Niema Moshiri niema@ucsd.edu — https://niema.net

Academic Positions

University of California, San Diego

Associate Teaching Professor, Computer Science & Engineering (2023 – Present)

- Affiliation: Bioinformatics and Systems Biology Graduate Program
- Affiliation: Department of Biomedical Informatics (School of Medicine)
- Affiliation: PREPARE Institute

Assistant Teaching Professor, Computer Science & Engineering (2019 – 2023)

Education

University of California, San Diego

Ph.D. in Bioinformatics and Systems Biology, 4.000 (June 2019)

- Advisors: Siavash Mirarab and Pavel Pevzner

B.S. in Bioengineering: Bioinformatics, 3.624 (June 2015)

- Minor: Economics

Funding

Sep 2023	*Contract* ($2,243,691; 3 years) Centers for Disease Control and Prevention (CDC)
Aug 2023	*Innovative Learning Technology Initiative* ($46,000; 1 year) UC Online, University of California Office of the President
Jul 2022	*NIH U54 Award 1U54HG012510-01* ($2,505,728; 5 years) National Institutes of Health (NIH)
Sep 2021	*NIH RM1 Award 1RM1HG011558-01A1* ($11,704,255; 5 years) National Institutes of Health (NIH)
Sep 2021	*COVID-19 HPC Consortium Award* (110,00 SUs; 6 months) COVID-19 High Performance Computing (HPC) Consortium
Jul 2021	*UC San Diego CDIIP Award* ($38,273; 1 year) UC San Diego Office of the Executive Vice Chancellor
Oct 2020	*Google exploreCSR Award* ($15,000) Google Research
May 2020	*NIH R25 Award 1R25HG011022-01* ($804,013; 5 years) National Institutes of Health (NIH)
May 2020	*UC-HSI DDI Award* ($350,000; 5 years) University of California Office of the President (UCOP)
May 2020	*NSF RAPID COVID-19 Award 2028040* ($200,000; 1 year) National Science Foundation (NSF)
Mar 2020	*Research Credits Program* ($5,000; 1 year) Google Cloud Platform (GCP)
Aug 2019	*Innovative Learning Technology Initiative* ($71,000; 5 years) University of California Office of the President (UCOP)

Honors and Awards

Jun 2023	*Outstanding Teaching Award* UC San Diego Sixth College
Nov 2022	*30 Under 30 — Healthcare (2023)* Forbes
Jun 2022	*Outstanding Teaching Award* UC San Diego Earl Warren College
Jun 2022	*Outstanding Teaching Award* UC San Diego Sixth College
Apr 2022	*Integrity Award* UC San Diego
Jun 2021	*Faculty of the Year Award* UC San Diego Tau Beta Pi
Jan 2021	*Best Teacher Award* UC San Diego Jacobs School of Engineering
Apr 2017	*Distinguished Teaching Award* UC San Diego Academic Senate
Jun 2015	*Distinguished Leadership/Service Award* UC San Diego Bioengineering Department
2011–2015	*Thurgood Marshall College Honors Program* Thurgood Marshall College, UC San Diego
2011–2015	*Provost Honors* University of California, San Diego

Research & Publications

Textbooks

Moshiri N (2024). "How to Teach Online." *GitHub Pages*. https://niema.net/How-to-Teach-Online (PDF)

Moshiri N (2022). "Learn Programming: Python – Remake." *Steam*. Steam App: 1882420

Moshiri N (2021). "Learn Programming: Python – Retro." *Steam*. Steam App: 1536770

Mansuri S, **Moshiri N** (2021). "Introduction to Computer Science and Object-Oriented Programming: Python." *Cogniterra (Stepik)*. https://cogniterra.org/326

Moshiri N, Izhikevich L (2018). "Design and Analysis of Data Structures." *Amazon KDP*. Paperback ISBN:1981017232, Kindle ASIN:B07CYM8ZWJ.

Moshiri N, Izhikevich L (2016). "Data Structures." *Cogniterra (Stepik)*. https://cogniterra.org/330

Papers/Articles

Moshiri N (2024). "Scalable Epidemic Simulation using FAVITES-Lite." *Computational Virology (Methods in Molecular Biology)*. Book Chapter. In Press.

Xu W, Hsu PK, **Moshiri N**, Yu S, Rosing T (2024). "HyperGen: Compact and Efficient Genome Sketching using Hyperdimensional Vectors." *Bioinformatics*. btae452. doi:10.1093/bioinformatics/btae452

Pinge S, Xu W, Kang J, Zhang T, **Moshiri N**, Bittremieux W, Rosing T (2024). "SpecHD: Hyperdimensional Computing Framework for FPGA-based Mass Spectrometry Clustering." *Design Automation and Test in Europe Conference (DATE) 2024*. In Press.

Kang J, Xu W, Bittremieux W, **Moshiri N**, Rosing T (2024). "DRAM-based Acceleration of Open Modification Search for Mass Spectrometry-based Proteomics." *IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems*. In Press. doi:10.1109/TCAD.2024.3382842

Keehner J, Abeles SR, Longhurst CA, Horton LE, Myers FE, Riggs-Rodriguez L, Ahmad M, Baxter S, Boussina A, Cantrell K, Cardenas P, De Hoff P, El-Kareh R, Holland J, Ikeda D, Kurashige K, Laurent LC, Aigner S, Andersen KG, Anderson C, Baer NA, Barber T, Bauk M, Beck JN, Belda-Ferre P, Betty M, Birmingham A, Castro-Martinez A, Cheung W, Fisch KM, Gangavarapu K, Gargano I, Hakim A, Harsono S, Henson B, Hobbs C, Holmes J, Jepsen K, Kurzban E, Marotz CA, Matteson NL, **Moshiri N**, Ngo TT, Ostrander TR, Perkins S, Plascencia A, Rivera An, Rivera Ar, Salido RA, Seaver P, Schwab M, Veder A, Zeller M, Lucas A, Pride D, Sathe S, Tran AR, Vasylyeva TI, Yeo G, Knight R, Wertheim JO, Torriani FJ (2024). "Integrated Genomic and Social Network Analyses of Severe Acute Respiratory Syndrome Coronavirus 2 Transmission in the Healthcare Setting." *Clinical Infectious Diseases*. ciad738. doi:10.1093/cid/ciad738

Cummins B, Johnson K, Schneider JA, Del Vecchio N, **Moshiri N**, Wertheim JO, Goyal R, Skaathun B (2024). "Leveraging social networks for identification of people living with HIV who are virally unsuppressed." *AIDS*. 38(2):245–254. doi:10.1097/QAD.0000000000003767

Ji D, Aboukhalil R, **Moshiri N** (2024). "ViralWasm: a client-side user-friendly web application suite for viral genomics." *Bioinformatics*. 40(1):btae018. doi:10.1093/bioinformatics/btae018

Matteson NL, Hassler GW, Kurzban E, Schwab MA, Perkins SA, Gangavarapu K, Levy JI, Parker E, Pride D, Hakim A, De Hoff P, Cheung W, Castro-Martinez A, Rivera A, Veder A Rivera A, Wauer C, Holmes J, Wilson J, Ngo SN, Plascencia A, Lawrence ES, Smoot EW, Eisner ER, Tsai R, Chacón M, Baer NA, Seaver P, Salido RA, Aigner S, Ngo TT, Barber T, Ostrander T, Fielding-Miller R, Simmons EH, Zazueta OE, Serafin-Higuera I, Sanchez-Alvarez M, Moreno-Camacho JL, GarcÃa-Gil A, Murphy Schafer AR, McDonald E, Corrigan J, Malone JD, Stous S, Shah S, **Moshiri N**, Weiss A, Anderson C, Aceves CM, Spencer EG, Hufbauer EC, Lee JJ, Ramesh KS, Nguyen KN, Saucedo K, Robles-Sikisaka R, Fisch KM, Gonias SL, Birmingham A, McDonald D, Karthikeyan S, Martin NK, Schooley RT, Negrete AJ, Reyna HJ, Chavez JR, Garcia ML, Cornejo-Bravo JM, Becker D, Isaksson M, Washington NL, Lee W, Garfein RS, Luna-Ruiz Esparza MA, Alcántar-Fernández J, Henson B, Jepsen K, Olivares-Flores B, Barrera-Badillo G, Lopez-Martínez I, Ramírez-González JE, Flores-León R, Kingsmore SF, Sanders A, Pradenas A, White B, Matthews G, Hale M, McLawhon RW, Reed SL, Winbush T, McHardy IH, Fielding RA, Nicholson L, Quigley MM, Harding A, Mendoza A, Bakhtar O, Browne SH, Olivas Flores J, Rincon RodrÃguez DG, Gonzalez Ibarra M, Robles Ibarra LC, Arellano Vera BJ, Gonzalez Garcia J, Harvey-Vera A, Knight R, Laurent LC, Yeo GW, Wertheim JO, Ji X, Worobey M, Suchard MA, Andersen KG, Campos-Romero A, Wohl S, Zeller M (2023). "Genomic surveillance reveals dynamic shifts in the connectivity of COVID-19 epidemics." *Cell*. 186(26):5690–5704.e20. doi:10.1016/j.cell.2023.11.024

Zhang T, González A, DeReus J, Armstrong G, Shaffer J, Sfigoli I, McDonald D, **Moshiri N**, Knight R, Rosing T (2023). "GenoMiX: Accelerated Simultaneous Analysis of Human Genomics, Microbiome Metagenomics, and Viral Sequences." *IEEE Biomedical Circuits and Systems Conference (BioCAS) 2023*. doi:10.1109/BioCAS58349.2023.10388531

Kang J, Xu W, Bittremieux W, **Moshiri N**, Rosing T (2023). "Accelerating Open Modification Spectral Library Searching on Tensor Core in Hyperdimensional Space." *Bioinformatics*. 39(7):btad404. doi:10.1093/bioinformatics/btad404

Xu W, Kang J, Bittremieux W, **Moshiri N**, Rosing T (2023). "HyperSpec: Ultrafast Mass Spectra Clustering in Hyperdimensional Space." *Journal of Proteome Research*. 22(6):1639–1648. doi:10.1021/acs.jproteome.2c00612

Moshiri N (2023). "ViralConsensus: A fast and memory-efficient tool for calling viral consensus genome sequences directly from read alignment data." *Bioinformatics*. 39(5):btad317. doi:10.1093/bioinformatics/btad317

Fielding-Miller RK, Karthikeyan S, Gaines T, Garfein RS, Salido RA, Cantu VJ, Kohn L, Martin NK, Wynn A, Wijaya FC, Flores M, Omaleki V, Majnoonian A, Gonzalez-Zuniga P, Nguyen M, Vo AV, Le T, Duong D, Hassani A, Tweeten S, Jepsen K, Henson B, Hakim A, Birmingham A, De Hoff P, Mark AM, Nasamran CA, Rosenthal SB, **Moshiri N**, Fisch KM, Humphrey G, Farmer S, Tubb H, Valles T, Morris J, Kang J, Khaleghi B, Young C, Akel AD, Eilert S, Eno J, Curewitz K, Laurent LC, Rosing T, Knight R (2023). "Safer at School Early Alert: An observational study of wastewater and surface monitoring to detect COVID-19 in elementary schools." *The Lancet Regional Health - Americas*. 19:100449. doi:10.1016/j.lana.2023.100449

Xu W, Gupta S, **Moshiri N**, Rosing T (2023). "RAPIDx: High-performance ReRAM Processing in-Memory Accelerator for Sequence Alignment." *IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems*. 42(10):3275–3288. doi:10.1109/TCAD.2023.3239537

Khaleghi B, Zhang T, Martino C, Armstrong G, Akel A, Curewitz K, Eno J, Eilert S, Knight R, **Moshiri N**, Rosing T (2022). "SALIENT: Ultra-Fast FPGA-based Short Read Alignment." *International Conference on Field Programmable. Technology (FPT) 2022*. doi:10.1109/ICFPT56656.2022.9974548

Khaleghi B, Zhang T, Shao N, Akel A, Curewitz K, Eno J, Eilert S, **Moshiri N**, Rosing T (2022). "FAST: FPGA-based Acceleration of Genomic Sequence Trimming." *IEEE Biomedical Circuits and Systems Conference (BioCAS) 2022*. doi:10.1109/BioCAS54905.2022.9948621

Pekar JE, Magee A, Parker E, **Moshiri N**, Izhikevich K, Havens JL, Gangavarapu K, Malpica Serrano LM, Crits-Christoph A, Matteson NL, Zeller M, Levy JI, Wang JC, Hughes S, Lee J, Park H, Park MS, Ching Zi Yan K, Tzer Pin Lin R, Mat Isa MN, Muhammad Noor Y, Vasylyeva TI, Garry RF, Homes EC, Rambaut A, Suchard MA, Andersen KG, Worobey M, Wertheim JO (2022). "The molecular epidemiology of multiple zoonotic origins of SARS-CoV-2." *Science*. 377(6609):960-966. doi:10.1126/science.abp8337

Karthikeyan S, Levy JI, De Hoff P, Humphrey G, Birmingham A, Jepsen K, Farmer S, Tubb HM, Valles T, Tribelhorn CE, Tsai R, Aigner S, Sathe S, **Moshiri N**, Henson B, Mark AM, Hakim A, Baer NA, Barber T, Belda-Ferre P, Chacon M, Cheung W, Crescini ES, Eisner ER, Lastrella AL, Lawrence ES, Marotz CA, Ngo TT, Ostrander T, Plascencia A, Salido RA, Seaver P, Smoot EW, McDonald D, Neuhard RM, Scioscia AL, Satterlund AM, Simmons EH, Abelman DB, Brenner D, Bruner JC, Buckley A, Ellison M, Gattas J, Gonias SL, Hale M, Hawkins F, Ikeda L, Jhaveri H, Johnson T, Kellen V, Kremer B, Matthews R, McLawhon RW, Ouillet P, Park D, Pradenas A, Reed S, Riggs L, Sanders A, Sollenberger B, Song A, White B, Winbush T, Aceves CM, Anderson C, Gangavarapu K, Hufbauer E, Kurzban E, Lee J, Matteson NL, Parker E, Perkins SA, Ramesh KS, Robles-Sikisaka R, Schwab MA, Spencer E, Wohl S, Nicholson L, McHardy IH, Dimmock DP, Hobbs CA, Bakhtar O, Harding A, Mendoza A, Bolze A, Becker D, Cirulli ET, Isaksson M, Schiabor Barrett KM, Washington NL, Malone JD, Murphy Schafer A, Gurfield N, Stous S, Fielding-Miller R, Garfein RS, Gaines T, Anderson C, Martin NK, Schooley R, Austin B, MacCannell DR, Kingsmore SF, Lee W, Shah S, McDonald E, Yu AT, Zeller M, Fisch KM, Longhurst C, Maysent P, Pride D, Khosla PK, Laurent LC, Yeo GW, Andersen KG, Knight R (2022). "Wastewater sequencing uncovers early, cryptic SARS-CoV-2 variant transmission." *Nature*. 609:101-108. doi:10.1038/s41586-022-05049-6

Jones D, Allen J, Yang Y, Bennett WF, Gokhale M, **Moshiri N**, Rosing T (2022). "Accelerators for Classical Molecular Dynamics Simulations of Biomolecules." *Journal of Chemical Theory and Computation*. 18(7):4047-4069.

Moshiri N (2022). "A scalable approach for detecting exam similarity in CS courses." *Journal of Computing Sciences in Colleges*. 37(10):8-16. doi:10.5555/3533760.3533761

Young C, Meng S, **Moshiri N** (2022). "An Evaluation of Phylogenetic Workflows in Viral Molecular Epidemiology." *Viruses*. 14(4):774. doi:10.3390/v14040774

Moshiri N, Fisch KM, Birmingham A, DeHoff P, Yeo GW, Jepsen K, Laurent LC, Knight R (2022). "The ViReflow pipeline enables user friendly large scale viral consensus genome reconstruction." *Scientific Reports*. 12:5077. doi:10.1038/s41598-022-09035-w

Armstrong G, Martino C, Morris J, Khaleghi B, Kang J, Dereus J, Zhu Q, Roush D, McDonald D, Gonzalez A, Shaffer J, Carpenter C, Estaki M, Wandro S, Eilert S, Akel A, Eno J, Curewitz K, Swafford A, **Moshiri N**, Rosing T, Knight R (2022). "Swapping metagenomics preprocessing pipeline components offers speed and sensitivity increases." *mSystems*. 7(2):e01378-21. doi:10.1128/msystems.01378-21

Moshiri N (2022). "NiemaGraphGen: A memory-efficient global-scale contact network simulation toolkit." *Gigabyte*. doi:10.46471/gigabyte.37

Salamat S, **Moshiri N**, Rosing T (2021). "FPGA Acceleration of Pairwise Distance Calculation for Viral Transmission Clustering." *IEEE Biomedical Circuits and Systems Conference (BioCAS) 2021*. PDF.

Salamat S, Kang J, Kim Y, Imani M, **Moshiri N**, Rosing T (2021). "FPGA Acceleration of Protein Back-Translation and Alignment." *Design Automation and Test in Europe Conference (DATE) 2021*.

Keehner J, Horton LE, Binkin NJ, Laurent LC, Pride D, Longhurst CA, Abeles SR, Torriani FJ, SEARCH Alliance (Aigner S, Andersen KG, Anderson C, Baer NA, Barber T, Belda-Ferre P, Betty M, Birmingham A, Castro-Martinez A, Chacón M, Cheung W, Crescini ES, De Hoff P, Eisner ER, Eisner ER, Fisch K, Vargas LF, Gangavarapu K, Hakim A, Henson B, Hobbs C, Humphrey G, Jepsen K, Kapadia BK, Knight R, Lastrella AL, Laurent LC, Lawrence ES, Machnicki M, Marotz CA, Matteson NL, Maunder DJ, **Moshiri N**, Ngo TT, Nouri A, Ostrander TR, Plascencia A, Ruiz CA, Salido RA, Sathe S, Seaver P, Smoot EW, Tsai R, Wu MY, Xia B, Yeo GW, Zeller M) (2021). "Resurgence of SARS-CoV-2 Infection in a Highly Vaccinated Health System Workforce." *The New England Journal of Medicine*. 385:1330-1332. doi:10.1056/NEJMc2112981

Zhou M, Wu L, Li M, **Moshiri N**, Skadron K, Rosing T (2021). "Ultra Efficient Acceleration for De Novo Genome Assembly via Near-Memory Computing." *International Conference on Parallel Architectures and Compilation Techniques (PACT) 2021*. doi:10.1109/PACT52795.2021.00022

Leininger E, Shaw K, **Moshiri N**, Neiles K, Onsongo G, Ritz A (2021). "Ten Simple Rules for Attending Your First Conference." *PLOS Computational Biology*. 17(7):e1009133. doi:10.1371/journal.pcbi.1009133

Almaraz K, Jang T, Lewis M, Ngo T, Song M, **Moshiri N** (2021). "SEPIA: Simulation-based Evaluation of Prioritization Algorithms." *BMC Medical Informatics and Decision Making*. 21:177. doi:10.1186/s12911-021-01536-4

Pekar J, Worobey M, **Moshiri N**, Scheffler K, Wertheim JO (2021). "Timing the SARS-CoV-2 Index Case in Hubei Province." *Science*. 372(6540):412-417. doi:10.1126/science.abf8003

Moshiri N, Smith DM, Mirarab S (2021). "HIV Care Prioritization using Phylogenetic Branch Length." *Journal of Acquired Immune Deficiency Syndromes*. 86(5):626-637. doi:10.1097/QAI.0000000000002612

Moshiri N (2021). "ViralMSA: Massively scalable reference-guided multiple sequence alignment of viral genomes." *Bioinformatics*. 37(5):714-716. doi:10.1093/bioinformatics/btaa743

Moshiri N (2020). "Here's how scientists are tracking the genetic evolution of COVID-19." *The Conversation*.

Kim Y, Imani M, **Moshiri N**, Rosing T (2020). "GenieHD: Efficient DNA Pattern Matching Accelerator Using Hyperdimensional Computing." *IEEE/ACM Design Automation and Test in Europe Conference (DATE) 2020*. doi:10.23919/DATE48585.2020.9116397

Moshiri N (2020). "TreeSwift: a massively scalable Python package for trees." *SoftwareX*. 11:100436. doi:10.1016/j.softx.2020.100436

Balaban M, **Moshiri N**, Mai U, Jia X, Mirarab S (2019). "TreeCluster: Clustering biological sequences using phylogenetic trees." *PLoS ONE*. 14(8):e0221068. doi:10.1371/journal.pone.0221068

Rule A, Birmingham A, Zuniga C, Altintas I, Huang SC, Knight R, **Moshiri N**, Nguyen M, Rosenthal SB, Perez F, Rose P (2019). "Ten Simple Rules for Reproducible Research in Jupyter Notebooks." *PLOS Computational Biology*. 15(7):e1007007. doi:10.1371/journal.pcbi.1007007

Moshiri N, Ragonnet-Cronin M, Wertheim JO, Mirarab S (2019). "FAVITES: simultaneous simulation of transmission networks, phylogenetic trees, and sequences." *Bioinformatics*. 35(11):1852-1861. doi:10.1093/bioinformatics/bty921

Moshiri N, Mirarab S (2018). "A Two-State Model of Tree Evolution and its Applications to *Alu* Retrotransposition." *Systematic Biology*. 67(3), 475-489. doi:10.1093/sysbio/syx088

Conference Presentations

Goldstein S, Feeley T, Babler K, Hilbert Z, Downhour D, **Moshiri N**, Elde N (2024). "Hidden evolutionary constraints dictate the retention of coronavirus accessory genes." *31st International Dynamics & Evolution of Human Viruses*. Poster.

Ji D, Aboukhalil R, **Moshiri N** (2024). "ViralWasm: a client-side user-friendly web application suite for viral genomics." *Workshop on Emerging Computer Systems Challenges and Applications in Biomedicine (BioSys) 2024*. Talk.

Hadjipieris P, **Moshiri N** (2023). "Hyflex Course Design: Student Experiences of Equity-centered Technology Enhanced Curriculum." *Professional and Organizational Development (POD) 2023*. Talk.

Cummins B, Johnson K, Schneider JA, Del Vecchio N, **Moshiri N**, Wertheim JO, Goyal R, Skaathun B (2023). "Leveraging social networks for identification of people living with HIV and high transmission potential." *International AIDS Society (IAS) 2023*. Poster.

Mkandawire W, Butler K, Varilly P, **Moshiri N**, Colubri A (2022). "Simulacres et Simulation: Using GAMA to debug a real-world genetic-epidemiology outbreak simulator." *GAMA Days 2022*. Talk.

Moshiri N (2022). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *San Diego Epidemiology Research Exchange Conference 2022*. Talk.

Moshiri N (2022). "A scalable approach for detecting exam similarity in CS courses." *Consortium for Computing Sciences in Colleges, Southwest (CCSC-SW) 2022*. Talk.

Moshiri N (2021). "Optimizing high-performance cloud computing to enable real-time high-throughput SARS-CoV-2 whole genome sequence analysis." *28th International Dynamics & Evolution of Human Viruses*. Poster.

Young C, Meng S, **Moshiri N** (2021). "An evaluation of phylogenetic workflows in viral molecular epidemiology." *28th International Dynamics & Evolution of Human Viruses*. Poster.

Kang J, Young C, Morris J, Akel A, Eilert S, Eno J, Curewitz K, **Moshiri N**, Rosing T (2021). "A GPU-Powered Phylogenetic Analysis for Large-scale Genomic Sequences." *28th International Dynamics & Evolution of Human Viruses*. Poster.

Salamat S, **Moshiri N**, Rosing T (2021). "FPGA-based acceleration of pairwise distance calculation for viral transmission clustering." *28th International Dynamics & Evolution of Human Viruses*. Poster.

Khaleghi B, Akel A, Curewitz K, Eno J, Eilert S, **Moshiri N**, Rosing T (2021). "FPGA-based acceleration of primer trimming." *28th International Dynamics & Evolution of Human Viruses*. Talk.

Moshiri N (2020). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *Cold Spring Harbor Laboratory (CSHL) Biological Data Science Meeting 2020*. Poster.

Moshiri N (2020). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *COVID-19 Dynamics & Evolution*. Talk.

Salamat S, Kang J, Kim Y, Imani M, **Moshiri N**, Rosing T (2020). "FPGA Acceleration of Protein Back-Translation and Alignment." *American Society of Human Genetics (ASHG) 2020*. Poster.

Gupta S, Imani M, Khaleghi B, **Moshiri N**, Rosing T (2020). "RAPIDx: A ReRAM Processing in-Memory Architecture for DNA Short Read Alignment." *American Society of Human Genetics (ASHG) 2020*. Poster.

Moshiri N (2020). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *Computing Research Association (CRA) Virtual Conference 2020*. Talk.

Moshiri N (2020). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *Bioinformatics Community Conference (BCC) 2020*. Poster.

Almaraz K, Jang T, Lewis M, Ngo T, Song M, **Moshiri N** (2020). "SEPIA: Simulation-based Evaluation of PrIoritization Algorithms." *27th International HIV Dynamics & Evolution*. Poster.

Lewis M, **Moshiri N** (2020). "Automated plagiarism detection in programming courses: a graph theoretical approach using MOSS." *Consortium for Computing Sciences in Colleges, Southwest (CCSC-SW) 2020*. Poster.

Mansuri S, Zhou H, Battu H, Fong A, Ho T, Xiao E, **Moshiri N** (2020). "What to do after AP CS? A case study on short technical modules for post-AP-exam high school students." *Consortium for Computing Sciences in Colleges, Southwest (CCSC-SW) 2020*. Poster.

Moshiri N, Pevzner P (2018). "Flipping computational courses using Massive Adaptive Interactive Texts." *Cold Spring Harbor Laboratory (CSHL) Biological Data Science Meeting 2018*. Talk.

Moshiri N (2018). "Open Computational Problems in HIV Epidemiology." *Workshop on the Future of Algorithms in Biology (FAB) 2018*. Talk.

Huang SC, **Moshiri N**, Reich M, Rose P (2018). "Challenges and Guidelines for Reproducible Research with Jupyter Notebook." *JupyterCon 2018*. Poster.

Moshiri N, Ragonnet-Cronin M, Wertheim J, Mirarab S (2018). "FAVITES: a framework for the simulation of compatible viral transmission networks, phylogenetic trees and sequences." *International AIDS Conference 2018*. Poster.

Moshiri N, Ragonnet-Cronin M, Wertheim J, Mirarab S (2018). "FAVITES: a framework for the simulation of compatible viral transmission networks, phylogenetic trees and sequences." *Society of Molecular Biology and Evolution (SMBE) 2018*. Poster.

Moshiri N, Ragonnet-Cronin M, Wertheim J, Mirarab S (2018). "FAVITES: a framework for the simulation of compatible viral transmission networks, phylogenetic trees and sequences." *25th International HIV Dynamics & Evolution*. Talk.

Moshiri N (2017). "Using Online Classes to Flip Bioinformatics Classrooms." *International Society for Computational Biology (ISMB) 2017*. Talk.

Moshiri N, Mirarab S (2017). "A two-state model of tree evolution and its applications to Alu retrotransposition." *Society of Molecular Biology and Society of Molecular Biology and Evolution (SMBE) 2017*. Poster.

Preprints/Reports

Moshiri N (2024). "CompactTree: A lightweight header-only C++ library for ultra-large phylogenetics." *bioRxiv*. doi:10.1101/2024.07.15.603593

Goldstein SA, Feeley TM, Babler KM, Hilbert ZA, Downhour DM, **Moshiri N**, Elde NC (2023). "Hidden evolutionary constraints dictate the retention of coronavirus accessory genes." *bioRxiv*. doi:10.1101/2023.10.12.561935

Crits-Christoph A, Levy JI, Pekar JE, Goldstein SA, Singh R, Hensel Z, Gangavarapu K, Rogers MB, **Moshiri N**, Garry RF, Holmes EC, Koopmans MPG, Lemey P, Popescu S, Rambaut A, Robertson DL, Suchard MA, Wertheim JO, Rasmussen AL, Andersen KG, Worobey M, Débarre F (2023). "Genetic tracing of market wildlife and viruses at the epicenter of the COVID-19 pandemic." *bioRxiv*. doi:10.1101/2023.09.13.557637

Soto Miranda M, Narváez Romo R, **Moshiri N** (2023). "Single-linkage molecular clustering of viral pathogens." *bioRxiv*. doi:10.1101/2023.08.03.551813

Jones D, Allen JE, Zhang X, Khaleghi B, Kang J, Xu W, **Moshiri N**, Rosing T (2023). "HD-Bind: Encoding of Molecular Structure with Low Precision, Hyperdimensional Binary Representations." *arXiv*:2303.15604

Crits-Christoph A, Gangavarapu K, Pekar JE, **Moshiri N**, Singh R, Levy JI, Goldstein SA, Suchard MA, Popescu S, Robertson DL, Lemey P, Wertheim JO, Garry RF, Rasmussen AL, Andersen KG, Holmes EC, Rambaut A, Worobey M, Débarre F (2023). "Genetic evidence of susceptible wildlife in SARS-CoV-2 positive samples at the Huanan Wholesale Seafood Market, Wuhan: Analysis and interpretation of data released by the Chinese Center for Disease Control." *Zenodo*. doi:10.5281/zenodo.7754298

Moshiri N (2022). "ViReaDB: A user-friendly database for compactly storing viral sequence data and rapidly computing consensus genome sequences." *bioRxiv*. doi:10.1101/2022.10.21.513318

Moshiri N (2020). "CoaTran: Coalescent tree simulation along a transmission network." *bioRxiv*. doi:10.1101/2020.11.10.377499

Velazquez A, Bustria M, Ouyang Y, **Moshiri N** (2020). "An analysis of clinical and geographical metadata of over 75,000 records in the GISAID COVID-19 database." *medRxiv*. doi:10.1101/2020.09.22.20199497

Song MJ, **Moshiri N** (2020). "An Analysis of SARS-CoV-2 Using ViReport." *bioRxiv*. doi:10.1101/2020.06.20.163162

Moshiri N (2018). "The dual-Barabási-Albert model." *arXiv*:1810.10538

Moshiri N (2018). "TreeN93: a non-parametric distance-based method for inferring viral transmission clusters." *bioRxiv*. doi:10.1101/383190

Moshiri N (2017). "A linear-time algorithm to sample the dual-birth model." *bioRxiv*. doi:10.1101/226423

Software

CoaTran: Simulate coalescent viral phylogenetic trees along a transmission network
https://github.com/niemasd/CoaTran

CompactTree: Parse and iterate over ultra-large tree structures in C++
https://github.com/niemasd/CompactTree

FAVITES: Simulate viral transmission, phylogenetic trees, and sequences
https://github.com/niemasd/FAVITES

NiemaGraphGen: Simulate ultra-large contact networks
https://github.com/niemasd/NiemaGraphGen

ProACT: Prioritize HIV care
https://github.com/niemasd/ProACT

TreeCluster: Infer transmission clusters from viral phylogenies
https://github.com/niemasd/TreeCluster

TreeN93: Infer transmission clusters non-parametrically from TN93 distances
https://moshiri-lab.github.io/TreeN93

TreeSAP: Simulate trees under various phylogenetic models
https://github.com/niemasd/TreeSAP

TreeSwift: Parse, manipulate, and iterate over ultra-large tree structures in Python
https://github.com/niemasd/TreeSwift

ViralConsensus: Call a viral consensus genome sequence
https://github.com/niemasd/ViralConsensus

ViralMSA: Estimate multiple sequence alignments of whole viral genomes
https://github.com/niemasd/ViralMSA

ViralWasm: Client-side web applications for viral molecular epidemiology
https://niema-lab.github.io/ViralWasm

ViReaDB: Compactly store viral sequence data
https://github.com/niemasd/ViReaDB

ViReflow: Produce consensus genome sequences from viral amplicon sequence data
https://github.com/niemasd/ViReflow

Invited Talks

Apr 2024	*Keynote Talk* DiamondHacks 2024
Feb 2024	*Improving HIV incidence estimation through integration of molecular data with epidemic modeling* AntiViral Research Center (AVRC), UC San Diego
Nov 2023	*Real-time genomic surveillance of pathogens through bioinformatics applications* PAHO Genomic Surveillance Regional Networks (PAHOGen)
Nov 2023	*Improving HIV incidence estimation through integration of molecular data with epidemic modeling* San Diego Center for AIDS Research (CFAR), UC San Diego
Sep 2023	*A scalable approach for detecting exam similarity in CS courses* Department of Computer Science, UC Davis
Sep 2023	*Massively-scalable tools for real-time viral molecular surveillance* Lawrence Livermore National Laboratory (LLNL)
Sep 2023	*Bioinformatics, AI, and Games* Sony Interactive Entertainment (PlayStation)
Jun 2023	*Computational Methods in Viral Molecular Epidemiology* San Diego Diplomacy Council
Jun 2023	*ViralConsensus: Fast and memory-efficient viral consensus calling* National University Hospital, Singapore – Laboratory Medicine
Apr 2023	*Massively scalable reference-guided multiple sequence alignment of viral genomes* COVID Information Commons
Mar 2023	*Invited Panelist* Exploring HyFlex Perspectives Through Research and Practice
Feb 2023	*Computational Methods in Viral Molecular Epidemiology* UC San Diego PREPARE Institute
Feb 2023	*Invited Panelist* SASE West Regional Conference
Oct 2022	*Applications of Bioinformatics in the Real-Time Molecular Surveillance of Viral Pathogens* Columbia University Emerging Infectious Diseases Seminar
Apr 2022	*A scalable approach for detecting exam similarity in CS courses* UC Berkeley Algorithms for Comp. & Education (ACE) Lab
Mar 2022	*Invited Panelist* Sweetwater Union High School District Career Night for CS
Feb 2022	*Keynote Talk* Bioinformatics Exchange (BEx) 2022

Nov 2021	*Transforming education through Massive Adaptive Interactive Texts (MAITs)* Digital Education Hackathon (DigiEduHack) 2021
Sep 2021	*Applications of Bioinformatics in the Real-Time Molecular Surveillance of Viral Pathogens* PAHO Genomic Epidemiology Webinar
Aug 2021	*ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes* Virus Evolution and Molecular Epidemiology (VEME) 2021
Aug 2021	*Optimizing high-performance cloud computing to enable real-time high-throughput SARS-CoV-2 whole genome sequence analysis* Virus Evolution and Molecular Epidemiology (VEME) 2021
Aug 2021	*Ten Simple Rules for Attending Your First Conference* NCF Natural Sciences Seminar
Aug 2021	*COVID-19 Genomic Analysis* Research Running on Cloud Compute & Emerging Technologies (RRoCCET) 2021
May 2021	*Bioinformatics workflows in viral amplicon sequencing* Micron Technology, Inc.
May 2021	*2021 Legacy Lecture* Scholars Society at UCSD
Apr 2021	*Workshop on Pandemic Preparedness* UC National Laboratories Fees Research Program
Feb 2021	*Tech Talk* SD Hacks 2021
Nov 2020	*RAPID: Real-time phylogenetic inference and transmission cluster analysis of COVID-19* COVID Information Commons
Oct 2020	*Keynote Talk* NCU Distance Education Symposium 2020
Sep 2020	*Workshop: A Viral Analysis Workflow* TheOpenCode Foundation
Sep 2020	*Scientists using AI to track, predict epidemics like COVID-19* Arirang News: Global Insight
Jul 2020	*Algorithms in Viral Phylogenetics and Molecular Epidemiology* Micron Technology, Inc.
Oct 2019	*Keynote Talk* SD Hacks 2019
Jan 2019	*Scalable methods for molecular epidemiology of rapidly-evolving pathogens* UCSD CSE Colloquium and Distinguished Lecture Series
Oct 2018	*Massively scalable tools for the analysis of viral epidemics* Temple University Institute for Genomics and Evolutionary Medicine (iGEM) Seminar

Apr 2018 *Standardized Environments using JupyterHub*
Reproducible Research and Interactive Education Meeting
Data Science Hub at the San Diego Supercomputer Center

Jun 2017 *The Era of Online Learning*
TEDxUCSD 2017, https://youtu.be/5JKgUoY9pTg

Campus Talks

Jun 2024 *GenAI Faculty Roundtable*
UC San Diego Teaching + Learning Commons

Feb 2024 *Professor Talk*
Eta Kappa Nu (IEEE-HKN) at UC San Diego

Jan 2024 *Chalk Talk*
Undergraduate Bioinformatics Club (UBIC) at UC San Diego

Oct 2023 *Professor Panel*
Computer Science & Engineering Society (CSES) at UCSD

Aug 2023 *Summer Internship Annual Symposium*
UC San Diego Department of Biomedical Informatics

Aug 2022 *Summer Internship Annual Symposium*
UC San Diego Department of Biomedical Informatics

May 2022 *Introduction to Research Panel*
Women in Computing (WIC) at UC San Diego

May 2022 *The Bioengineering Experience 2022*
Biomedical Engineering Society (BMES) at UC San Diego

Feb 2022 *First-Year Experience: Coding in Biology – Professor Panel*
Undergraduate Bioinformatics Club (UBIC) at UC San Diego

Feb 2022 *Dining with Professionals*
Society of Asian Scientists & Engineers (SASE) at UCSD

Oct 2021 *Admissions Virtual Fall Showcase Faculty Panel*
UC San Diego Office of Undergraduate Admissions

Sep 2021 *Meet the Profs*
EnVisionaries at UC San Diego

Aug 2021 *Summer Internship Annual Symposium*
UC San Diego Department of Biomedical Informatics

Jul 2021 *CSE Summer Transfer Series*
UC San Diego Computer Science & Engineering Department

Jul 2021 *Virtual Transfer Summer Prep Program*
Jacobs School of Engineering (JSOE) at UC San Diego

Jul 2021 *BISB Bootcamp Summer Seminar Series*
Bioinformatics & Systems Biology (BISB) at UC San Diego

Jul 2021 *Inaugural UCSD CSE Twitch Live Stream*
UC San Diego Computer Science & Engineering (CSE)

Jun 2021 *Lunch & Learn*
UC San Diego IT Services (ITS)

May 2021 *Student-Faculty Mixer*
UC San Diego Tau Beta Pi Engineering Honors Society

May 2021 — *AAPI Month STEM Faculty Q&A Panel*
UC San Diego Tau Beta Pi and SASE

May 2021 — *Science and Engineering Student-Faculty Mixer*
UC San Diego Associated Students Office of Academic Affairs

Feb 2021 — *ECE USC Professor AMA (Ask Me Anything)*
ECE Undergraduate Student Council (ECE USC)

Feb 2021 — *ACM AI Speaker Series*
ACM AI at UC San Diego

Feb 2021 — *ACM Cyber Speaker Series*
ACM Cyber at UC San Diego

Aug 2020 — *UBIC Reddit AMA (Ask Me Anything)*
Undergraduate Bioinformatics Club (UBIC) at UC San Diego

Jan 2020 — *UBIC Chalk Talk*
Undergraduate Bioinformatics Club (UBIC) at UC San Diego

Dec 2019 — *Halıcıoğlu Data Science Institute Seminar*
Halıcıoğlu Data Science Institute

May 2019 — *The Bioengineering Experience 2019*
Biomedical Engineering Society (BMES) at UC San Diego

Sep 2018 — *Bioinformatics Expo (BEx) 2018*
Bioinformatics and Systems Biology Program, UC San Diego

Sep 2018 — *Bioinformatics and Systems Biology Boot Camp 2018*
Bioinformatics and Systems Biology Program, UC San Diego

Jun 2018 — *Bioinformatics Industry + Academia Symposium 2018*
Undergraduate Bioinformatics Club (UBIC) at UC San Diego

Apr 2018 — *The Bioengineering Experience 2018*
Biomedical Engineering Society (BMES) at UC San Diego

Jan 2018 — *Bioinformatics Podcast*
Undergraduate Bioinformatics Club (UBIC) at UC San Diego

Sep 2017 — *Bioinformatics Expo (BEX) 2017*
Bioinformatics and Systems Biology Program, UC San Diego

May 2017 — *Bioinformatics Industry + Academia Symposium 2017*
Undergraduate Bioinformatics Club (UBIC) at UC San Diego

Apr 2017 — *The Bioengineering Experience 2017*
Biomedical Engineering Society (BMES) at UC San Diego

April 2017 — *Population and Medical Genetics Seminar*
Bioinformatics and Systems Biology Program, UC San Diego

May 2016 — *Bioinformatics Industry + Academia Symposium 2016*
Undergraduate Bioinformatics Club (UBIC) at UC San Diego

Apr 2016 — *The Bioengineering Experience 2016*
Biomedical Engineering Society (BMES) at UC San Diego

May 2015 — *Bioinformatics Industry + Academia Symposium 2015*
Undergraduate Bioinformatics Club (UBIC) at UC San Diego

Online Courses

Analyze Your Genome! (UC San Diego & edX, 2017 to Present)

Applied Bioinformatics Specialization (UC San Diego & Coursera, 2019 to Present)

Bioinformatics Algorithms Specialization (UC San Diego & Coursera, 2015 to Present)

Data Structures: An Active Learning Approach (UC San Diego & edX, 2018 to Present)

Hacking COVID-19 Course 1: Identifying a Deadly Pathogen (UC San Diego & Coursera, 2021 to Present)

Hacking COVID-19 Course 2: Decoding SARS-CoV-2's Secrets (UC San Diego & Coursera, 2021 to Present)

Hacking COVID-19 Course 3: Unraveling COVID-19's Origins (UC San Diego & Coursera, 2022 to Present)

Hacking COVID-19 Course 4: Metabolic Pathway Analysis Yields SARS-CoV-2 Drug Targets (UC San Diego & Coursera, 2023 to Present)

Hacking COVID-19 Course 5: Tracing SARS-CoV-2's Evolution (UC San Diego & Coursera, 2024 to Present)

Introduction to Genomic Data Science (UC San Diego & edX, 2017 to Present)

Teaching Experience

Computer Science

Advanced Data Structures (CSE 100)

Basic Data Structures and Object-Oriented Design (CSE 12)

Design and Analysis of Algorithms (CSE 101)

Introduction to Computer Science and OOP: Python (CSE 6R)

Introduction to Programming and Computational Problem Solving (I) (CSE 8A)

Introduction to Programming and Computational Problem Solving (II) (CSE 8B)

Introduction to Programming and Computational Problem Solving (Accel) (CSE 11)

Summer Program for Incoming Students (SPIS)

Teaching Methods in Computer Science (CSE 599)

Bioinformatics

Advanced Bioinformatics Laboratory (BIMM 185)

Biological Databases (CSE 182)

Biology Meets Computing (CSE 180)

Current Issues in Bioinformatics (CSE 191)

Introduction to Bioinformatics (Academic Connections, UCSD Extension)

Introduction to Bioinformatics Algorithms (CSE 282)

Molecular Sequence Analysis (CSE 181)

Biology

Genetics (BICD 100)

Economics

International Trade (ECON 101)

Principles of Microeconomics (ECON 1)

Editor/Reviewer

Grants

California Education Learning Lab

Journals

BMC Bioinformatics

Bioinformatics

Briefings in Bioinformatics

eLife (Guest Reviewing Editor)

Evolutionary Bioinformatics

F1000Research

IEEE/ACM Transactions on Computational Biology and Bioinformatics

Journal of Theoretical Biology

Patterns

PeerJ

PeerJ Computer Science

PLOS Computational Biology

PLOS ONE

Scientific Reports

Virus Evolution

Viruses

Conferences

ACM Conference on Bioinf., Comp. Bio., and Health Inf. (ACM-BCB) 2022

ACM Global Computing Education Conference (CompEd) 2019

Consortium for Computing Sciences in Colleges, Southwest (CCSC-SW) 2019

Consortium for Computing Sciences in Colleges, Southwest (CCSC-SW) 2020

Consortium for Computing Sciences in Colleges, Southwest (CCSC-SW) 2023

Consortium for Computing Sciences in Colleges, Southwest (CCSC-SW) 2024

Innovation and Technology in Computer Science Education (ITiCSE) 2020

Research in Computational Molecular Biology (RECOMB) 2023

Research in Computational Molecular Biology (RECOMB) 2024

Special Interest Group on Computer Science Education (SIGCSE) 2019

Special Interest Group on Computer Science Education (SIGCSE) 2020

Institutional Service

2024–Present *Inclusive Instruction Working Group Member*
UCSD Collective Impact

2021–Present *Research Committee Member*
UCSD PREPARE Institute

2021–Present *Training Committee Member*
UCSD PREPARE Institute

2021–Present *Member (Community and Data Science & Management Cores)*
UCSD PREPARE Institute

2020–Present *Diversity, Equity, and Inclusion (DEI) Committee Member*
UCSD Bioinformatics & Systems Biology Graduate Program

2019–Present *Outreach and Student Affairs Committee Member*
UCSD Bioinformatics and Systems Biology (BISB) Program

2024–2024 *Senior Faculty Mentor*
National Center of Leadership in Academic Medicine (NCLAM)

2023–2024 *Chair of the Faculty*
UCSD Seventh College

2019–2024 *M.S. Admissions Committee Member*
UCSD Computer Science & Engineering (CSE) Department

2020–2022 *Ph.D. Admissions Committee Member*
UCSD Bioinformatics & Systems Biology Graduate Program

2020–2022 *Steering Committee Member*
UCSD CAMSEE

2021–2021 *Founding Director, Mentor*
UCSD CBAM Research Mentorship Program

2020–2021 *Executive Committee Member*
UCSD Seventh College

Outreach

2019–Present *Early Research Scholars Program (ERSP) Mentor*
UCSD Computer Science & Engineering Department

2018–Present *Skype a Scientist Volunteer*
Skype a Scientist

2017–Present *SciChats@Salk Volunteer*
Salk Institute for Biological Studies

2017–Present *SalkEducation Volunteer*
Salk Institute for Biological Studies

May 2024 *CRAE Workshop 4: How do I combine my interests + computing?*
UR2PhD, Computing Research Association (CRA)

Apr 2024 *Viral Phylogenetics Workshop*
High Tech High Chula Vista

Apr 2024 *Undergraduate Virtual Symposium Organizer*
JUMP 2.0, Semiconductor Research Corporation (SRC)

Apr 2024 *CRAE Workshop 3: How will my research change the world?*
UR2PhD, Computing Research Association (CRA)

Mar 2024 *CRAE Workshop 2: What do careers in comp. research look like?*
UR2PhD, Computing Research Association (CRA)

	Feb 2024	*CRAE Workshop 1: So you've done some research, what's next?* UR2PhD, Computing Research Association (CRA)
	Oct 2023	*Viral Phylogenetics Workshop* Bonita Vista High School
	2022–2023	*HTHCV Internship Mentor* High Tech High Chula Vista (HTHCV)
	2019–2023	*Summer Program for Incoming Students (SPIS) Professor* UCSD Computer Science & Engineering Department
	Apr 2023	*Guest Speaker* Bonita Vista High School
	Nov 2022	*Guest Speaker* University City High School
	Jun 2021	*TritonHacks 2021 Judge* TritonHacks
	Sep 2020	*Workshop Guest Speaker* TheOpenCode Foundation
	Feb 2020	*DataHacks 2020 Mentor* DataHacks
	Oct 2019	*SD Hacks Judge* SD Hacks
	2018–2019	*STEMTaught Author* STEMTaught
	2018–2019	*eMENTOR* Del Lago Academy
	2016–2019	*Mentor Teaching Assistant* UCSD Computer Science & Engineering Department
	Jan 2019	*High Tech Fair* Fleet Science Center
	2017–2018	*Group Mentor* Women in Computing (WIC) at UCSD
	Oct 2018	*Park Clean-Up Volunteer* San Jose Dept. of Parks, Recreation & Neighborhood Services
	Oct 2017	*Protein Modeling Project Mentor* Mission Bay High School
	Apr 2015	*High School Outreach Event Organizer and Volunteer* Undergraduate Bioinformatics Club (UBIC) at UC San Diego
	Feb 2015	*Envision Volunteer* Society of Women Engineers (SWE) at UCSD
Professional Organizations	2018–2024	*Evolutionary Bioinformatics* 2024–2024 Editorial Review Board Member
	2023–2024	*Undergraduate Research to PhD (UR2PhD), CRA* 2024–2024 UR2PhD + CTI-Accelerate Course Developer 2023–2024 Bridge Workshop Series Designer-Facilitator

	2023–2024	*PRISM Center, Semiconductor Research Corporation (SRC)* 2023–2024 Diversity Director / BPC
	2019–2024	*Association for Computing Machinery (ACM)* 2019–2024 Member
	2018–2024	*Computer Science Teachers Association (CSTA)* 2018–2024 Member
	2021–2022	*Research in Computational Molecular Biology (RECOMB) 2023* 2023–2023 Highlights Program Committee
	2021–2022	*2022 RECOMB-BE Satellite Conference* 2021–2022 Conference Chair
	2020–2021	*2021 CCSC Southwestern Conference* 2020–2021 Conference Chair
	2019–2021	*Consortium for Comp. Sci. in Colleges, Southwest (CCSC-SW)* 2019–2021 Treasurer, Registrar
	2020–2020	*ACM-BCB 2020 Conference* 2020–2020 Orientation Organizer
	2018–2020	*International AIDS Society (IAS)* 2018–2020 Member
	2018–2020	*American Go Association (AGA)* 2018–2020 Member
	2018–2019	*Special Interest Group on Computer Science Education (SIGCSE)* 2017–2019 Member
	2017–2019	*International Society of Computational Biology (ISCB)* 2017–2019 Fundraising Committee Member
	2017–2019	*Society of Molecular Biology and Evolution (SMBE)* 2017–2019 Member
University Organizations	2018–2019	*CS foreach at UCSD* 2018–2019 Member
	2017–2019	*Graduate Women in Computing (GradWIC) at UCSD* 2017–2018 Outreach Committee Member
	2015–2019	*Graduate Bioinformatics Council (GBIC) at UCSD* 2018–2019 President 2017–2018 Director of Onboarding 2016–2017 Director of Finance 2015–2016 Director of Internal
	2013–2018	*Women in Computing (WIC) at UCSD* 2013–2018 Member 2017–2018 Group Mentor
	2014–2015	*Engineering World Health (EWH) at UCSD* 2014–2015 Member
	2013–2015	*Society of Women Engineers (SWE) at UCSD* 2013–2015 Member

2012–2015 *Undergraduate Bioinformatics Club (UBIC) at UCSD*
2014–2015 President
2013–2014 Administrative Officer