

Mohsen Zakeri

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<https://github.com/mohsenzakeri>

CURRENT POSITION

Postdoctoral Fellow, Computer Science Department

Johns Hopkins University, Baltimore, MD

Advisor: Ben Langmead

2022 - present

EDUCATION

PhD | Computer Science, Advisor: Prof. Rob Patro

University of Maryland

Dec. 2021

College Park, MD

MS | Computer Science, Advisor: Prof. Rob Patro

Stony Brook University

May. 2017

Stony Brook, NY

BS | Computer Engineering, Major: Software Engineering

University of Tehran

Jun. 2015

Tehran, Iran

RESEARCH AND PROFESSIONAL EXPERIENCE

Scalable full-text pangenome indexes

Postdoc fellow at Johns Hopkins University

2022 - present

- Designed and developed [Movi](#), a data structure based on the Move-Structure for indexing pangenomes. Movi is a full-text index which scales very well for highly similar references while being very fast to query. | *C++*

Oxford Nanopore reads classification

Postdoc fellow at Johns Hopkins University

2022 - present

- Developed a method to compute exact matching queries (pseudo-matching lengths) with [Movi](#) for real-time classification of Oxford Nanopore reads and fast host depletion with pangenomes. | *C++*
- Contributed to the design of [Sigmoni](#) for multi-class classification of Nanopore signals using a compressed full-text index (r-index).

Converting genomic to transcriptomic coordinates

Computational biologist intern at Ocean Genomics, Pittsburgh, PA

Summer 2021

- Developed [Mudskipper](#), a software tool that converts alignments in SAM files - commonly used for storing sequence alignments - from genomic coordinates to transcriptomic coordinates. | *Rust*

Efficient and accurate methods for single-cell RNA-seq preprocessing

Research assistant at University of Maryland

2020 - 2021

- Contributed to the design and development of a variation of pseudoalignment with structural constraints (sketch mode) for mapping single-cell RNA-seq reads, used in [Alevin-fry](#). | *C++ and Rust*

A fast and accurate aligner for short reads

Research assistant at Stony Brook University and University of Maryland

2019 - 2020

- Collaborated on the design and development of [Puffaligner](#), an aligner based on Pufferfish (a ccdbg index) that aligns various types of short reads to a collection of references. | *C++*

A pipeline for abundance estimation of metagenomics sequencing reads

Research assistant at Stony Brook University

2018 - 2019

- Collaborated on the design and development of [Cedar](#), a fast and accurate method for quantifying metagenomics sequencing reads. Cedar focuses on eliminating spurious reads in an iterative manner during the EM optimization. | *C++*

Improving the accuracy of fast RNA-seq quantification methods

Research assistant at Stony Brook University

2016 - 2019

- Collaborated on the design and development of [Selective-alignment](#) to enhance the specificity and sensitivity of lightweight alignment methods used in fast RNA-seq quantification approaches. | *C++*
- Enhanced the probabilistic model of bulk RNA-seq in [Salmon](#) to improve the fidelity of the equivalence class-based [factorization](#) models for RNA-seq data. This new model improved the accuracy of abundance estimations, particularly in challenging cases, i.e., paralogous genes. | *C++*

TEACHING EXPERIENCE

Instructor of a HEART course Johns Hopkins University, Baltimore, MD Needle in a haystack: Finding the origin of shredded sequences	Fall 2023
Co-Instructor of a HEART course Johns Hopkins University, Baltimore, MD Software Engineering in Bio-medical Research	Fall 2022
Teaching assistant of undergraduate courses Stony Brook University, Stony Brook, NY Social Networks, Discrete Mathematics, Computer Programming III	2015 - 2017
Teaching assistant of a graduate course Stony Brook University, Stony Brook, NY Analysis of Algorithms	Fall 2016
Teaching assistant of undergraduate courses University of Tehran, Tehran, Iran Advanced Programming, Artificial Intelligence	2014 - 2015

PEER REVIEWED PUBLICATIONS

*: co-first authorship

- [1] Vikram S Shivakumar, Omar Y Ahmed, Sam Kovaka, **Mohsen Zakeri**, and Ben Langmead. “Sigmoni: classification of nanopore signal with a compressed pangenome index”. In: *Bioinformatics (ISMB Proceedings)* 40.Supplement_1 (2024), pp. i287–i296.
- [2] Euphy Y Wu, Noor P Singh, Kwangbom Choi, **Mohsen Zakeri**, Matthew Vincent, Gary A Churchill, Cheryl L Ackert-Bicknell, Rob Patro, and Michael I Love. “SEESAW: detecting isoform-level allelic imbalance accounting for inferential uncertainty”. In: *Genome biology* 24.1 (2023), p. 165.
- [3] Dongze He, **Mohsen Zakeri**, Hirak Sarkar, Charlotte Soneson, Avi Srivastava, and Rob Patro. “Alevin-fry unlocks rapid, accurate and memory-frugal quantification of single-cell RNA-seq data”. In: *Nature Methods* 19.3 (2022), pp. 316–322.
- [4] Giorgos Skoufos, Fatemeh Almodaresi, **Mohsen Zakeri**, Joseph N Paulson, Rob Patro, Artemis G Hatzigeorgiou, and Ioannis S Vlachos. “AGAMEMNON: an Accurate metaGenomics And METatranscriptOMics quaNtificationON analysis suite”. In: *Genome biology* 23.1 (2022), pp. 1–27.
- [5] Fatemeh Almodaresi, **Mohsen Zakeri***, and Rob Patro. “Puffaligner: A Fast, Efficient, and Accurate Aligner Based on the Pufferfish Index”. In: *Bioinformatics* (2021).
- [6] Avi Srivastava, Laraib Malik, Hirak Sarkar, **Mohsen Zakeri**, Fatemeh Almodaresi, Charlotte Soneson, Michael I Love, Carl Kingsford, and Rob Patro. “Alignment and mapping methodology influence transcript abundance estimation”. In: *Genome biology* 21.1 (2020), pp. 1–29.
- [7] Hirak Sarkar, **Mohsen Zakeri***, Laraib Malik, and Rob Patro. “Towards selective-alignment: Bridging the accuracy gap between alignment-based and alignment-free transcript quantification”. In: (2018), pp. 27–36.
- [8] **Mohsen Zakeri**, Avi Srivastava, Fatemeh Almodaresi, and Rob Patro. “Improved data-driven likelihood factorizations for transcript abundance estimation”. In: *Bioinformatics (ISMB Proceedings)* 33.14 (2017), pp. i142–i151.

PRE-PRINTS

- [1] Lore Depuydt, Omar Ahmed, Andrej Baláž, Nathaniel K Brown, Adrián Goga, Alessia Petescia, **Mohsen Zakeri**, Jan Fostier, Travis Gagie, Ben Langmead, et al. “r-indexing without backward searching”. In: *arXiv e-prints* (2023), arXiv–2312.
- [2] **Mohsen Zakeri**, Nathaniel K Brown, Omar Y Ahmed, Travis Gagie, and Ben Langmead. “Movi: a fast and cache-efficient full-text pangenome index”. In: *bioRxiv* (2023).
- [3] Avi Srivastava, **Mohsen Zakeri**, Hirak Sarkar, Charlotte Soneson, Carl Kingsford, and Rob Patro. “Accounting for Fragments of unexpected origin improves transcript quantification in RNA-seq simulations focused on increased realism”. In: *bioRxiv* (2021).

- [4] **Mohsen Zakeri**, Avi Srivastava, Hirak Sarkar, and Rob Patro. “A Like-for-Like Comparison of Lightweight-Mapping Pipelines for Single-Cell RNA-seq Data Pre-Processing”. In: *bioRxiv* (2021).

CONFERENCES AND PRESENTATIONS

- [1] **Movi: a fast and cache-efficient full-text pangenome index (talk)**. In: *Recomb-seq, Cambridge, MA*. 2024.
- [2] **Real-time nanopore adaptive sampling with Movi (talk)**. In: *Genome Informatics, Cold Spring Harbor, NY*. 2023.
- [3] **Real-time nanopore adaptive sampling with move data structure (talk)**. In: *Workshop on Emerging Methods for Sequencing Analysis, State College, PA*. 2023.
- [4] **Augmented-data bootstrap reveals missing uncertainty during RNA-seq quantification (poster)**. In: *RECOMB, San Diego*. 2022.
- [5] **Cedar: scalable, accurate and fast metagenomic abundance estimation (poster)**. In: *RECOMB, Washington D.C.* 2019.

EXTERNAL RESEARCH SUPPORT

I contributed to the writing of the grant:

Efficient and scalable pangenomes with the move structure
NIH/NHGRI R21 grant R21HG013433 (\$377K)

2/1/2024 - 2/28/2026

COMMUNITY INVOLVEMENT

Hackathon Judge

September 2023

[Hophacks](#), Johns Hopkins University

- Volunteered as a judge at an annual health-focused hackathon, where participants developed and presented applications over three days in a science fair format.
- Assessed projects on creativity, usefulness, polish, and technical difficulty, contributing to the development and recognition of innovative health technologies.

REFERENCES

Ben Langmead
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Rob Patro
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Associate Professor, Department of Computer Science, University of Maryland

Travis Gagie
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Associate Professor, Faculty of Computer Science, Dalhousie University