Niema Moshiri

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Education

- **Ph.D.**, Bioinformatics & Systems Biology, *UC San Diego* (2015–2019)
- **B.S.**, Bioengineering: Bioinformatics, *UC San Diego* (2011–2015)

Academic Positions

- **Associate Teaching Professor**, Computer Science & Engineering, *UC San Diego* (2023–Present)
- **Assistant Teaching Professor**, Computer Science & Engineering, *UC San Diego* (2019–2023)

Non-Academic Positions

- **Consultant**, Future Technology Group, *Sony Interactive Entertainment* (2025–2026)
- **Program Specialist**, NCHHSTP/DHP/DRB, *CDC* (2023–2026)
- **Machine Learning Consultant**, GI Machine Learning & AI, *Blizzard Entertainment* (2025–2026)

Funding

- Anthropic AI for Science (**$15,000 Credits**; 2026–2027)
  - *Bringing 500 bioinformatics tools to the browser with Claude*
- Northeastern University Center for Inclusive Computing (**$394,850**; 2026–2028)
  - *CIC Implementation Grant*
- Minderoo Foundation (**$10,667,599**; 2025–2027)
  - *eDNAID: Environmental DNA and AI as tools for Ocean Aid*
- UCOP UC Online (**$45,000**; 2025–2026)
  - *Scalable foundational AI course: CSE 25 - Introduction to Artificial Intelligence*
- CDC U01IP001238 (**$13,331,272**; 2024–2027)
  - *PREVENT: Preparedness through Respiratory Virus Epidemiology and Community Engagement*
- CDC Contract 75D30123C17580 (**$2,243,691**; 2023–2026)
  - *Operation and Maintenance (O&M), and Development, Modernization, and Enhancement (DME) Services for HIV-TRACE*
- UCOP UC Online (**$46,000**; 2023–2024)
  - *An Online Training Module to Provide Instructors Guidance in Developing and Offering Fully Online and Hybrid Courses*

- Google GCP Research Credits Program (**$5,000**; 2023–2024)
  - *Scalable methods for viral molecular epidemiology*
- NIH U54 1U54HG012510-01 (**$2,505,728**; 2022–2026)
  - *A FAIR Bridge2AI Center (FABRIC)*
- NIH RM1 1RM1HG011558-01A1 (**$11,704,255**; 2021–2026)
  - *Genetic & Social Determinants of Health: Center for Admixture Science and Technology*
- COVID-19 High Performance Computing (**110,000 SUs**; 2021–2022)
  - *Weekly updated phylogenetic inference of San Diego SARS-CoV-2 sequences*
- UC San Diego Course Development and Instructional Improvement Program (**$38,273**; 2021–2022)
  - (*More*) *Free, Interactive, Open Educational Resources for Lower-Division Programming Courses*
- Google exploreCSR (**$15,000**; 2020–2021)
  - *Computational Biology and Medicine (CBAM) Research Mentorship Program*
- NIH R25 1R25HG011022-01 (**$804,013**; 2020–2025)
  - *Development of Online Computational Genomics Specialization*
- UCOP UC-HSI DDI (**$350,000**; 2020–2025)
  - *Recruitment and Retention Doctoral Diversity Informatics Initiative (R2D2)*
- NSF Rapid Response Research 2028040 (**$200,000**; 2020–2022)
  - *Real-time phylogenetic inference and transmission cluster analysis of COVID-19*
- Google GCP Research Credits Program (**$5,000**; 2020–2021)
  - *Real-time phylogenetic inference and transmission cluster analysis of COVID-19*
- UCOP Innovative Learning Technology Initiative (**$71,000**; 2019–2024)
  - *Online Cross-UC Introductory Python Programming Course*

Honors and Awards

- **Faculty Service Excellence Award**, Seventh College, *UC San Diego* (2026)
- **Outstanding Teaching Innovation Award**, Jacobs School of Engineering, *UC San Diego* (2026)
- **Outstanding Teaching Award**, Seventh College, *UC San Diego* (2025)
- **Outstanding Teaching Award**, Sixth College, *UC San Diego* (2023)
- **30 Under 30 (2023): Healthcare**, *Forbes* (2022)
- **Outstanding Teaching Award**, Sixth College, *UC San Diego* (2022)
- **Outstanding Teaching Award**, Earl Warren College, *UC San Diego* (2022)

- **Integrity Award**, Academic Integrity Office, *UC San Diego* (2022)
- **Faculty of the Year Award**, Tau Beta Pi Honors Society, *UC San Diego* (2021)
- **Best Teacher Award: Computer Science & Engineering (CSE)**, Jacobs School of Engineering, *UC San Diego* (2021)
- **Distinguished Teaching Award**, Academic Senate, *UC San Diego* (2017)
- **Distinguished Leadership and Service Award**, Department of Bioengineering, *UC San Diego* (2015)

Research

Papers

- Jones D, Yang Y, Lightstone FC, **Moshiri N**, Allen JE, Rosing TŠ (2026). "SurGBSA: learning representations from molecular dynamics simulations." *Digital Discovery*. doi:10.1039/d6dd00174b.
- Zhang T, Zhou M, **Moshiri N**, Rosing TŠ (2026). "PoreMap: Unlocking High-Throughput Raw Nanopore Signal Mapping with Near-Memory Processing." *2026 International Conference on Software, Telecommunications and Computer Networks (SoftCOM)*, Split, Croatia. In Press.
- **Moshiri N** (2026). "MultiVirusConsensus: an accurate and efficient open-source pipeline for identification and consensus sequence generation of multiple viruses from mixed samples." *Bioinformatics Advances*. 6(1):vbag256. doi:10.1093/bioadv/vbag256.
- Laflen B, Li Z, Urbina M, Rosing TŠ, **Moshiri N** (2026). "QPL-enabled HTSlib library: accelerating sequence file compression using Intel IAA." *Bioinformatics Advances*. 6(1):vbag250. doi:10.1093/bioadv/vbag250.
- LaMere S, Xiong H, Wang W, LaMere B, **Moshiri N** (2025). "Epigenetic motifs distinguishing endogenous from exogenous retroviral integrants." *Journal of Virology*. 99:e00775–25. doi:10.1128/jvi.00775-25.
- **Moshiri N** (2025). "Scalable Epidemic Simulation Using FAVITES-Lite." *Methods in Molecular Biology (Computational Virology)*. 2927:173–193. Book Chapter. doi:10.1007/978-1-0716-4546-8_10.
- Wertheim JO, Vasylyeva TI, Wood RJ, Cantrell K, Piña Contreras S, Feldheim A, Goyal R, Havens JL, Knight R, Laurent LC, **Moshiri N**, Neuhard R, Sathe S, Satterlund A, Scioscia A, Song AY, Schooley RT, Anderson CM, Martin NK (2025). "Phylogeographic and genetic network assessment of COVID-19 mitigation protocols on SARS-CoV-2 transmission in university campus residences." *eBioMedicine*. 116:105729. doi:10.1016/j.ebiom.2025.105729.
- **Moshiri N** (2025). "CompactTree: a lightweight header-only C++ library and Python wrapper for ultra-large phylogenetics." *Gigabyte*. doi:10.46471/gigabyte.152.
- Pekar JE, **Moshiri N**, Lemey P, Crits-Christoph A, Débarre F, Goldstein SA, Hensel Z, Rambaut A, Worobey M, Holmes EC, Wertheim JO (2025). "Recently reported SARS-CoV-2 genomes suggested to be intermediate between the two early main lineages are instead likely derived." *Virus Evolution*. 11(1):veaf008. doi:10.1093/ve/veaf008.
- Goldstein SA, Feeley TM, Babler KM, Hilbert ZA, Downhour DM, **Moshiri N**, Elde NC (2024). "Hidden evolutionary constraints dictate the retention of coronavirus accessory genes." *Current Biology*. 34(24):5685–5696.E3. doi:10.1016/j.cub.2024.10.050.
- Jones D, Zhang X, Bennion BJ, Pinge S, Xu W, Kang J, Khaleghi B, **Moshiri N**, Allen JE, Rosing TŠ (2024). "HDBind: encoding of molecular structure with hyperdimensional binary representations." *Scientific Reports*. 14:29025. doi:10.1038/s41598-024-80009-w.

- Pinge S, Xu W, Bittremieux W, **Moshiri N**, Jun SW, Rosing TŠ (2024). "RapidOMS: FPGA-based Open Modification Spectral Library Searching with HD Computing." *2024 IEEE Biomedical Circuits and Systems Conference* (*BioCAS*), Xi'an, China. 1–5. doi:10.1109/BioCAS61083.2024.10798176.

- Crits-Christoph A, Levy JI, Pekar JE, Goldstein SA, Singh R, Hensel Z, Gangavarapu K, Rogers MB, **Moshiri N**, Garry RF, Holmes EC, Koopmans MP, Lemey P, Peacock TP, Popescu S, Rambaut A, Robertson DL, Suchard MA, Wertheim JO, Rasmussen AL, Andersen KG, Worobey M, Débarre F (2024). "Genetic tracing of market wildlife and viruses at the epicenter of the COVID-19 pandemic." *Cell*. 187(19):5468–5482.E11. doi:10.1016/j.cell.2024.08.010.

- Kang J, Xu W, Bittremieux W, **Moshiri N**, Rosing TŠ (2024). "DRAM-Based Acceleration of Open Modification Search in Hyperdimensional Space." *IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems*. 43(9):2592–2605. doi:10.1109/TCAD.2024.3382842.

- Xu W, Hsu PK, **Moshiri N**, Yu S, Rosing TŠ (2024). "HyperGen: compact and efficient genome sketching using hyperdimensional vectors." *Bioinformatics*. 40(7):btae452. doi:10.1093/bioinformatics/btae452.

- 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 A, Rivera A, Salido RA, Seaver P, Schwab M, Veder A, Yeo GW, 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 SARS-CoV-2 Transmission in the Healthcare Setting." *Clinical Infectious Diseases*. 78(5):1204–1213. doi:10.1093/cid/ciad738.

- Pinge S, Xu W, Kang J, Zhang T, **Moshiri N**, Bittremieux W, Rosing TŠ (2024). "SpecHD: Hyperdimensional Computing Framework for FPGA-Based Mass Spectrometry Clustering." *2024 Design, Automation & Test in Europe Conference & Exhibition* (*DATE*), Valencia, Spain. 1–6. doi:10.23919/DATE58400.2024.10546776.

- 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 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-Alavez M, Moreno-Camacho JL, García-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, King AJ, 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 Rodríguez 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, **Moshiri N**, Knight R, Rosing TŠ (2023). "GenoMiX: Accelerated Simultaneous Analysis of Human Genomics, Microbiome Metagenomics, and Viral Sequences." *2023 IEEE Biomedical Circuits and Systems Conference* (*BioCAS*), Toronto, Ontario, Canada. 1–5. doi:10.1109/BioCAS58349.2023.10388531.

- Kang J, Xu W, Bittremieux W, **Moshiri N**, Rosing TŠ (2023). "Accelerating open modification spectral library searching on tensor core in high-dimensional space." *Bioinformatics*. 39(7):btad404. doi:10.1093/bioinformatics/btad404.
- **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.
- Xu W, Kang J, Bittremieux W, **Moshiri N**, Rosing TŠ (2023). "HyperSpec: Ultrafast Mass Spectra Clustering in Hyperdimensional Space." *Journal of Proteome Research*. 22(6):1639–1648. doi:10.1021/acs.jproteome.2c00612.
- Fielding-Miller R, Karthikeyan S, Gaines T, Garfein RS, Salido RA, Cantu VJ, Kohn L, Martin NK, Wynn A, Wijaya C, 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 HM, Valles T, Morris J, Kang J, Khaleghi B, Young C, Akel AD, Eilert S, Eno J, Curewitz K, Laurent LC, Rosing TŠ, 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 TŠ (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 TŠ (2022). "SALIENT: Ultra-Fast FPGA-based Short Read Alignment." *2022 International Conference on Field-Programmable Technology (ICFPT)*, Hong Kong. 1–10. doi:10.1109/ICFPT56656.2022.9974548.
- Khaleghi B, Zhang T, Shao N, Akel A, Curewitz K, Eno J, Eilert S, **Moshiri N**, Rosing TŠ (2022). "FAST: FPGA-based Acceleration of Genomic Sequence Trimming." *2022 IEEE Biomedical Circuits and Systems Conference (BioCAS)*, Taipei, Taiwan. 510–514. 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, Yan KCZ, Lin RTP, Mat Isa MN, Noor YM, Vasylyeva TI, Garry RF, Holmes 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, Chacón M, Cheung W, Cresini 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 G, 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 reveals early cryptic SARS-CoV-2 variant transmission." *Nature*. 609:101–108. doi:10.1038/s41586-022-05049-6.
- Jones D, Allen JE, Yang Y, Drew Bennett WF, Gokhale M, **Moshiri N**, Rosing TŠ (2022). "Accelerators for Classical Molecular Dynamics Simulations of Biomolecules." *Journal of Chemical Theory and Computation*. 18(7):4047–4069. doi:10.1021/acs.jctc.1c01214.
- 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** (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.

- **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, Gonazlez A, Shaffer JP, Carpenter C, Estaki M, Wandro S, Eilert S, Akel A, Eno J, Curewitz K, Swafford AD, **Moshiri N**, Rosing TŠ, Knight R (2022). "Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases." *mSystems*. 7: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 TŠ (2021). "FPGA Acceleration of Pairwise Distance Calculation for Viral Transmission Clustering." *2021 IEEE Biomedical Circuits and Systems Conference* (*BioCAS*), Berlin, Germany. Link.

- Zhou M, Wu L, Li M, **Moshiri N**, Skadron K, Rosing TŠ (2021). "Ultra Efficient Acceleration for De Novo Genome Assembly via Near-Memory Computing." *2021 30th International Conference on Parallel Architectures and Compilation Techniques* (*PACT*), Atlanta, Georgia, USA. 199–212. doi:10.1109/PACT52795.2021.00022.

- Keehner J, Horton LE, Binkin NJ, Laurent LC, 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, Fisch K, Franco Vargas L, Gangavarapu K, Hakim A, Henson B, Hobbs C, Humphrey G, Jepsen K, Kapadia BK, Knight R, Lastrella AL, 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, Pride D, Longhurst CA, Abeles SR, Torriani FJ (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.

- 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.

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

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

- Salamat S, Kang J, Kim Y, Imani M, **Moshiri N**, Rosing TŠ (2021). "FPGA Acceleration of Protein Back-Translation and Alignment." *2021 Design, Automation & Test in Europe Conference & Exhibition* (*DATE*), Grenoble, France. 822–827. doi:10.23919/DATE51398.2021.9474103.

- Kim Y, Imani M, **Moshiri N**, Rosing TŠ (2020). "GenieHD: Efficient DNA Pattern Matching Accelerator Using Hyperdimensional Computing." *2020 Design, Automation & Test in Europe Conference & Exhibition* (*DATE*), Grenoble, France. 115–120. doi:10.23919/DATE48585.2020.9116397.

- **Moshiri N** (2020). "TreeSwift: A massively scalable Python tree package." *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 MH, Rosenthal SB, Pérez F, Rose PW (2019). "Ten simple rules for writing and sharing computational analyses 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.

Talks

- **Moshiri N** (2026). "Massively-scalable auto-graded online assessments with adaptive feedback using PrairieLearn." *UC Santa Barbara Robert Mehrabian College of Engineering*, Santa Barbara, California, USA.
- **Moshiri N** (2026). "Sequential Recommendation Exploration." *Blizzard Entertainment*, Virtual.
- **Moshiri N** (2026). "AI and Data-Driven Discovery in Complex Systems." *2026 Sony Interactive Entertainment (PlayStation) Academic Day*, San Mateo, California, USA.
- **Moshiri N** (2026). "Niema's super flexible code auto-grading PyTest-to-PrairieLearn translation layer." *UC San Diego Jacobs School of Engineering (JSOE) AI Show-and-Tell*, La Jolla, California, USA.
- **Moshiri N** (2025). "Panelist." *Computing Research Association (CRA) Undergraduate to PhD (UR2PhD) Undergraduate Research Methods*, Virtual.
- **Moshiri N** (2025). "Real-time genomic surveillance of pathogens through bioinformatics applications." *Blizzard Entertainment*, Virtual.
- **Moshiri N** (2025). "Real-time genomic surveillance of pathogens through bioinformatics applications." *UC Irvine Department of Computer Science*, Irvine, California, USA.
- **Moshiri N** (2024). "Computational Methods in Viral Molecular Epidemiology." *Vi Technology Group*, San Diego, California, USA.
- **Moshiri N** (2024). "Panelist." *Computing Talent Initiative (CTI) Research Panel*, Virtual.
- **Moshiri N** (2024). "A scalable approach for detecting exam similarity in CS courses." *UC Berkeley Algorithms for Computing and Education (ACE) Lab*, Virtual.
- **Moshiri N** (2024). "Real-time genomic surveillance of pathogens through bioinformatics applications." *The University of Tokyo (UTokyo) Division of Systems Virology*, Tokyo, Japan.
- **Moshiri N** (2024). "Keynote." *2024 DiamondHacks*, La Jolla, California, USA.
- Goyal R, Martin N, **Moshiri N** (2024). "Improving HIV incidence estimation through integration of molecular data with epidemic modeling." *AntiViral Research Center (AVRC)*, La Jolla, California, USA.
- **Moshiri N** (2024). "Real-time genomic surveillance of pathogens through bioinformatics applications." *California Institute of Technology (Caltech) Computational Tools for Decoding Microbial Ecosystems (ESE/GE/BI/IDS 184)*, Pasadena, California, USA.
- **Moshiri N** (2023). "Real-time genomic surveillance of pathogens through bioinformatics applications." *1st Meeting of the Pan American Health Organization (PAHO) Genomic Surveillance Regional Networks (PAHOGen)*, Virtual.
- Goyal R, Martin N, **Moshiri N** (2023). "Improving HIV incidence estimation through integration of molecular data with epidemic modeling." *San Diego Center for AIDS Research (CFAR)*, La Jolla, California, USA.
- **Moshiri N** (2023). "A scalable approach for detecting exam similarity in CS courses." *UC Davis Department of Computer Science*, Davis, California, USA.
- **Moshiri N** (2023). "Massively-scalable tools for real-time viral molecular surveillance." *Lawrence Livermore National Laboratory (LLNL)*, Livermore, California, USA.

- **Moshiri N** (2023). "Bioinformatics, AI, and Games." *Sony Interactive Entertainment* (*PlayStation*), San Mateo, California, USA.
- **Moshiri N** (2023). "Computational Methods in Viral Molecular Epidemiology." *San Diego Diplomacy Council*, San Diego, California, USA.
- **Moshiri N** (2023). "ViralConsensus: Fast and memory-efficient viral consensus calling." *National University Hospital* (*NUH*) *Singapore Molecular Diagnosis Centre*, Virtual.
- **Moshiri N** (2023). "Massively scalable reference-guided Multiple Sequence Alignment of viral genomes." *Columbia University COVID Information Commons* (*CIC*), Virtual.
- Ditta AS, Liu B, Maduro M, Siddiqui-Ali S, Pion-Berlin D, Hadjipieris P, Moore C, **Moshiri N**, Stern-Lockerman R, Johns E (2023). "Panelist." *UC Riverside Exploring HyFlex Perspectives Through Research and Practice Meeting*, Riverside, California, USA. Link.
- **Moshiri N** (2023). "Computational Methods in Viral Molecular Epidemiology." *UC San Diego Pandemic Response to Emerging Pathogens, Antimicrobial Resistance and Equity* (*PREPARE*) *Institute*, La Jolla, California, USA.
- **Moshiri N** (2023). "Panelist." *2023 Society of Asian Scientists and Engineers* (*SASE*) *West Regional Conference*, La Jolla, California, USA.
- **Moshiri N** (2022). "Applications of Bioinformatics in the Real-Time Molecular Surveillance of Viral Pathogens." *Columbia University Emerging Infectious Diseases Seminar*, Virtual.
- **Moshiri N** (2022). "A scalable approach for detecting exam similarity in CS courses." *UC Berkeley Algorithms for Computing and Education* (*ACE*) *Lab*, Virtual.
- **Moshiri N** (2022). "Panelist." *Sweetwater Union High School District* (*SUHSD*) *Career Night for Computer Science*, Virtual.
- **Moshiri N** (2022). "Keynote." *2022 Bioinformatics Exchange* (*BEx*), Virtual.
- **Moshiri N** (2021). "Transforming education through Massive Adaptive Interactive Texts (MAITs)." *2021 Digital Education Hackathon* (*DigiEduHack*), Virtual. Link.
- **Moshiri N** (2021). "Applications of Bioinformatics in the Real-Time Molecular Surveillance of Viral Pathogens." *Pan American Health Organization* (*PAHO*) *Genomic Epidemiology Webinar*, Virtual.
- **Moshiri N** (2021). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *2021 Virus Evolution and Molecular Epidemiology* (*VEME*) *Workshop*, Virtual.
- **Moshiri N** (2021). "Ten Simple Rules for Attending Your First Conference." *New College of Florida Natural Sciences Seminar*, Virtual.
- **Moshiri N** (2021). "Optimizing high-performance cloud computing to enable real-time high-throughput SARS-CoV-2 whole genome sequence analysis." *2021 Virus Evolution and Molecular Epidemiology* (*VEME*) *Workshop*, Virtual.
- **Moshiri N** (2021). "COVID-19 Genomic Analysis." *2021 Research Running on Cloud Compute & Emerging Technologies* (*RRoCCET*), Virtual.
- **Moshiri N** (2021). "Bioinformatics workflows in viral amplicon sequencing." *Micron Technology*, Virtual.
- **Moshiri N** (2021). "Legacy Lecture." *Scholars Society at UC San Diego*, Virtual. Link.
- **Moshiri N** (2021). "Scalable methods in viral molecular epidemiology." *UC National Laboratory Fees Program Workshop on Pandemic Preparedness*, Virtual.
- **Moshiri N** (2021). "Tech Talk." *2021 SD Hacks*, Virtual.
- **Moshiri N** (2020). "RAPID: Real-time phylogenetic inference and transmission cluster analysis of COVID-19." *Columbia University COVID Information Commons* (*CIC*), Virtual.

- **Moshiri N** (2020). "Enabling scalable online learning through the development of Massive Adaptive Interactive Texts (MAITs)." *Northern Caribbean University 2020 Distance Education Symposium*, Virtual.
- **Moshiri N** (2020). "A Viral Analysis Workflow." *TheOpenCode Foundation*, Virtual.
- **Moshiri N** (2020). "Scientists using AI to track, predict epidemics like COVID-19." *Arirang News: Global Insight*, Virtual. Link.
- **Moshiri N** (2020). "Algorithms in Viral Phylogenetics and Molecular Epidemiology." *Micron Technology*, Virtual.
- **Moshiri N** (2019). "Keynote." *2019 SD Hacks*, La Jolla, California, USA.
- **Moshiri N** (2019). "Scalable methods for molecular epidemiology of rapidly-evolving pathogens." *UC San Diego Department of Computer Science & Engineering (CSE)*, La Jolla, California, USA.
- **Moshiri N** (2018). "Massively scalable tools for the analysis of viral epidemics." *Temple University Institute for Genomics and Evolutionary Medicine (iGEM)*, Philadelphia, Pennsylvania, USA.
- **Moshiri N** (2018). "Standardized Environments using JupyterHub." *Data Science Hub*, La Jolla, California, USA.
- **Moshiri N** (2017). "The Era of Online Learning." *2017 TEDxUCSD*, La Jolla, California, USA. Link.

Conferences

- **Moshiri N** (2026). "Massively-scalable auto-graded online assessments with adaptive feedback using PrairieLearn." *2026 Teaching Professor Network (TPN) Conference*, Riverside, California, USA. Talk.
- **Moshiri N** (2025). "Massively-scalable auto-graded online assessments with adaptive feedback using PrairieLearn." *2025 Education Innovation Expo*, La Jolla, California, USA. Talk.
- Goldstein SA, Feeley TM, Babler KM, Hilbert ZA, Downhour DM, **Moshiri N**, Elde NC (2024). "Hidden evolutionary constraints dictate the retention of coronavirus accessory genes." *31st International Dynamics & Evolution of Human Viruses*, Squamish, British Columbia, Canada. Poster.
- Ji D, Aboukhalil R, **Moshiri N** (2024). "ViralWasm: a client-side user-friendly web application suite for viral genomics." *2024 Workshop on Emerging Computer Systems Challenges and Applications in Biomedicine (BioSys)*, La Jolla, California, USA. Talk.
- Hadjipieris P, **Moshiri N** (2023). "Hyflex Course Design: Student Experiences of Equity-centered Technology Enhanced Curriculum." *2023 Professional and Organizational Development (POD)*, Pittsburgh, Pennsylvania, USA. 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." *2023 International AIDS Society (IAS)*, Brisbane, Queensland, Australia. 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." *2022 GAMA Days*, Virtual. Talk.
- **Moshiri N** (2022). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *2022 San Diego Epidemiology Research Exchange Conference*, San Diego, California, USA. Talk.
- **Moshiri N** (2022). "A scalable approach for detecting exam similarity in CS courses." *2022 Consortium for Computing Sciences in Colleges, Southwest (CCSC-SW)*, Irvine, California, USA. Talk.
- Salamat S, **Moshiri N**, Rosing TŠ (2021). "FPGA Acceleration of Pairwise Distance Calculation for Viral Transmission Clustering." *28th International Dynamics & Evolution of Human Viruses*, Virtual. Poster.

- **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*, Virtual. Poster.
- Kang J, Young C, Morris J, Akel A, Eilert S, Eno J, Curewitz K, **Moshiri N**, Rosing TŠ (2021). "A GPU-Powered Phylogenetic Analysis for Large-scale Genomic Sequences." *28th International Dynamics & Evolution of Human Viruses*, Virtual. Poster.
- Young C, Meng S, **Moshiri N** (2021). "An Evaluation of Phylogenetic Workflows in Viral Molecular Epidemiology." *28th International Dynamics & Evolution of Human Viruses*, Virtual. Poster.
- Khaleghi B, Akel A, Curewitz K, Eno J, Eilert S, **Moshiri N**, Rosing TŠ (2021). "FPGA-based acceleration of primer trimming." *28th International Dynamics & Evolution of Human Viruses*, Virtual. Talk.
- **Moshiri N** (2020). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *2020 Cold Spring Harbor Laboratory* (*CSHL*) *Biological Data Science Meeting*, Virtual. Poster. Link.
- Gupta S, Imani M, Khaleghi B, **Moshiri N**, Rosing TŠ (2020). "RAPIDx: A ReRAM Processing in-Memory Architecture for DNA Short Read Alignment." *2020 American Society of Human Genetics* (*ASHG*), Virtual. Poster.
- Salamat S, Kang J, Kim Y, Imani M, **Moshiri N**, Rosing TŠ (2020). "FPGA Acceleration of Protein Back-Translation and Alignment." *2020 American Society of Human Genetics* (*ASHG*), Virtual. Poster.
- **Moshiri N** (2020). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *COVID-19 Dynamics & Evolution*, Virtual. Talk.
- **Moshiri N** (2020). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *2020 Computing Research Association* (*CRA*) *Virtual Conference*, Virtual. Talk. Link.
- **Moshiri N** (2020). "ViralMSA: massively scalable reference-guided multiple sequence alignment of viral genomes." *2020 Bioinformatics Community Conference* (*BCC*), Virtual. Poster. Link.
- 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*, Virtual. Talk.
- 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." *2020 Consortium for Computing Sciences in Colleges, Southwest* (*CCSC-SW*), San Marcos, California, USA. Poster. Link.
- Lewis M, **Moshiri N** (2020). "Automated plagiarism detection in programming courses: a graph theoretical approach using MOSS." *2020 Consortium for Computing Sciences in Colleges, Southwest* (*CCSC-SW*), San Marcos, CA, USA. Poster.
- **Moshiri N**, Pevzner PA (2018). "Flipping computational courses using Massive Adaptive Interactive Texts." *2018 Cold Spring Harbor Laboratory* (*CSHL*) *Biological Data Science Meeting*, Cold Spring Harbor, New York, USA. Talk.
- **Moshiri N** (2018). "Open Computational Problems in HIV Epidemiology." *2018 Workshop on the Future of Algorithms in Biology* (*FAB*), Pittsburgh, Pennsylvania, USA. Talk. Link.
- Huang SC, **Moshiri N**, Reich M, Rose PW (2018). "Challenges and Guidelines for Reproducible Research with Jupyter Notebook." *2018 JupyterCon*, New York City, New York, USA. Poster.
- **Moshiri N**, Ragonnet-Cronin M, Wertheim JO, Mirarab S (2018). "FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences." *2018 International AIDS Conference*, Amsterdam, Netherlands. Poster.
- **Moshiri N**, Ragonnet-Cronin M, Wertheim JO, Mirarab S (2018). "FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences." *2018 Society for Molecular Biology and Evolution* (*SMBE*), Yokohama, Japan. Poster.

- **Moshiri N**, Ragonnet-Cronin M, Wertheim JO, Mirarab S (2018). "FAVITES: simultaneous simulation of transmission networks, phylogenetic trees and sequences." *25th International HIV Dynamics & Evolution*, Leavenworth, Washington, USA. Talk.
- **Moshiri N** (2017). "Using Online Classes to Flip Bioinformatics Classrooms." *2017 International Society for Computational Biology (ISMB)*, Prague, Czech Republic. Talk.
- **Moshiri N**, Mirarab S (2017). "A Two-State Model of Tree Evolution and Its Applications to Alu Retrotransposition." *2017 Society for Molecular Biology and Evolution (SMBE)*, Austin, Texas, USA. Poster.

Preprints

- Stadler K, Phillips K, **Moshiri N** (2024). "Improved user-friendliness in the design and analysis of FAVITES-Lite simulations." *medRxiv*. doi:10.1101/2024.06.10.24308702.
- Soto Miranda M, Narváez Romo R, **Moshiri N** (2023). "Single-linkage molecular clustering of viral pathogens." *bioRxiv*. doi:10.1101/2023.08.03.551813.
- 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 M, **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*. 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.

Books

- **Moshiri N** (2024). "How to Teach Online." *GitHub Pages*. Link.
- Mansuri S, **Moshiri N** (2021). "Introduction to Computer Science and Object-Oriented Programming: Python." *Cogniterra (Stepik)*. Link.
- **Moshiri N**, Izhikevich L (2018). "Design and Analysis of Data Structures." *Amazon KDP*. ISBN:9781981017232. ASIN:B07CYM8ZWJ.
- **Moshiri N**, Izhikevich L (2016). "Data Structures." *Cogniterra (Stepik)*. Link.

Games

- Blizzard Entertainment (2026). "Diablo IV: Lord of Hatred." *Blizzard Entertainment*. MobyGames:259985. Steam:3958690.
- **Moshiri N** (2022). "Learn Programming: Python – Remake." *Niema Moshiri*. Steam:1882420.
- **Moshiri N** (2021). "Learn Programming: Python – Retro." *Niema Moshiri*. Steam:1536770.

Teaching

UC San Diego

- Academic Connections: Introduction to Bioinformatics
- COSMOS: California State Summer School for Mathematics and Science
- CSE 6R: Introduction to Computer Science and Object-Oriented Programming: Python
- CSE 11: Introduction to Computer Science in Java (Accelerated)
- CSE 87: First-Year Student Seminar: A Technical History of Video Games
- CSE 87: First-Year Student Seminar: Tracking Viral Epidemics
- CSE 100: Advanced Data Structures
- CSE 180: Biology Meets Computing
- CSE 185: Advanced Bioinformatics Laboratory
- CSE 599: Teaching Methods in Computer Science
- PRISM: High School Research Program
- SEV 1: First Year Experience: Seventh College
- SPIS: Summer Program for Incoming Students

Online

- Analyze Your Genome!
- Applied Bioinformatics Specialization Track
- Bioinformatics Algorithms Specialization Track
- Data Structures: An Active Learning Approach
- Hacking COVID-19 — Course 1: Identifying a Deadly Pathogen
- Hacking COVID-19 — Course 2: Decoding the Secrets of SARS-CoV-2
- Hacking COVID-19 — Course 3: Unraveling COVID-19's Origins
- Hacking COVID-19 — Course 4: Metabolic Pathway Analysis Yields SARS-CoV-2 Drug Targets
- Hacking COVID-19 — Course 5: Tracing SARS-CoV-2's Evolution
- Introduction to Computer Science and Object-Oriented Programming: Python

- Introduction to Genomic Data Science

Editor

- eLife (Reviewing Editor)
- Scientific Reports (Editorial Board Member)

Reviewer

- ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)
- ACM Global Computing Education Conference (CompEd)
- ACM Technical Symposium on Computer Science Education (SIGCSE / SIGCSE-TS)
- AIDS Research and Human Retroviruses
- Bioinformatics
- Bioinformatics Advances
- BMC Bioinformatics
- BMC Genomics
- Briefings in Bioinformatics
- California Education Learning Lab
- Cell Reports Methods
- Computational and Structural Biotechnology
- Consortium for Computing Sciences in Colleges, Southwest (CCSC-SW)
- Czech Science Foundation (GAČR)
- Evolutionary Bioinformatics
- F1000Research
- Gigabyte
- IEEE Journal of Biomedical and Health Informatics
- IEEE/ACM Transactions on Computational Biology and Bioinformatics
- Innovation and Technology in Computer Science Education (ITiCSE)
- Journal of Theoretical Biology
- Molecular Biology and Evolution
- NAR Genomics and Bioinformatics
- Nature Communications
- Nature Computational Science
- Neural Information Processing Systems (NeurIPS)

- Patterns
- PeerJ
- PeerJ Computer Science
- PLOS Computational Biology
- PLOS ONE
- Research in Computational Molecular Biology (RECOMB)
- Transactions of the Kansas Academy of Science
- Virus Evolution
- Viruses

Organizations

- **Editorial Board Member**, *Scientific Reports* (2026–Present)
- **Editorial Review Board Member**, *Evolutionary Bioinformatics* (2024–Present)
- **Broadening Participation Champion (BPC)**, *Semiconductor Research Corporation* (2023–Present)
- **Member**, *Association for Computing Machinery* (2019–Present)
- **San Diego Chapter Member**, *Computer Science Teachers Association* (2018–Present)
- **Faculty Research Mentor**, *Computing Research Association* (2025–2025)
- **CTI Accelerate Course Developer**, *Computing Research Association* (2024–2024)
- **Bridge Workshop Series Designer-Facilitator**, *Computing Research Association* (2023–2024)
- **2023 Conference Highlights Program Committee Member**, *International Conference on Research in Computational Molecular Biology* (2023–2023)
- **2022 Conference Chair**, *International Conference on Research in Computational Molecular Biology* (2022–2022)
- **2021 Conference Chair**, *Consortium for Computing Sciences in Colleges, Southwest* (2019–2021)
- **Treasurer**, *Consortium for Computing Sciences in Colleges, Southwest* (2019–2021)
- **Registrar**, *Consortium for Computing Sciences in Colleges, Southwest* (2019–2021)
- **Member**, *American Go Association* (2018–2020)
- **Organizer: Conference Orientation for Undergraduates**, *2020 ACM Conference on Bioinformatics, Computational Biology, and Health Informatics* (2020–2020)
- **Member**, *International AIDS Society* (2018–2020)
- **Member**, *Society for Molecular Biology and Evolution* (2017–2019)
- **Member**, *ACM Technical Symposium on Computer Science Education* (2018–2019)
- **Fundraising Committee Member**, *International Society for Computational Biology* (2017–2019)

Institutional Service

- **Inclusive Instruction Working Group Member**, *UC San Diego* (2024–Present)
- **Faculty Co-Advisor (with Professor Terry Gaasterland)**, *UC San Diego* (2023–Present)
- **Training Committee Member**, *UC San Diego* (2021–Present)
- **Research Committee Member**, *UC San Diego* (2021–Present)
- **Ph.D. Admissions Committee Member**, *UC San Diego* (2020–Present)
- **M.S. Admissions Committee Member**, Computer Science & Engineering, *UC San Diego* (2019–Present)
- **Outreach and Student Affairs Committee Member**, *UC San Diego* (2019–Present)
- **Diversity, Equity, and Inclusion (DEI) Committee Member**, *UC San Diego* (2020–2025)
- **Senior Faculty Mentor**, *UC San Diego* (2024–2024)
- **Chair of the Faculty**, *UC San Diego* (2023–2024)
- **Faculty Co-Advisor (with Professor Bradley Voytek)**, *UC San Diego* (2023–2024)
- **Steering Committee Member**, *UC San Diego* (2020–2022)
- **Executive Committee Member**, *UC San Diego* (2020–2021)
- **Founding Director**, *UC San Diego* (2020–2021)
- **President**, *UC San Diego* (2018–2019)
- **Member**, *UC San Diego* (2018–2019)
- **Member**, *UC San Diego* (2017–2019)
- **Director of Onboarding**, *UC San Diego* (2017–2018)
- **Director of Finance**, *UC San Diego* (2016–2017)
- **Director of Internal Affairs**, *UC San Diego* (2015–2016)

Outreach

- **Faculty Advocate**, *UC San Diego* (2022–Present)
- **Research Mentor**, *UC San Diego* (2019–Present)
- **Volunteer**, *Skype a Scientist* (2018–Present)
- **SciChats @ Salk Volunteer**, *Salk Institute for Biological Studies* (2017–Present)
- **SalkEducation Volunteer**, *Salk Institute for Biological Studies* (2017–Present)
- **Guest Speaker: Viral Phylogenetics Workshop**, *Bonita Vista High School* (2025–2025)
- **Guest Speaker: Viral Phylogenetics Workshop**, *High Tech High Chula Vista* (2024–2024)
- **Guest Speaker: Viral Phylogenetics Workshop**, *Bonita Vista High School* (2023–2023)
- **Internship Program Mentor**, *High Tech High Chula Vista* (2022–2023)
- **Guest Speaker: Introduction to Bioinformatics**, *Bonita Vista High School* (2023–2023)

- **Guest Speaker: Introduction to Bioinformatics**, *University City High School* (2022–2022)
- **2021 TritonHacks Judge**, *UC San Diego* (2021–2021)
- **2020 DataHacks Mentor**, *UC San Diego* (2020–2020)
- **Author: Inherited Traits, 3rd Grade**, *STEMTaught* (2018–2019)
- **2019 SD Hacks Judge**, *UC San Diego* (2019–2019)
- **eMENTOR**, *Del Lago Academy* (2018–2019)
- **Mentor Teaching Assistant**, Computer Science & Engineering, *UC San Diego* (2016–2019)
- **High Tech Fair Volunteer**, *Fleet Science Center* (2019–2019)
- **Park Clean-Up Volunteer**, *San Jose Department of Parks, Recreation & Neighborhood Services* (2018–2018)
- **Group Mentor**, *UC San Diego* (2017–2018)
- **Project Mentor: Protein Modeling**, *Mission Bay High School* (2017–2017)