SINA MAJIDIAN

sina.majidian@unil.ch ◇ sinamajidian.github.io

3400 North Charles St, Baltimore, MD, USA.

PROFESSIONAL EXPERIENCE

Postdoctoral Fellow *May 2024 - Present*
Ben Langmead Lab,
Department of Computer Science, Johns Hopkins University, USA.
Developing methods for estimating evolutionary distances between genomes.

Postdoctoral Fellow *May 2021 - Apr. 2024*
Comparative Genomics Lab (Christophe Dessimoz & Natasha Glover),
Department of Computational Biology, University of Lausanne, Switzerland.
Developing algorithms for orthology inference at the tree-of-life scale.

Remote intern *Nov. 2019 - Jan. 2020*
Fritz Sedlazeck Lab
Human Genome Sequencing Center, Baylor College of Medicine, USA.
Designing methods for improving haplotype phasing using population data from 1000 Genomes Project.

Guest Researcher *Oct. 2018 - Oct. 2019*
Bioinformatics Group (Dick de Ridder),
Wageningen University, The Netherlands.
Developing haplotype phasing method using linked-read data (10X Genomics) for polyploids.

EDUCATION

Iran University of Science & Technology, Tehran. Iran.
Ph.D., Electrical Engineering, Signal processing. *Sep. 2015 – Jul. 2020*
Thesis: *Haplotype assembly using matrix completion.*
Advisor: Mohammad Hossein Kahaei

M.Sc., Electrical Engineering, Signal processing. *Sep. 2013 – Sep. 2015*
Thesis: *Cramer–Rao bound for correlation matrix estimation.*

Shahid Beheshti University, Tehran. Iran.
B.S., Electrical Engineering. *Sep. 2008 - Mar. 2013*
Thesis: *Adaptive differential pulse code modulation for speech processing.*

PEER REVIEWED PUBLICATIONS

My Google Scholar, seven first-author and five senior-author publications, h-index=7, *=corresponding author.

21. **S. Majidian**, Y. Nevers, A. Yazdizadeh, A. Vesztrocy, S. Pascarelli, D. Moi, N. Glover, A. Altenhoff, C. Dessimoz, Orthology inference at scale with FastOMA. *Nature Methods*, 2025.

20. N. Dwarshuis, N. Kalra, ..., J. Wagner, **S. Majidian***, J. Zook*. The GIAB genomic stratifications resource for human reference genomes. *Nature Communications*, 15.1:9029, 2024.

19. D. Dylus, A. Altenhoff, **S. Majidian**, F. Sedlazeck, C. Dessimoz. Read2Tree: scalable and accurate phylogenetic trees from raw reads. *Nature Biotechnology*, 42:139–147, 2024.

18. M. Ndiaye, S. Banos, L. Fitzgerald, A. Yazdizadeh, S. Oreshkov, C. Dessimoz, F. Sedlazeck, N. Glover, **S. Majidian***. When less is more: applications of minimizers in genomics. *Genome Biology*, 25.1:270, 2024.

17. S. Lamei, A. Beyraghdar, A. Shojaeiyan, **S. Majidian***. Transcriptomic data reveals the dynamics of terpenoids biosynthetic pathway of fenugreek. *BMC Genomics*, 25.1:390, 2024.

16. A. Altenhoff, A.W Vesztrocy, C. Bernard, C. Train, A. Nicheperovich, S. PrietoBanos, I. Julca, D. Moi, Y. Nevers, **S. Majidian**, C. Dessimoz, N. Glover, OMA orthology in 2024: improved prokaryote coverage, ancestral and extant GO enrichment, a revamped synteny viewer and more in the OMA Ecosystem. *Nucleic Acids Research*, 52.D1:D513–D521, 2024.

15. F. Langschied, ..., **S. Majidian**, ..., C. Dessimoz, I. Ebersberger. New developments for the Quest for Orthologs benchmark service. *NAR Genomics and Bioinformatics*, 6.4:lqae167, 2024.

14. F. Langschied, .., **S. Majidian**, .., I. Ebersberger. Quest for Orthologs in the Era of Biodiversity Genomics. *Genome Biology and Evolution*, 16.10:evae224, 2024.

13. **S. Majidian**, D. Paiva Agustinho, F. Sedlazeck, M. Mahmoud, Genomic variant benchmark: if you cannot measure it, you cannot improve it. *Genome Biology*, 24.1:221, 2023.

12. P. Liakopoulos, B., Banfalvi, X. Wang, **S. Majidian**, T. de Farias, C. Dessimoz, A. Sima, Towards predicting essential proteins via federated SPARQL queries. Proceeding Semantic Web Applications and Tools for Health Care and Life Sciences. 45: 173-174, 2023.

11. A. Nicheperovich, A. Altenhoff, C. Dessimoz, **S. Majidian***, OMAMO: orthology-based model organism selection. *Bioinformatics*, 38:10. 2022.

10. K. Walker, ..., **S. Majidian**, ..., Fritz J Sedlazeck, Ben Busby. The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. *F1000 Research*, PMID 36262335, 2022.

9. A. Ahmadi, **S. Majidian**, M. Kahaei, Matrix completion using graph total variation based on directed laplacian matrix. *Circuits, Systems, and Signal Processing Springer*, 40:3099–3106, 2021.

8. R. Ezazi, M. Ahmadzadeh, **S. Majidian**, E. Stefani, M. Pindo, C. Donati, Responses of cucumber (Cucumis sativus L.) rhizosphere microbial community to some agronomic management practices, *FEMS Microbiology Ecology*, 97.8:fiab107, 2021.

7. **S. Majidian**, M. Mohades, M. Kahaei, Matrix completion with weighted constraint for haplotype estimation, *Digital Signal Processing Elsevier*, 108:102880, 2021.

6. **S. Majidian**, M. Kahaei, D. de Ridder, Hap10: reconstructing accurate and long polyploid haplotypes using linked reads, *BMC Bioinformatics*, 21.253, 2020.

5. **S. Majidian** F. Sedlazeck, PhaseME: automatic rapid assessment of phasing quality and phasing improvement, *GigaScience*, 9.7:giaa078, 2020.

4. **S. Majidian**, M. Kahaei, D. de Ridder, Minimum error correction-based haplotype assembly: considerations for long read data, *PLOS one*, 15.6:e0234470, 2020.

3. **S. Majidian**, M. Kahaei, NGS based haplotype assembly using matrix completion, PLOS one, 14.3:e0214455, 2020.

2. E. Valipour, V. Nooshabadi, S. Mahdipour, S. Shabani, L. Farhady, **S. Majidian**, Z. Noroozi, F. Motevaseli, M. Modarressi. Anti-angiogenic effects of testis-specific gene antigen 10 on primary endothelial cells, *Gene Elsevier*, 754:144856, 2020.

1. M. Mohades, **S. Majidian**, M. Kahaei, Haplotype assembly using manifold optimization and error correction mechanism, *IEEE Signal Processing Letters*, 26.6:868-872, 2019.

PREPRINTS & SUMISSIONS

5. **S. Majidian**, S. Hwang, M. Zakeri, B Langmead. Challenges for sketch-based estimation of evolutionary distance. Under review in *Briefings in Bioinformatics*, 2025.

4. S.A., Malekpour, A. Kalirad, **S. Majidian**. Inferring the selective history of CNVs using a maximum likelihood model. *bioRxiv*, Under review in *Genome Biology and Evolution* after revision, 2025.

3. F. Jaryani, ..., **S. Majidian**, ..., Ben Busby. The Sixth Annual Structural Variant and Pangenomics Hackathon at BCM, *F1000 Research*, 2025.

2. Z. Kubica, ..., **S. Majidian**, ..., Fritz Sedlazeck. The fifth international hackathon for developing computational cloud-based tools and resources for pan-structural variation and genomics. *F1000 Research*, 2024.

1. S. Moix, N. Glover, **S. Majidian**. Phylogenetic placement of whole genome duplications in yeasts through quantitative analysis of hierarchical orthologous groups. *F1000 Research*, 2023.

CONFERENCE AND INVITED TALKS

10. Nov. 2024. EvANI—Genomic distance evaluation pipeline and benchmarking dataset. Lightning Talk, Biological Data Science 2024, *Cold Spring Harbor Laboratory*, NY, US.
9. Orthology inference at scale with FastOMA.
    - Aug. 2024. *Workshop on Emerging Methods for Sequence Analysis WEMSA*. Pennsylvania State University, US.
    - July 2023. *ISMB/ECCB 2023*, Evolution and Comparative Genomics (EvolCompGen) COSI, Lyon, France.
    - Oct. 2023. *Biodiversity Genomics Conference 2023*, Welcome Sanger Institute. Online.
8. Mar. 2024. Computational comparative genomics with FastOMA and Read2Tree. *Institut Pasteur*, France.
7. Nov. 2023. Computational comparative genomics in the era of BioGenome projects. *University of Zurich*, Switzerland.
6. May 2023. Inference of phylogenetic trees directly from raw sequencing reads using Read2Tree. *Department of Microbiology, University of Lausanne.* Switzerland.
5. Sept. 2022. Toward a representative benchmark dataset of biological questions/answers involving orthology, gene expression, and complementary omics data. European Conference on Computational Biology ECCB 2022, Barcelona, Spain.
4. Aug. 2021. A fast pipeline for species tree inference using placement in Hierarchical Orthologous Groups. *Biodiversity Genomics Conference,* Wellcome Sanger Institute. Online.
3. Dec 2021. Towards pathway-specific model organisms with orthology relationships. *International Conference on Genetics and Human Genomics*, Iran.
2. Jan. 2018. Haplotype assembly using rank minimization. *The 7th Conference on Bioinformatics*, Iran.
1. May 2018. Haplotype assembly using matrix completion. *International Workshop in Signal Processing*, Iran.

TEACHING

- Workshop Instructor, OMA and OMArk Biodiversity Genomics Academy, Sep 2023 & Oct 2024. omabrowser.org/oma/academy/
- Workshop Instructor, Biodiversity Bioinformatics and Comparative Genomics. SIB Swiss Institute of Bioinformatics, 30 Aug. 2023.
- **Lecturer**, Reviews in Quantitative Biology. 20 PhD students, University of Lausanne, Nov. 2022.
- Workshop Instructor, Intensive practical genome sequencing course, University of Konstanz, Germany, March 2024 & 2025 (arranged).
- Teaching assistant, Bioinformatics Algorithms, 15 Master/PhD students. University of Lausanne, Mar-Apr 2023.
- Teaching assistant, Introduction to Bioinformatics, 110 undergraduate students. University of Lausanne, 20 hours, Apr-May 2022 & 2023.
- Teaching assistant, Introduction to UNIX. SIB, University of Zurich, 27 Sep. 2022. 4 hours.
- Teaching assistant, Introduction to Python. SIB, University of Lausanne, 29-30 Sep. 2022. 24 hours.
- Workshop instructor, Introduction to DNA data analysis. Yazd, Iran. Nov. 2021. 40 participants. 4 hours.
- Workshop instructor, Gene expression analysis using GEO2R. Iran. Nov. 2021. 40 participants. 2 hours.
- Workshop instructor, R programming. University of Tehran, Iran, 2020. 20 participants. 8 hours.
- **Lecturer**, Intro to Bioinformatics, University of Tehran, Iran, 2020, 20 students.
- **Lecturer**, 'Mathematics 1', Nahavand Institute, Iran, 2016. 20 students. 3 hours per week for 14 weeks.
- **Lecturer**, 'Wireless Communications' and 'Microwave and Antenna', Sadra Institute, Iran, 2017, 10 undergraduate students in each course. 3 hours per week for 14 weeks.
- Teaching assistant. 'Convex optimization', 'Stochastic process', 'Digital signal processing'. Iran University of Science & Technology, 2016-2018. Each course 25 students, 2 hours per week for 14 weeks.
- Teaching Assistant. 'Physics 1', 'Physics lab', 'Circuits lab'. Beheshti University, 2013. 10 students each course. 3 hours per week for 14 weeks.
- Participating in a training module, 'Introduction to University Teaching' covering: principles of instructional design, facilitating group learning activities and presentation techniques. University of Lausanne. 3 days, Aug. 2022.

MENTORSHIP

- Supervisor of undergraduate students, *Abisola Adeusi* and *Natalie Vallejo*. Genomic analysis of bacterial diversity and taxonomic classification. Johns Hopkins University, 2025.
- Supervisor of PhD visit, *Fahimeh Palizban*. Discovering copy number variation profiles in maternal cell-free DNA using long-read sequencing. University of Lausanne & University of Tehran, 2023-2024.
- Co-supervisor of PhD student, *Karim Farmanpour Kalalagh*, MEP and MEV biosynthetic pathway in Tanacetum parthenium L. Tarbiat Modares University 2023-2025.

- Supervisor of Master student, *Arung Maurya*. Reconstructing phylogenies and copy number variants using spatial transcriptomics. University of Lausanne, 2023.
- Supervisor of Summer intern, *Alina Nicheperovich*. Orthology guided model organism selection. University College London, Aug. 2021. Resulted in one paper published in Bioinformatics.
- Co-supervisor of Master student, *Sara Lamei*. Analyzing biosynthetic pathway of terpenoids in fenugreek using RNA-seq data. Tarbiat Modares University, 2022. Resulted in one paper published in BMC Genomics.
- Supervisor of Summer intern, *Ali Yazdizadeh*. Importance of phylogenetic rooting for orthology inference. Summer Undergraduate Research (SUR) Programme, University of Lausanne, 2022.
- Co-supervisor of a team of interns: *Borbala Banfalvi*, *Claire Wang*, and *Petros Liakopoulos*, Natural Language Question Answering over Knowledge Graphs. University of Lausanne, summer 2022.
- Supervisor of Master student, *Samuel Moix*. Detecting whole genome duplication using hierarchical orthologous groups. University of Lausanne, Dec. 2021.
- Co-supervision of Master student, *Mathijs van Kooten*. Creating an ensemble method combining haplotype estimates. Wageningen university, Dec. 2019.

RESPONSIBILITIES, ACTIVITIES, AND MEMBERSHIPS

- Conference Manager and Program Committee Member. Quest for orthologs 8th (ISCB-affiliated), 17-18 July, Montreal, Canada. fourwaves.com/qfo8.
- Manuscript reviewer for journals: Genome Biology, Genome Research, NAR genomics and bioinformatics, GigaScience, Computers in Biology and Medicine, Genome, Mitochondrial DNA, IET systems biology journal, Frontiers in systems biology, Frontiers in Genetics, Computational and Structural Biotechnology Journal. Reviewer for RECOMB Conference. Co-review with PIs for Nature methods and Bioinformatics. 2019-2025.
- Grants reviewer: Zurich University of Applied Sciences Research Partnership Grant proposal. 2024.
- ...

GRANTS AND AWARDS

- ...

SOFTWARES

- *FastOMA* for orthology inference: https://github.com/DessimozLab/FastOMA
- *Read2Tree* for tree inference: https://github.com/DessimozLab/Read2Tree
- *Hap10* for haplotype assembly of polyploids:https://github.com/sinamajidian/Hap10
- *PhaseME* for quality assessment of haplotype phasing information: https://github.com/sinamajidian/phaseme

REFERENCES

- Prof. Ben Langmead (PostDoc supervisor), *Johns Hopkins University*, USA,
- Prof. Christophe Dessimoz (PostDoc supervisor), *University of Lausanne*, Switzerland,
- Prof. Fritz Sedlazeck (Internship supervisor), *Baylor College of Medicine*, USA,
- Prof. Dick de Ridder (PhD rotation supervisor), *Wageningen University*, The Netherlands,
- Prof. Mohmmadhossein Kahaei (PhD supervisor), *Iran University of Science & Technology*, Iran,
- Alina Nicheperovich (former mentee), DPhil Candidate in Clinical Medicine, *University of Oxford*,
- Borbala Banfalvi (former mentee), PhD Candidate in Health Data, *Queen Mary University of London, UK*,
- Ali Yazdizadeh (former mentee), Incoming PhD candidate in Computational Biology, *Carnegie Mellon University, USA*,