *Nature*, 629:851–860 2024.
8. [Siavash Mirarab](#), Iker Rivas-González, Shaohong Feng et al. A region of suppressed recombination misleads neoavian phylogenomics. *Proceedings of the National Academy of Sciences*, 121(15):e2319506121 2024.
9. Yueyu Jiang, Daniel McDonald, Daniela Perry, Rob Knight and [Siavash Mirarab](#). Scaling DEPP phylogenetic placement to ultra-large reference trees: a tree-aware ensemble approach. *Bioinformatics*, btac361 2024.
10. Shayesteh Arasti, Puoya Tabaghi, Yasamin Tabatabaee and [Siavash Mirarab](#). Optimal Tree Metric Matching Enables Phylogenomic Branch Length Estimation. In *Research in Computational Molecular Biology*, 462–465, Cham, 2024. Springer Nature Switzerland.
11. Metin Balaban, Yueyu Jiang, Qiyun Zhu, Daniel McDonald, Rob Knight and [Siavash Mirarab](#). Generation of accurate, expandable phylogenomic trees with uDance. *Nature Biotechnology*, Online 2023.
12. Daniel McDonald, Yueyu Jiang, Metin Balaban et al. Greengenes2 unifies microbial data in a single reference tree. *Nature Biotechnology*, Online 2023.
13. Yasamin Tabatabaee, Chao Zhang, Tandy Warnow and [Siavash Mirarab](#). Phylogenomic branch length estimation using quartets. *Bioinformatics*, 39(Supplement_1):i185–i193 2023.
14. Ali Osman Berk Sapci, Eleonora Rachtman and [Siavash Mirarab](#). CONSULT-II: Accurate taxonomic identification and profiling using locality-sensitive hashing. *Bioinformatics*, btac150 2024.
15. Shayesteh Arasti and [Siavash Mirarab](#). Median quartet tree search algorithms using optimal subtree prune and regraft. *Algorithms for Molecular Biology*, 19(1):12 2024.
16. Aff 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 2023.
17. 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.
18. Chao Zhang and [Siavash Mirarab](#). Weighting by Gene Tree Uncertainty Improves Accuracy of Quartet-based Species Trees. *Molecular Biology and Evolution*, 39(12):msac215 2022.
19. Chao Zhang and [Siavash Mirarab](#). ASTRAL-Pro 2: ultrafast species tree reconstruction from multi-copy gene family trees. *Bioinformatics*, 38(21):4949–4950 2022.
20. Metin Balaban, Nishat A 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.
21. Maryam Rabiee and [Siavash Mirarab](#). QuCo: quartet-based co-estimation of species trees and gene trees. *Bioinformatics*, 38(Supplement_1):i413–i421 2022.
22. Yueyu Jiang, Puoya Tabaghi and [Siavash Mirarab](#). Learning Hyperbolic Embedding for Phylogenetic Tree Placement and Updates. *Biology*, 11(9):1256, 2022.
23. Navid Bin Hasan, Metin Balaban, Avijit Biswas, Md. Shamsuzzoha Bayzid and [Siavash Mirarab](#). Distance-Based Phylogenetic Placement with Statistical Support. *Biology*, 11(8):1212 2022. ISBN: 2079-7737.
24. 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 2022.
25. Yueyu Jiang, Metin Balaban, Qiyun Zhu and [Siavash Mirarab](#). DEPP: Deep Learning Enables Extending Species Trees using Single Genes. *Systematic Biology*, 72(1):17–34 2022.
26. Uyen Mai and [Siavash Mirarab](#). Completing gene trees without species trees in sub-quadratic time. *Bioinformatics*, 38(6):1532–1541 2022.
27. 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 2022.

28. 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 2021.
29. [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 2021.
30. 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 2021.
31. 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 2021.
32. 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 2021.
33. Maryam Rabiee and [Siavash Mirarab](#). SODA: multi-locus species delimitation using quartet frequencies. *Bioinformatics*, 36(24):5623–5631 2021.
34. Shaohong Feng, Josefin Stiller, Yuan Deng et al. Dense sampling of bird diversity increases power of comparative genomics. *Nature*, 587(7833):252–257 2020.
35. Uyen Mai and [Siavash Mirarab](#). Log Transformation Improves Dating of Phylogenies. *Molecular Biology and Evolution*, 38(3):1151–1167 2021.
36. 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 2020.
37. Metin Balaban and [Siavash Mirarab](#). Phylogenetic double placement of mixed samples. *Bioinformatics*, 36(Supplement_1):i335–i343 2020.
38. 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.
39. Francesco Asnicar, Andrew Maltez Thomas, Francesco Beghini et al. Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. *Nature Communications*, 11(1):2500 2020. Publisher: Springer US ISBN: 0348556977.
40. 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 2020.
41. Metin Balaban, Shahab Sarmashghi and [Siavash Mirarab](#). APPLES: Scalable Distance-Based Phylogenetic Placement with or without Alignments. *Systematic Biology*, 69(3):566–578 2020.
42. Maryam Rabiee and [Siavash Mirarab](#). INSTRAL: Discordance-Aware Phylogenetic Placement Using Quartet Scores. *Systematic Biology*, 69(2):384–391 2020.
43. Maryam Rabiee and [Siavash Mirarab](#). Forcing external constraints on tree inference using AS-TRAL. *BMC Genomics*, 21(S2):218 2020.
44. Qiyun Zhu, Uyen Mai, Wayne Pfeiffer et al. Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. *Nature Communications*, 10(1):5477 2019.
45. James H Leebens-Mack, Michael S Barker, Eric J Carpenter et al. One thousand plant transcriptomes and the phylogenomics of green plants. *Nature*, 574(7780):679–685 2019.
46. Erfan Sayyari, Ban Kawas and [Siavash Mirarab](#). TADA: phylogenetic augmentation of microbiome samples enhances phenotype classification. *Bioinformatics*, 35(14):i31–i40 2019.
47. Lei Chen, Qiang Qiu, Yu Jiang et al. Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. *Science*, 364(6446):eaav6202 2019.
48. 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 2019.
49. 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.
50. 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.
51. 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.

52. Maryam Rabiee, Erfan Sayyari and [Siavash Mirarab](#). Multi-allele species reconstruction using ASTRAL. *Molecular Phylogenetics and Evolution*, 130:286–296 2019.
53. Shyam Gopalakrishnan, Mikkel-Holger S. Sinding, Jazmín Ramos-Madriral et al. Interspecific Gene Flow Shaped the Evolution of the Genus *Canis*. *Current Biology*, 28(21):3441–3449.e5 2018.
54. Daniel McDonald, Embriette Hyde, Justine W. Debelius et al. American Gut: an Open Platform for Citizen Science Microbiome Research. *mSystems*, 3(3) 2018.
55. Wolf L. Eiserhardt, Alexandre Antonelli, Dominic J. Bennett et al. A roadmap for global synthesis of the plant tree of life. *American Journal of Botany*, 105(3):614–622 2018.
56. Stefan Janssen, Daniel McDonald, Antonio Gonzalez et al. Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. *mSystems*, 3(3):e00021–18 2018.
57. 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.
58. 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. ISBN: 9783319679785.
59. Erfan Sayyari and [Siavash Mirarab](#). Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. *Genes*, 9(3):132 2018. Publisher: Multidisciplinary Digital Publishing Institute.
60. Erfan Sayyari, James B. Whitfield and [Siavash Mirarab](#). DiscoVista: Interpretable visualizations of gene tree discordance. *Molecular Phylogenetics and Evolution*, 122:110–115 2018. arXiv: 1709.09305.
61. Ali Akbari, Joseph J. Vitti, Arya Iranmehr et al. Identifying the favored mutation in a positive selective sweep. *Nature Methods*, 15(4):279–282 2018. Publisher: Nature Publishing Group.
62. 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.
63. 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.
64. 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. Publisher: Public Library of Science ISBN: 1111111111.
65. [Siavash Mirarab](#). Phylogenomics: Constrained gene tree inference. *Nature Ecology & Evolution*, 1(2):0056 2017. Publisher: Nature Publishing Group.
66. Erfan Sayyari and [Siavash Mirarab](#). Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. *BMC Genomics*, 17(S10):101–113 2016.
67. Nam-phuong N.-P. Nguyen, Michael Nute, [Siavash Mirarab](#) and Tandy Warnow. HIPPI: highly accurate protein family classification with ensembles of HMMs. *BMC Genomics*, 17(S10):765 2016.
68. James E Tarver, Mario dos Reis, [Siavash Mirarab](#) et al. The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. *Genome Biology and Evolution*, 8(2):330–344 2016.
69. [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.
70. Joel Cracraft, Peter Houde, Simon Y W Ho et al. Response to Comment on “Whole-genome analyses resolve early branches in the tree of life of modern birds”. *Science*, 349(6255):1460 2015.
71. 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.
72. Jed Chou, Ashu Gupta, Shashank Yaduvanshi et al. A comparative study of SVDquartets and other coalescent-based species tree estimation methods. *BMC Genomics*, 16(Suppl 10):S2, 2015.
73. [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.
74. Nam-phuong Nguyen, [Siavash Mirarab](#), Keerthana Kumar and Tandy Warnow. Ultra-large alignments using phylogeny-aware profiles. *Genome Biology*, 16(1):124 2015.
75. 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. Publisher: Public Library of Science.

76. Erich D Jarvis, [Siavash Mirarab](#), Andre J Aberer et al. Phylogenomic analyses data of the avian phylogenomics project. *GigaScience*, 4(1):1–9 2015. Publisher: BioMed Central.
77. [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(5):377–86 2015.
78. E. D. Jarvis, [Siavash Mirarab](#), A. J. Aberer et al. Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science*, 346(6215):1320–1331 2014.
79. [Siavash Mirarab](#), M. S. Bayzid, Bastien Boussau and Tandy Warnow. Statistical binning enables an accurate coalescent-based estimation of the avian tree. *Science*, 346(6215):1250463–1250463 2014.
80. Naim Matasci, Ling-Hong L.-H. Hung, Zhixiang Yan et al. Data access for the 1,000 Plants (1KP) project. *GigaScience*, 3(1):17, 2014. Publisher: BioMed Central.
81. Norman J. Wickett, [Siavash Mirarab](#), Nam Nguyen et al. Phylotranscriptomic analysis of the origin and early diversification of land plants. *Proceedings of the National Academy of Sciences*, 111(45):E4859–4868 2014. arXiv: 1301.5277v2 ISBN: 0027-8424.
82. [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 2016. Publisher: Oxford University Press ISBN: 1063-5157.
83. [Siavash Mirarab](#), Rezwana Reaz, Md. Shamsuzzoha Bayzid, Théo Zimmermann, M. S. Swenson and Tandy Warnow. ASTRAL: genome-scale coalescent-based species tree estimation. *Bioinformatics*, 30(17):i541–i548 2014.
84. Nam-phuong Nguyen, [Siavash Mirarab](#), Bo Liu, Mihai Pop and Tandy Warnow. TIPP: taxonomic identification and phylogenetic profiling. *Bioinformatics*, 30(24):3548–3555 2014.
85. Arlin Stoltzfus, Hilmar Lapp, Naim Matasci et al. Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. *BMC bioinformatics*, 14(1):158, 2013. Publisher: BioMed Central Ltd ISBN: 1471-2105 (Electronic)\r1471-2105 (Linking).
86. Nam Nguyen, [Siavash Mirarab](#) and Tandy Warnow. MRL and SuperFine+ MRL: new supertree methods. *Algorithms for Molecular Biology*, 7(1):3 2012.
87. [Siavash Mirarab](#), Nam Nguyen and Tandy Warnow. SEPP: SATé-Enabled Phylogenetic Placement. In *Pacific Symposium On Biocomputing*, 247–58. WORLD SCIENTIFIC 2012.
88. [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. Publisher: IEEE.
89. [Siavash Mirarab](#) and Tandy Warnow. FastSP: linear time calculation of alignment accuracy. *Bioinformatics*, 27(23):3250–8, 2011. ISBN: 1367-4811; 1367-4803.
90. 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(5):593–617, 2010. Publisher: IEEE.
91. [Siavash Mirarab](#) and Ladan Tahvildari. An empirical study on bayesian network-based approach for test case prioritization. In *Software Testing, Verification, and Validation, 2008 1st International Conference on*, 278–287. IEEE, 2008.
92. [Siavash Mirarab](#), Afshar Ganjali, Ladan Tahvildari, Shimin Li, Weining Liu and Mike Morrissey. A requirement-based software testing framework: An industrial practice. In *Software Maintenance, 2008. ICSM 2008. IEEE International Conference on*, 452–455. IEEE, 2008.
93. 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 the 16th ACM SIGSOFT International Symposium on Foundations of software engineering*, 71–82. ACM, 2008.
94. Mehdi Amoui, Mazeiar Salehie, [Siavash Mirarab](#) and Ladan Tahvildari. Adaptive action selection in autonomic software using reinforcement learning. In *Autonomic and Autonomous Systems, 2008. ICAS 2008. Fourth International Conference on*, 175–181. IEEE, 2008.
95. [Siavash Mirarab](#) and Ladan Tahvildari. A prioritization approach for software test cases based on bayesian networks. In *Fundamental Approaches to Software Engineering*, volume 4422 LNCS, 276–290. Springer Berlin Heidelberg, 2007. ISSN: 03029743.
96. [Siavash Mirarab](#), Alaa Hassouna and Ladan Tahvildari. Using bayesian belief networks to predict change propagation in software systems. In *Program Comprehension, 2007. ICPC’07. 15th IEEE International Conference on*, 177–188. IEEE, 2007.
97. Mehdi Amoui, [Siavash Mirarab](#), Sepand Ansari and Caro Lucas. A genetic algorithm approach to design evolution using design pattern transformation. *International 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

DEPP (<https://github.com/yueyujiang/DEPP>)
 Deep learning for phylogenetic placement

ASTER (<https://github.com/chaoszhang/ASTER>)
 Species tree estimation from both gene trees and alignments

krepp (<https://github.com/bo1929/krepp>)
 Read mapping to many genomes using k -mers

This list has recently grown too long to reproduce. See below for more.
<http://eceweb.ucsd.edu/~smirarab/software.html>