

# Mohammadamin Edrisi

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## EDUCATION

**Rice University**, Houston, TX  
*Ph.D. in Computer Science*  
Expected May, 2024

**Rice University**, Houston, TX  
*M.Sc. in Computer Science*  
November, 2020

**Sharif University of Technology**, Tehran, Iran  
*B.S. in Electrical Engineering*  
January, 2017

## PUBLICATIONS

**MaCroDNA: Accurate integration of single-cell DNA and RNA data for a deeper understanding of tumor heterogeneity**

Mohammadamin Edrisi, Xiru Huang, Huw A. Ogilvie, Luay Nakhleh  
*Accepted for publication in Nature Communications, 2023.*  
<https://doi.org/10.1101/2022.08.21.504709>

**MoTERNN: Classifying the Mode of Cancer Evolution Using Recursive Neural Networks**

Mohammadamin Edrisi, Huw A. Ogilvie, Meng Li, Luay Nakhleh  
*RECOMB International Workshop on Comparative Genomics, 232-247, 2023*  
[https://doi.org/10.1007/978-3-031-36911-7\\_15](https://doi.org/10.1007/978-3-031-36911-7_15)

**NestedBD: Bayesian Inference of Phylogenetic Trees From Single-Cell DNA Copy Number Profile Data Under a Birth-Death Model**

Yushu Liu, Mohammadamin Edrisi, Huw A. Ogilvie, Luay Nakhleh  
*Under review in PLOS Computational Biology, 2023.*  
<https://doi.org/10.1101/2022.01.16.476510>

**Phylovar: Towards scalable phylogeny-aware inference of single-nucleotide variations from single-cell DNA sequencing data**

Mohammadamin Edrisi, Monica V. Valecha, Sunkara B. V. Chowdary, Sergio Robledo, Huw A. Ogilvie, David Posada, Hamim Zafar, Luay Nakhleh  
*In proceedings of the 30<sup>th</sup> annual conference on Intelligent Systems for Molecular Biology (ISMB), Bioinformatics 38 (Supplement\_1): i195-i202, 2022.*  
<https://doi.org/10.1093/bioinformatics/btac254>

**Current progress and open challenges for applying deep learning across the biosciences**

Nicolae Sapoval, Amirali Aghazadeh, Michael G. Nute, Dinler A. Antunes, Advait Balaji, Richard Baraniuk, C. J. Barberan, Ruth Dannenfesler, Chen Dun, Mohammadamin Edrisi, R. A. Leo Elworth, Bryce Kille, Anastasios Kyrillidis, Luay Nakhleh, Cameron R. Wolfe, Zhi Yan, Vicky Yao and Todd J. Treangen  
*Nature Communications, 13 (1): 1728, 2022.*  
<https://doi.org/10.1038/s41467-022-29268-7>

**Methods for copy number aberration detection from single-cell DNA sequencing data**

Xian Fan Mallory, Mohammadamin Edrisi, Nicholas Navin, Luay Nakhleh  
*Genome Biology, 21 (1): 208, 2020.*  
<https://doi.org/10.1186/s13059-020-02119-8>

**Assessing the performance of methods for copy number aberration detection from single-cell DNA sequencing data**

Xian Fan Mallory, **Mohammadamin Edrisi**, Nicholas Navin, Luay Nakhleh  
*PLOS Computational Biology*, 16 (7): 124, 2020.  
<https://doi.org/10.1371/journal.pcbi.1008012>

**Methods developed during the first National Center for Biotechnology Information Structural Variation Codeathon at Baylor College of Medicine**

Medhat Mahmoud, Alejandro Rafael Gener, Michael M. Khayat, [and 43 authors including **Mohammadamin Edrisi**]  
*F1000Research*, 9:1141, 2020.  
<https://doi.org/10.12688/f1000research.23773.1>

**A Combinatorial Approach for Single-cell Variant Detection via Phylogenetic Inference**

**Mohammadamin Edrisi**, Hamim Zafar, Luay Nakhleh  
*19th International Workshop on Algorithms in Bioinformatics (WABI 2019)* (Vol. 143, p. 22:1-22:13). Schloss DagstuhlLeibniz-Zentrum fuer Informatik, 2019.  
<https://doi.org/10.4230/LIPIcs.WABI.2019.22>

**Meta-aligner: long-read alignment based on genome statistics**

Damoon Nashta-ali, Ali Aliyari, Ahmad Ahmadian Moghadam, **Mohammadamin Edrisi**, Seyed Abolfazl Motahari, Babak Hossein Khalaj  
*BMC Bioinformatics*, 18 (1): 126, 2017.  
<https://doi.org/10.1186/s12859-017-1518-y>

**SOFTWARE**

**MaCroDNA**: Python implementation of the method introduced in [MaCroDNA: Accurate integration of single-cell DNA and RNA data for a deeper understanding of tumor heterogeneity](#), available on: <https://github.com/NakhlehLab/MaCroDNA>

**MoTERNN**: PyTorch implementation of the method presented in [MoTERNN: Classifying the Mode of Cancer Evolution Using Recursive Neural Networks](#), available on: <https://github.com/NakhlehLab/MoTERNN>

**Phylovar**: Python implementation of the method presented in [Phylovar: Towards scalable phylogeny-aware inference of single-nucleotide variations from single-cell DNA sequencing data](#), available on: <https://github.com/NakhlehLab/Phylovar>

**scVILP**: implementation of the method presented in [A Combinatorial Approach for Single-cell Variant Detection via Phylogenetic Inference](#), available on: <https://github.com/mae6/scVILP>

**TEACHING & MENTORSHIP EXPERIENCES**

<b>Mentor</b> , REU Data Science, 10-week summer program	Summer 2022
<b>Mentor</b> , Google-Rice Research Experience for Undergraduates (REU), 10-week summer program	Summer 2021
<b>Teaching Assistant</b> , Reasoning About Algorithms (COMP 382)	Fall 2019
<b>Teaching Assistant</b> , Probabilistic Algorithms (COMP 580)	Spring 2019
<b>Teaching Assistant</b> , Bioinformatics: Sequence Alignment (COMP 571)	Fall 2018

**HONORS & AWARDS**

Honorable Mention of Ian Lawson Van Toch Memorial Award for Outstanding Student Paper in 30<sup>th</sup> Conference on Intelligent Systems for Molecular Biology (ISMB)  
<https://www.iscb.org/ismb2022-general-info/award-winners>  
<https://cswb.rice.edu/news/rice-cs-phd-student-mohammadamin-edrisi-wins-honorable-mention-ismb-0> 2022

Rice Computer Science Graduate Fellowship 2017-2018

