

# VIKRAM SHIVAKUMAR

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## EDUCATION

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| <b>Johns Hopkins University</b><br>PhD Candidate, Computer Science (expected graduation: Feb 2026)<br>Advisor: Ben Langmead<br>Qualifying project advisor: Adam Phillippy | <i>2021-</i>     |
| <b>Johns Hopkins University</b><br>M.S. in Biomedical Engineering                                                                                                         | <i>2021-2023</i> |
| <b>University of California, Berkeley</b><br>B.S. in Bioengineering (Honors)<br>Minor in Computer Science                                                                 | <i>2017-2020</i> |

## PROFESSIONAL EXPERIENCE

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| <b>Undergraduate Researcher</b><br>UC Berkeley, Department of Bioengineering<br>Berkeley, CA<br>Advisor: Liana Lareau                             | <i>2020-2021</i> |
| <b>Research Intern</b><br>Georgetown University, Innovation Center for Biomedical Informatics (ICBI)<br>Washington D.C.<br>Advisor: Matthew McCoy | <i>2018-2019</i> |
| <b>Research Intern</b><br>National Museum of Natural History, Lab of Analytical Biology (LAB)<br>Washington D.C.<br>Advisor: Elizabeth Zimmer     | <i>2015-2017</i> |

## FELLOWSHIPS AND AWARDS

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| National Science Foundation Graduate Research Fellowship (Total amount: \$138,000) | <i>2021-2026</i> |
| <b>Best Short Talk and Poster</b> — RECOMB-seq (Istanbul, Turkey)                  | <i>2023</i>      |
| <b>Best Proceedings Paper and Talk</b> — ISMB HitSeq (Montreal, QC)                | <i>2024</i>      |
| <b>Best Poster (2<sup>nd</sup> place)</b> — JHU ARCH HPC Symposium (Baltimore, MD) | <i>2025</i>      |
| <b>Best Poster</b> — ISMB EvolCompGen (Liverpool, UK)                              | <i>2025</i>      |

## PUBLICATIONS

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See [Google Scholar](#) and ORCID [0000-0002-1424-3711](#) for more information.

### Research Articles

10. **V.S. Shivakumar**, B. Langmead (2025). Mumemto: efficient maximal matching across pangenomes. *Genome Biology*, 26, 169. doi:10.1186/s13059-025-03644-0

9. A. Zheng, I. Lee, **V.S. Shivakumar**, O.Y. Ahmed, B. Langmead (2025). Fast and flexible minimizer digestion with digest. *Bioinformatics*, 41(7), btaf368. [doi:10.1093/bioinformatics/btaf368](https://doi.org/10.1093/bioinformatics/btaf368)
8. S. Kovaka, P.W. Hook, K.M. Jenike, **V. Shivakumar**, L.B. Morina, R. Razaghi, W. Timp, M.C. Schatz (2025). Uncalled4 improves nanopore DNA and RNA modification detection via fast and accurate signal alignment. *Nature Methods*, 1–11. [doi:10.1038/s41592-025-02631-4](https://doi.org/10.1038/s41592-025-02631-4)
7. N.K. Brown, **V.S. Shivakumar**, B. Langmead (2025). Improved pangenomic classification accuracy with chain statistics. *International Conference on Research in Computational Molecular Biology (RECOMB), Lecture Notes in Bioinformatics (LNBI)*, 15647, 190–208. [doi:10.1007/978-3-031-90252-9\\_12](https://doi.org/10.1007/978-3-031-90252-9_12)
6. **V.S. Shivakumar**, O.Y. Ahmed, S. Kovaka, M. Zakeri, B. Langmead (2024). Sigmoni: classification of nanopore signal with a compressed pangenome index. *Bioinformatics*, 40(Supplement\_1), i287–i296. [doi:10.1093/bioinformatics/btae213](https://doi.org/10.1093/bioinformatics/btae213)
5. A.L. Cope, F. Anderson, J. Favate, M. Jackson, A. Mok, A. Kurowska, J. Liu, E. MacKenzie, **V. Shivakumar**, P. Tilton, S.M. Winterbourne, S. Xue, K. Kavoussanakis, L.F. Lareau, P. Shah, E.W.J. Wallace (2022). riboviz 2: a flexible and robust ribosome profiling data analysis and visualization workflow. *Bioinformatics*, 38(8), 2358–2360. [doi:10.1093/bioinformatics/btac093](https://doi.org/10.1093/bioinformatics/btac093)
4. M.D. McCoy, **V. Shivakumar**, S. Nimmagadda, M.S. Jafri, S. Madhavan (2019). SNP2SIM: a modular workflow for standardizing molecular simulation and functional analysis of protein variants. *BMC Bioinformatics*, 20, 1–8. [doi:10.1186/s12859-019-2774-9](https://doi.org/10.1186/s12859-019-2774-9)
3. G. Damasco, **V.S. Shivakumar**, T.M. Misciewicz, D.C. Daly, P.V.A. Fine (2019). Leaf transcriptome assembly of Protium copal (Burseraceae) and annotation of terpene biosynthetic genes. *Genes*, 10(5), 392. [doi:10.3390/genes10050392](https://doi.org/10.3390/genes10050392)
2. **V.S. Shivakumar**, G. Johnson, E.A. Zimmer (2019). Transcriptome analysis of the curry tree (*Berbera koenigii* L., Rutaceae) during leaf development. *Scientific Reports*, 9(1), 4230. [doi:10.1038/s41598-019-40227-z](https://doi.org/10.1038/s41598-019-40227-z)
1. **V.S. Shivakumar**, M.S. Appelhans, G. Johnson, M. Carlsen, E.A. Zimmer (2017). Analysis of whole chloroplast genomes from the genera of the Clauseneae, the curry tribe (Rutaceae, Citrus family). *Molecular Phylogenetics and Evolution*, 117, 135–140. [doi:10.1016/j.ympev.2016.12.015](https://doi.org/10.1016/j.ympev.2016.12.015)

## Preprints

3. D. Diaz-Dominguez, T. Gagie, V. Guerrini, B. Langmead, Z. Liptak, G. Manzini, F. Masillo, **V. Shivakumar** (2025). Prefix-free parsing for merging big BWTs. *arXiv*. [doi:10.48550/arXiv.2506.03294](https://doi.org/10.48550/arXiv.2506.03294) (Accepted at SPIRE 2025)
2. **V.S. Shivakumar**, B. Langmead (2025). Partitioned Multi-MUM finding for scalable pangenomics. *bioRxiv*. [doi:10.1101/2025.05.20.654611](https://doi.org/10.1101/2025.05.20.654611) (In review at Genome Research)
1. **V. Shivakumar**, W. Reid, S. Madhavan, M.D. McCoy (2020). Simulating Protein Structure to Support Clinical Decisions: Predicting the Ligand Specific Impact of Genomic Variation on Opioid Binding. *Research Square*.

## PRESENTATIONS

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### Invited Talks

7. **Workshop on Algorithms in Bioinformatics (WABI)**, College Park, MD. August 20, 2025. Partitioned Multi-MUM finding for scalable pangenomics

6. **Tree of Life seminar series**, Wellcome Sanger Institute, Hinxton, UK. July 30, 2025.  
Multi-MUM finding across pangenomes with Mumemto
5. **Human Pangenome Reference Consortium (HPRC) meeting**, presented remotely. March 24, 2025.  
Multi-MUM finding across pangenomes with Mumemto
4. **Intelligent Systems for Molecular Biology (ISMB)**. Montreal, Canada. July 13, 2024.  
Sigmoni: efficient pangenome multi-classification of nanopore signal (**Best Talk Award**)
3. **RECOMB-seq**, Cambridge, MA. April 27, 2024.  
Mumemto: efficient maximal matching across multiple genomes
2. **Workshop on efficient methods for sequence analysis (WEMSA)**, State College, PA. May 24, 2023.  
Sigmoni: efficient pangenome multi-classification of nanopore signal
1. **Research on Computational Molecular Biology: Satellite Conference on Biological Sequence Analysis (RECOMB-seq)**. Istanbul, Turkey. April 14, 2023.  
Sigmoni: efficient pangenome multi-classification of nanopore signal

## Poster Presentations

3. **Mumemto: efficient maximal matching across pangenomes**
  - **Best Poster Award**: Intelligent Systems for Molecular Biology (ISMB). Liverpool, UK. July 21-24, 2025.
  - Biology of Genomes. Cold Spring Harbor Laboratory, NY, USA. May 9, 2025.
  - **Best Poster Award (2<sup>nd</sup> place)** High Performance Computing Symposium, Johns Hopkins University. Baltimore, MD. April 2, 2025.
  - Workshop on efficient methods for sequence analysis (WEMSA). State College, PA. August 9, 2024.
  - RECOMB-seq, Cambridge, MA. April 27, 2024.
2. **Sigmoni: efficient pangenome multi-classification of nanopore signal**
  - Genome Informatics. Cold Spring Harbor Laboratory, NY, USA. December 8, 2023.
  - Workshop on efficient methods for sequence analysis (WEMSA). State College, PA. May 24, 2023.
  - **Best Poster Award**: Research on Computational Molecular Biology (RECOMB). Istanbul, Turkey. April 16, 2023.
  - Biological Data Science. Cold Spring Harbor Laboratory, NY, USA. November 10, 2022.
1. **Analysis of whole Chloroplast genomes from the genera of the Clauseneae, the Curry tribe (Rutaceae, Citrus family)**
  - Botany. Savannah, GA. August 1st, 2016.

## TEACHING AND MENTORSHIP

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## Teaching

- 2020 Undergraduate Student Instructor (uGSI)  
BioE/CompBio 131, Introduction to Computational Biology – Prof. Ian Holmes
- 2021 Course Assistant (CA)  
BioE/CompBio 145, Introduction to Computational Biology – Prof. Liana Lareau
- 2023 Teaching Assistant (TA) (and guest lecturer)  
Sketching and Indexing for Sequences – Prof. Ben Langmead
- 2024 Course Assistant (CA) (and guest lecturer)  
Sketching and Indexing for Sequences – Prof. Ben Langmead

## Mentorship

Students supervised:

- Alan Zheng, undergraduate researcher
- Ishmael Lee, undergraduate researcher
- Andrew Raptis, high school intern
- Arjun Garg, high school intern

## SOFTWARE

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**Mumemto - Exact matching across pangenomes**

<https://github.com/vikshiv/mumemto>

**Sigmoni - fast Nanopore signal classification using compressed indexing**

<https://github.com/vikshiv/sigmoni>

**Digest - C++ and Python API for minimizer digestion schemes**

<https://github.com/VeryAmazed/digest>

**riboviz - visualizing ribosome profiling sequencing data**

<https://github.com/riboviz/riboviz>

**SNP2SIM - variant-based molecular dynamics**

<https://github.com/mccoymd/snp2sim>

## SERVICE AND MEMBERSHIPS

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### Peer Review Experience

- 2025 – Bioinformatics (reviewer)
- 2023 – RECOMB (sub-reviewer)
- 2023 – ISMB (sub-reviewer)

### Memberships

- 2023 – International Society for Computational Biology (ISCB)
- 2025 – Human Pangenome Reference Consortium (HPRC)

### Service

- 2023 – Peer mentorship program - Computer Science department
- 2021 Volunteer - Orientation, Biomedical Engineering department
- 2018 – 2020 Treasurer of UC Berkeley Molecular and Cell Biology Student Organisation (MCBcDNA)