# VIKRAM SHIVAKUMAR

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## EDUCATION

**Johns Hopkins University** *2021-*
PhD Candidate, Computer Science
Advisor: Ben Langmead

**Johns Hopkins University** *2023*
M.S. in Biomedical Engineering

**University of California, Berkeley** *2020*
B.S. in Bioengineering (Honors)
Minor in Computer Science

## PROFESSIONAL EXPERIENCE

**Undergraduate Researcher** *2021*
UC Berkeley, Department of Bioengineering
Berkeley, CA
Advisor: Liana Lareau

**Research Intern** *2018-2019*
Georgetown University, Innovation Center for Biomedical Informatics (ICBI)
Washington D.C.
Advisor: Matthew McCoy

**Research Intern** *2015-2017*
National Museum of Natural History, Lab of Analytical Biology (LAB)
Washington D.C.
Advisor: Elizabeth Zimmer

## FELLOWSHIPS AND AWARDS

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| National Science Foundation Graduate Research Fellowship (Total amount: $138,000) | *2021-2026* |
| Best Short Talk and Poster — **RECOMB-seq** (Istanbul, Turkey) | *2023* |
| Best Proceedings Paper and Talk — **ISMB** (Montreal, QC) | *2024* |
| Best Poster (2nd place) — **ARCH HPC Symposium** (JHU) | *2025* |

## PUBLICATIONS

See Google Scholar and ORCID 0000-0002-1424-3711 for more information.

### Research Articles

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.

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)*, 190–208.

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.
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.
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.
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.
2. **V.S. Shivakumar**, G. Johnson, E.A. Zimmer (2019). Transcriptome analysis of the curry tree (*Bergera koenigii L.*, Rutaceae) during leaf development. *Scientific Reports*, 9(1), 4230.
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.

### Preprints

3. **V.S. Shivakumar**, B. Langmead (2025). Mumemto: efficient maximal matching across pangenomes. *bioRxiv*. (In review at Genome Biology)
2. A. Zheng, I. Lee, **V.S. Shivakumar**, O.Y. Ahmed, B. Langmead (2025). Fast and flexible minimizer digestion with digest. *bioRxiv*. (In review at Bioinformatics)
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

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

### Poster Presentations

3. **Mumemto: efficient maximal matching across pangenomes**
    - Intelligent Systems for Molecular Biology (ISMB). Liverpool, UK. July 21-24, 2025.
    - Biology of Genomes. Cold Spring Harbor Laboratory, NY, USA. May 9, 2025.
    - 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.
    - 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

### Teaching

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| 2020 | TA – BioE/CompBio 131, Introduction to Computational Biology (Prof. Ian Holmes) |
| 2021 | CA – BioE/CompBio 145, Introduction to Computational Biology (Prof. Liana Lareau) |
| 2023 | TA (and guest lecturer) – Sketching and Indexing for Sequences (Prof. Ben Langmead) |
| 2024 | CA (and guest lecturer) – Sketching and Indexing for Sequences (Prof. Ben Langmead) |

### Mentorship

Students supervised:

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

## SOFTWARE

**Mumemto - Exact matching across pangenomes**
https://github.com/vikshiv/mumemto
**Sigmoni - fast Nanopore signal classificaiton 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

### Peer Review Experience

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

### Memberships

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

### Service

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| 2021 | Volunteer - Orientation, Biomedical Engineering department |
| 2018 –2020 | Treasurer of UC Berkeley Molecular and Cell Biology Student Organisation (MCBcDNA) |