

Hao Yuan

Ph.D. candidate

Genetic and Genome Science Program

Ecology, Evolution and Behavior Program

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Education

2021-Now	Ph.D. in Genetics and Genome Sciences Program; Ecology, Evolution and Behavior Program, in progress Advisor: Ingo Braasch, Arjun Krishnan	Michigan State University, MI, USA
2016-2019	MS in Biology Topic: Assembly and Filtering of Enriched Data from Exon Capture Across Species Advisor: Chenhong Li	Shanghai Ocean University, Shanghai, China
2012-2016	BS in Marine Biology Advisor: Chenhong Li	Shanghai Ocean University, Shanghai, China

Professional Experience

2021-Now Braasch Lab & Krishnan Lab, Graduate Assistant

2020-2021 Shanghai Amplicongene Bioscience Co. LTD., Bioinformatician

2019 Genergy Biotechnology Co. LTD., Bioinformatician

Skills

Computational background and skills

- Well-versed with Python, R, Linux command line and version control using GitHub
- Experience working with high-performance computing resources

Genomic analysis skills

- Well-versed with genomic data analysis including genomic sequences, transcriptomics, single-cell transcriptomics
- Well-versed with graph learning methods and integrated analysis with omic data

Statistics, Data science, and Machine learning background and skills

- Data wrangling and visualization in Python with pandas, matplotlib, and seaborn
- Statistical modeling and machine learning in Python with statsmodel, scipy, scikit-learn and pytorch

Biological and Biomedical background and skills

- Heterogeneity of complex diseases, genomics, gene networks, research organisms, evolution, cross-species knowledge transfer

Publications

[* Joint Primary Author]

10. Computational strategies for cross-species knowledge transfer and translational biomedicine.

Yuan, H., Mancuso, C. A., Johnson, K., Braasch, I., & Krishnan, A.

arXiv (2024) preprint arXiv:2408.08503.

<https://doi.org/10.48550/arXiv.2408.08503>

Accepted by *Nature Methods*

9. Annotating publicly-available samples and studies using interpretable modeling of unstructured metadata.

Yuan, H., Hicks, P., Ahmadian, M., Johnson, K. A., Valtadoros, L., & Krishnan, A.

Briefings in Bioinformatics (2024), 26(1).

<https://doi.org/10.1093/bib/bbae652>

8. Estimation of Species Abundance Based on the Number of Segregating Sites using Environmental DNA (eDNA)

Ai, Q.*, **Yuan, H.***, Wang, Y., Li, C.

Molecular Ecology Resources (2025), 25(6), e14076.

<https://doi.org/10.1111/1755-0998.14076>

7. CONE: COntext-specific Network Embedding via Contextualized Graph Attention.

Liu, R.*, **Yuan, H.***, Johnson, K.A. and Krishnan, A.

Proceedings of Machine Learning Research (2024) 261:53-71.

<https://proceedings.mlr.press/v261/liu24a.html>

6. Exon-capture data and locus screening provide new insights into the phylogeny of flatfishes (Pleuronectoidei).

Atta, C. J., **Yuan, H.**, Li, C., Arcila, D., Betancur-R, R., Hughes, L. C., Ortí, G., & Tornabene, L.

Molecular Phylogenetics and Evolution (2022) 166, 107315.

<https://doi.org/10.1016/j.ympev.2021.107315>

5. Inline index helped in cleaning up data contamination generated during library preparation and the subsequent steps.

Wang, Y., **Yuan, H.**, Huang, J., & Li, C.

Molecular Biology Reports (2022) 49(1), 385–392.

<https://doi.org/10.1007/s11033-021-06884-y>

4. Assexon: Assembling Exon Using Gene Capture Data.

Yuan, H., Atta, C., Tornabene, L., & Li, C.

Evolutionary Bioinformatics (2019) 15, 117693431987479.

<https://doi.org/10.1177/1176934319874792>

3. Gene markers for exon capture and phylogenomics in ray-finned fishes.

Jiang, J.*, **Yuan, H.***, Zheng, X., Wang, Q., Kuang, T., Li, J., Liu, J., Song, S., Wang, W., Cheng, F., Li, H., Huang, J., & Li, C.

Ecology and Evolution (2019) 9(7), 3973–3983.

<https://doi.org/10.1002/ece3.5026>

2. A phylogenomic approach to reconstruct interrelationships of main clupeocephalan lineages with a critical discussion of morphological apomorphies.

Straube, N., Li, C., Mertzen, M., **Yuan, H.**, & Moritz, T.

BMC Evolutionary Biology (2018) 18(1), 158.

<https://doi.org/10.1186/s12862-018-1267-1>

1. Target gene enrichment in the cyclophyllidean cestodes, the most diverse group of tapeworms.

Yuan, H., Jiang, J., Jiménez, F. A., Hoberg, E. P., Cook, J. A., Galbreath, K. E., & Li, C.

Molecular Ecology Resources (2016) 16(5), 1095–1106.

<https://doi.org/10.1111/1755-0998.12532>

Conference and Meeting Presentations

Talk

Outside MSU

- Sep 2024 CONE: CONtext-specific Network Embedding via Contextualized Graph Attention. Machine Learning in Computational Biology 2024, Seattle, WA
- Mar 2024 Discovering context-specific functionally equivalent genes in research organisms using cross species transcriptome-based machine learning. The Allied Genetics Conference 2024, Metro Washington, DC
- Dec 2022 An ML framework for precision medicine: from patient-specific gene networks to translational animal models. Rocky 2022 Bioinformatics Conference, Snowmass, CO
- Oct 2016 Genome-wide detection of sites under selection using a modified method of evolutionary probability - a case study on adaptive evolution of Homo species. 23rd Academic Annual Meeting of China Zoological Society. Wuhan, China

Within MSU

Genetics and Genome Sciences Program

- Oct 2024 Annotating public omics samples and studies using interpretable modeling of unstructured metadata by txt2onto 2.0, Genetics and Genome Sciences Forum
- Feb 2024 An ML framework for precision medicine: from patient-specific gene networks to translational research organisms, Genetics and Genome Sciences Forum
- Oct 2023 Reconstruct patient-specific gene networks from transcriptomic data, Genetics and Genome Sciences Forum

Computational Mathematics, Science and Engineering Program

- Oct 2022 An ML framework for precision medicine: from patient-specific gene networks to translational animal models, Computational Biology Forum

Poster

Outside MSU

- 2025 Evolutionary Implications of the Teleost Genome Duplication Revealed by Cross-Species Single-Cell Transcriptomic Comparison. American Society for Biochemistry and Molecular Biology 2025 Evolution and core processes in gene expression, Kansas City, MO
- 2025 ICePop: Identifying Disease-Affected Cell Types Through Network-Based Analysis of Gene Module Overexpression in Single-Cell Data. Network Biology 2025, Cold Spring Harbor, NY
- 2024 ICePop: Identifying Disease-Affected Cell Types Through Network-Based Analysis of Gene Module Overexpression in Single-Cell Data. Biological Data Science 2024, Cold Spring Harbor, NY
- 2024 Tracking dynamic regulatory changes in rare diseases using single sample networks. Annual

Meeting of American Society of Human Genetics 2024, Denver, CO

- 2024 CONE: COntext-specific Network Embedding via Contextualized Graph Attention. Machine Learning in Computational Biology 2024, Seattle, WA
- 2023 Interpretable text-based machine learning for inferring systematic tissue and disease annotations of public transcriptome samples. Genome Informatics 2023, Cold Spring Harbor, NY
- 2023 An ML framework for precision medicine: from patient-specific gene networks to translational animal models. Network Biology 2023, Cold Spring Harbor, NY
- 2022 An ML framework for precision medicine: from patient-specific gene networks to translational animal models. Rocky 2022 Bioinformatics Conference, Snowmass, CO
- 2022 Cross-species transcriptome-based regression to discover equivalents of human samples and genes in biomedical research organisms. 30th Conference on Intelligent Systems for Molecular Biology, Madison, WI
- 2018 EXpipe: An Assembly Pipeline for Exon Capture Data Across Large Scales of Divergence. 1st AsiaEvo Conference, Shenzhen, China.

Honors and Awards

2023 Summer College of Natural Science Outstanding Scholar Fellowship

Teaching and Mentoring Experience

Teaching

- 2023 IBIO341: Fundamental Genetics, Teaching Assistant

Mentoring

Post baccalaureate

- 2023-2025 Lydia Valtadoros, Department of Biomedical Informatics, The University of Colorado Anschutz Medical Campus

Junior graduate student

- 2023-now Parker Hicks, Department of Biomedical Informatics, The University of Colorado Anschutz Medical Campus

Professional Service

Reviewing Service

- 2024 Journal of Experimental Zoology Part B: Molecular and Developmental Evolution (co-review with Dr. Ingo Braasch)
- 2023 Genome Biology (co-review with Dr. Arjun Krishnan)
- 2022 Genome Research (co-review with Dr. Arjun Krishnan)

Community Service

- 2023-2025 Genetics and Genome Sciences Program Seminar Coordinator
- 2023-2025 Genetics and Genome Sciences Program Graduate Student Organization

Outreach

Career Development Activities

- Jan 2023 Graduate Student Career Forum
- Apr 2022 APIDA Virtual Career Panel: Careers in Data, Analytics, Technology, & Engineering
- Apr 2022 Boost your professional power skills

STEM Outreach

- Dec 2023 AP Biology DeWitt High School Visit Day