

# SINA MAJIDIAN

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I am a computational biologist with expertise in data science. I strive to understand genome variation and evolution across different genomic regions by developing interpretable and efficient methods in pan-genomics.

## PROFESSIONAL EXPERIENCE

<b>Postdoctoral Fellow</b> Ben Langmead Lab, Department of Computer Science, Johns Hopkins University, USA. Developing scalable methods for evolutionary and human genomics using pangenomes.	<i>May 2024 - Present</i>
<b>Postdoctoral Fellow</b> Comparative Genomics Lab Department of Computational Biology, University of Lausanne, Switzerland. Developing algorithms for orthology and phylogeny inference at the tree-of-life scale.	<i>May 2021 - Apr. 2024</i>
<b>Remote intern</b> 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.	<i>Nov. 2019 - Jan. 2020</i>

## EDUCATION

<b>Iran University of Science &amp; Technology, Tehran. Iran.</b> Ph.D., Electrical Engineering, Signal processing. Advisor: Mohammad Hossein Kahaei Thesis: <i>Haplotype assembly using matrix completion.</i>	<i>Sep. 2015 – Jul. 2020</i>
<b>Wageningen University, The Netherlands.</b> PhD Student Research Visit, Bioinformatics Group Supervisor: Dick de Ridder <i>Developing haplotype phasing method using linked-read data (10X Genomics) for polyploids.</i>	<i>Oct. 2018 - Oct. 2019</i>
<b>Iran University of Science &amp; Technology, Tehran. Iran.</b> M.Sc., Electrical Engineering, Signal processing. <i>Cramer–Rao bound for correlation matrix estimation.</i>	<i>Sep. 2013 – Sep. 2015</i>
<b>Shahid Beheshti University, Tehran. Iran.</b> B.S., Electrical Engineering, Signal processing.	<i>Sep. 2008 - Mar. 2013</i>

## PEER REVIEWED PUBLICATIONS

Eight first-author and six senior-author (\*) publications. [My Google Scholar.](#)

23. **S. Majidian**, S. Hwang, M. Zakeri, B Langmead. EvANI benchmarking workflow for evolutionary distance estimation. *Briefings in Bioinformatics*, 26:3, bbaf267, 2025.
22. **S. Majidian**, Y. Nevers, A. Yazdizadeh, A. Vesztrycy, S. Pascarelli, D. Moi, N. Glover, A. Altenhoff, C. Dessimoz, Orthology inference at scale with FastOMA. *Nature Methods*, 22, 269–272, 2025.
21. S.A., Malekpour, A. Kalirad, **S. Majidian\***. Inferring the selective history of CNVs using a maximum likelihood model. *Genome Biology and Evolution*, 17:3, evaf050, 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*, 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*, 2024.
15. A. Altenhoff, ..., **S. Majidian**, ..., Erik Sonnhammer. New developments for the Quest for Orthologs benchmark service. *NAR Genomics and Bioinformatics*, 6.4:1qae167, 2024.
14. F. Langschie, ..., **S. Majidian**, Erik Sonnhammer, P. Thomas, C. Dessimoz, I. Ebersberger. Quest for Orthologs in the Era of Biodiversity Genomics. *Genome Biology and Evolution*, 16.10:evae224, 2024.
13. **S. Majidian**, D. Paiva Agostinho, 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. [ceur-ws.org/Vol-3415/paper-45.pdf](https://ceur-ws.org/Vol-3415/paper-45.pdf).
11. A. Nicheperovich, A. Altenhoff, C. Dessimoz, **S. Majidian\***, OMAMO: orthology-based model organism selection. *Bioinformatics*, 38:10. 2022.
10. K. Walker, ..., **S. Majidian**, ..., F. Sedlazeck, B. Busby. The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. *Front 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** F. Sedlazeck, PhaseME: automatic rapid assessment of phasing quality and phasing improvement. *GigaScience*, 9.7:giaa078, 2020.
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**, M. Kahaei, D. de Ridder, Minimum error correction-based haplotype assembly: considerations for long read data. *PLOS one*, 15.6:e0234470, 2020.
4. **S. Majidian**, M. Mohades, M. Kahaei, Matrix completion with weighted constraint for haplotype estimation, *Digital Signal Processing Elsevier*, 108:102880, 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

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13. **S. Majidian**, B. Langmead. MetaKpick: machine learning-based metagenomic classification with multi k-mer-based pangenome indexes. Asbtract submitted to the WABI Conference on Algorithms in Bioinformatics, 2025.
12. S. Tan, **S. Majidian**, B Langmead, M. Zakeri. Movi Color: fast and accurate long-read classification with the move structure. Accept Score in the 16th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2025), 2025, *bioRxiv*.
11. K. Vaddadi, M. Lin, **S. Majidian**, T. Mun, B. Langmead. Minimizing reference bias with an imputed personalized reference. Submitted, 2025, Previous version on *bioRxiv*.
10. R. Chikhi. ... **S. Majidian**..., A. Babaian. Logan: Planetary-Scale Genome Assembly Surveys Life's Diversity. Previous version on *bioRxiv*.
9. L. Hug, ... **S. Majidian**..., A. Probst. A roadmap for fair reuse of public microbiome data. Accepted for publication in *Nature Microbiology*. Previous version on *bioRxiv*.
8. F. Palizban, **S. Majidian\***. cfCNV: an optimized pipeline for detecting copy number variations for cell free DNA data. Published Abstract in the *European Journal of Human Genetics*. 32. 57th ESHG European Society of Human Genetics.
7. **S. Majidian**, A. Hadziahmetovic, ..., A. Ouangraoua, I. Julca. Quest for orthologs in the era of data deluge and AI: Challenges and innovations in orthology prediction and data integration. Submitted. 2025.

6. A. Yazdizadeh, A. Altenhoff, C. Dessimoz, **S. Majidian\***. OrthoXML-tools: a toolkit for manipulating OrthoXML files for orthology data. Submitted, 2025.
5. G. Sarton-Loheac, N. Romashchenko, C. Train, **S. Majidian**, N. Glover, Reconstructing evolutionary histories with hierarchical orthologous groups. Submitted, 2025.
4. C. Train, A. Altenhoff, **S. Majidian**, D. Dylus, C. Dessimoz, N. Glover. Phylo.io v2: an improved web-based tool for viewing, comparing, and customizing large phylogenetic trees. 2025.
3. F. Jaryani, ..., **S. Majidian**, ..., B. Busby. The Sixth Annual Structural Variant and Pangenomics Hackathon at BCM, *F1000 Research*, 2025.
2. Z. Kubica, ..., **S. Majidian**, ..., F. 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.

## INVITED AND CONFERENCE TALKS

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10. Computational comparative genomics in the era of BioGenome projects.
  - May. 2025. *The Zeavolution community*, Online.
  - Mar. 2024. *Bioinformatics-Biostatistics Hub*, Institut Pasteur, France.
  - Nov. 2023. *Department of Systematic and Evolutionary Botany*, University of Zurich, Switzerland.
9. May. 2025. Scalable metagenomic classification in the era of long-read sequencing. Slam Talk, *Johns Hopkins University, School of Medicine*, USA. PDA Annual Conference 2025.
8. Nov. 2024. EvANI—Genomic distance evaluation pipeline and benchmarking dataset. Lightning Talk, Biological Data Science 2024, *Cold Spring Harbor Laboratory*, NY, USA.
7. Orthology inference at scale with FastOMA.
  - Aug. 2024. *WEMSA Workshop on Emerging Methods for Sequence Analysis*. Pennsylvania State University, USA.
  - July 2023. *ISMB/ECCB 2023*, Evolution and Comparative Genomics (EvolCompGen) COSI, Lyon, France.
  - Oct. 2023. *Biodiversity Genomics Conference 2023*, Wellcome Sanger Institute. Online.
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

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- Workshop Instructor, OMA and OMArk Biodiversity Genomics Academy, Sep 2023 & 2024. [omabrowser.org/oma/academy/](https://omabrowser.org/oma/academy/)
- Workshop Instructor, Biodiversity Bioinformatics and Comparative Genomics. SIB Swiss Institute of Bioinformatics, 30 Aug. 2023.
- **Guest 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.
- 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. University of Zurich & SIB, 27 Sep. 2022. 4 hours.
- Teaching assistant, Introduction to Python. SIB, University of Lausanne & SIB, 29-30 Sep. 2022. 24 hours.
- Workshop instructor, Introduction to DNA data analysis. Yazd, Iran. Nov. 2021. 40 participants. 4 hours.
- Workshop instructor, R programming. University of Tehran, Iran, 2020. 20 participants. 8 hours.
- **Guest Lecturer**, Intro to Bioinformatics, University of Tehran, Iran, 2020, 20 students.
- 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.
- 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 AND SUPERVISION

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- *Natalie Vallejo* and *Abisola Adeusi* (Undergraduate students). Johns Hopkins University, 2025.
- *Fahimeh Palizban* (PhD candidate). Invited to the University of Lausanne, 2024 (Currently at Children's Hospital of Philadelphia).
- *Karim Farmanpour* (PhD candidate), Tarbiat Modares University, 2023-2025.
- *Arun Maurya* (Master project). University of Lausanne, 2023 (Currently Research Engineer at Institut Pasteur, France.).
- *Alina Nicheperovich* (Summer intern). University College London, 2021 (Currently PhD student at University of Oxford).
- *Sara Lamei* (Master project). Tarbiat Modares University, 2022. (Now at Saarland University, Germany.)
- *Ali Yazdizadeh* (Summer intern). University of Lausanne, 2022 (Incoming PhD student at Carnegie Mellon University).
- *Borbala Banfalvi* (Summer intern), University of Lausanne, 2022 (Currently PhD student at Queen Mary University London).
- *Claire Wang* (Summer intern), University of Lausanne, 2022 (Currently PhD student at University of Cambridge).
- *Samuel Moix* (First master project). University of Lausanne, 2021 (Currently PhD student at University of Lausanne).
- *Mathijs van Kooten* (Master project). Wageningen university, 2019

## RESPONSIBILITIES, MEMBERSHIPS, AND OUTREACH ACTIVITIES

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- Conference Manager and Program Committee Member. Quest for orthologs 8th (an ISCB-affiliated conference), 17-18 July, Montreal, Canada. [event.fourwaves.com/qfo8](http://event.fourwaves.com/qfo8). Secured \$9000 in funding from Canadian Institutes of Health Research (CIHR).
- Student member, Society for Molecular Biology and Evolution SMOB. 2025.
- ISCB member. International Society for Computational Biology. 2023.
- ISCB Student Council Education Committee. team member. 2023.
- Member of European reference genomes (ERGA) consortium, with publication as a member: "Biodiversity: an atlas of European reference genomes". *Nature* 619 (2023): 252-252.
- Active Member of the Quest for orthologs consortium. 2021-2025.
- Award Committee of HopHacks, Hackathon at Johns Hopkins University, 15 Sept. 2024.
- Best Poster Committee for Genopod event, University of Lausanne, Sep 2023.
- SIB member, Swiss Institute of Bioinformatics. 2021-2024.
- Student member, Iranian Bioinformatics Society. 2018-2020.
- Conference co-organiser, IEEE day event, 500 participants, Shahid Beheshti University, Iran. 2009.
- Participated in the course "Responsible Conduct of Research", covering topics of conflicts of interest, responsible human and animal subjects research, and ethics. Johns Hopkins University, 2024.
- Manuscript reviewer for journals: *Genome Biology*, *Genome Research*, *PLOS Computational Biology*, *NAR Genomics and Bioinformatics*, *GigaScience*, *Computers in Biology and Medicine*, *Genome*, *Mitochondrial DNA*, *IET Systems Biology*, *Frontiers in Systems Biology*, *Frontiers in Genetics*, *Computational and Structural Biotechnology Journal*. Reviewer for RE-COMB and WABI conferences. Co-review with PIs for *Nature methods* and *Bioinformatics*. 2019-2025.
- Grants reviewer: Zurich University of Applied Sciences Research Partnership Grant proposal. 2024.

## SOFTWARES

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- *FastOMA* for orthology inference: <https://github.com/DessimozLab/FastOMA>.
- *Impute-First* for variant calling <https://github.com/kvaddad1/impute-first>.
- *Read2Tree* for tree inference: <https://github.com/DessimozLab/Read2Tree>.
- *Haplo* for haplotype assembly: <https://github.com/sinamajidian/Hap10>.
- *PhaseME* for assessment of haplotype phasing: <https://github.com/sinamajidian/phaseme>.