

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 Genetic and Genome Science 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

Teaching Experience

2023 IBIO341: Fundamental Genetics, Teaching Assistant

Honors and Awards

2023 Summer College of Natural Science Outstanding Scholar Fellowship
2018 National Scholarship for Graduate Students
#10 scholarships awarded in the Shanghai Ocean University that year

Publications

[* Joint Primary Author]

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

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

bioRxiv (2023): 2023-10.

<https://doi.org/10.1101/2023.10.21.563390>

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., Merten, 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

Oral Presentations

- 2022 An ML framework for precision medicine: from patient-specific gene networks to translational animal models. Rocky 2022 Bioinformatics Conference, Snowmass, CO
- 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.

Poster Presentations

- 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: A Assembly Pipeline for Exon Capture Data Across Large Scales of Divergence. 1st AsiaEvo Conference, Shenzhen, China.

Skills

Computational background and skills

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

Statistics, Data science, and Machine learning background and skills

- Relevant courses: IBIO830/1 Statistical Methods in Ecology and Evolution I & II, CSE847 Machine Learning
- Data wrangling and visualization in Python with pandas, matplotlib, and seaborn
- Statistics and machine learning in Python with scipy and scikit-learn

Biological and Biomedical background and skills

- Relevant courses: BMB801 Molecular Biology, PLB849 Evolutionary biology
- Areas of interest: Heterogeneity of complex diseases, genomics, gene networks, research organisms, evolution, cross-species knowledge transfer