

PROFILE

I am currently a PhD candidate in Computational Genetics at Uppsala University, and I consider myself a friendly and approachable person. I specialize in Bioinformatics and have experience in advanced computational methods to solve complex genetic problems. My primary focus is on developing and applying innovative bioinformatic tools and statistical models to analyze genomic data and gain insights into population genetics and quantitative traits. I am skilled in statistical software and proficient in using high-throughput sequencing data and complex genetic modeling to drive research conclusions.

EDUCATION

- | | |
|--|---------------------|
| ❖ PhD in Computational Genetics | 2021-Current |
| <ul style="list-style-type: none">▪ Uppsala University, Uppsala, Sweden▪ Thesis: Exploring the Genetic Landscape of Chicken Populations: Admixture, Growth QTLs, and Long-Term Selection Dynamics <p>Uncover the domestication history of global chicken, the complex genetic architecture of chicken body weight, and the selection response after 40 generations of intense bi-directional selection.</p> | |
| ❖ MSc in Biometry | 2018-2019 |
| <ul style="list-style-type: none">▪ National Taiwan University, Taipei, Taiwan▪ Thesis: Training Set Determination for Genomic Selection (doi: 10.1007/s00122-019-03387-0) <p>Provide a new optimality criterion to determine a training set that is expected to result in the highest Pearson's correlation between the genomic estimated breeding value and the actual phenotype.</p> | |
| ❖ BSc in Agronomy | 2016-2018 |
| <ul style="list-style-type: none">▪ National Taiwan University, Taipei, Taiwan | |

EXPERIENCES & ACHIEVEMENTS

- | | |
|---|------------------|
| ❖ Speaker of Slice of Science Series | 2024 |
| <ul style="list-style-type: none">▪ After-hour speech of sharing own research with other researchers | |
| ❖ ISAG Conference Bursary Winner (ISAG 2023) | 2023 |
| <ul style="list-style-type: none">▪ International Society for Animal Genetics Conference in South Africa | |
| ❖ Organizer and Host of the Department Workshop (IMBIM day 2023) | 2023 |
| <ul style="list-style-type: none">▪ A full-day scientific workshop and banquet | |
| ❖ TA for Comparative Genomics for Biomedicine Course | 2021-2024 |
| <ul style="list-style-type: none">▪ Master-level course at Uppsala University, Uppsala, Sweden | |
| ❖ Teaching Bioinformatic Course | 2021-2024 |
| <ul style="list-style-type: none">▪ Master-level course at Uppsala University, Uppsala, Sweden▪ Responsible for managing one module, giving main lectures, serving as an examiner, and practicing TA | |
| ❖ Research Assistant | 2019-2020 |
| <ul style="list-style-type: none">▪ Uppsala Biomedical Centre, Uppsala University, Uppsala, Sweden▪ NGS data alignment, quality control, server maintenance, teaching, and software development | |
| ❖ Research Assistant | 2019-2020 |
| <ul style="list-style-type: none">▪ National Taiwan University, Taipei, Taiwan▪ Software developed for simulation studies, server maintenance, and manuscript writing. | |
| ❖ TA & 3 Times Excellent Teaching Assistants | 2018-2019 |
| <ul style="list-style-type: none">▪ National Taiwan University, Taipei, Taiwan▪ TA for statistics labs. Teaching the R programming language and practical application of statistics. | |

PUBLICATIONS & SOFTWARE

- ❖ **Ou, J.H.** (2024). Exploring the genetic landscape of chicken populations: Admixture, growth QTLs, and long-term selection dynamics. *Doctoral thesis, Uppsala dissertations from the Faculty of Medicine 2053*.
- ❖ **Ou, J.H.** (2024). geno2r: Functions for reading genotype data in R. *R package version 1.6.2*. <https://www.oumark.net/geno2r/>
- ❖ **Ou, J.H.**, Rönneburg, T., Carlborg, Ö., Honaker, C.F., Siegel, P.B., Rubin, C.J. (2024). Complex genetic architecture of the chicken *Growth1* QTL region. *PLoS One*, Accepted.
- ❖ **Ou, J.H.**, Wu, P.Y., Liao, C.T., (2023). TSDFGS: Training set determination for genomic selection. *R package version 2.4.2*. <https://www.oumark.net/TSDFGS>
- ❖ Wu, P.Y., **Ou, J.H.**, & Liao, C.T. (2023). Sample size determination for training set optimization in genomic prediction. *Theoretical and Applied Genetics*, 136(3).
- ❖ Rönneburg, T., **Ou, J.H.**, Pettersson, M., Honaker, C.F., Siegel, P.B., Caroborg, Ö. (2023). Within-line segregation as contributors to long-term, single-trait selection-responses in the Virginia chicken lines. Manuscript in thesis, Uppsala University.
- ❖ Guo, Y., **Ou, J.H.**, Zan, Y., Wang, Y., Li, H., Zhu, C., Chen, K., Zhou, X., Hu, X., Caroborg, Ö. (2022). Researching on the fine structure and admixture of the worldwide chicken population reveal connections between populations and important events in breeding history. *Evolutionary Applications*, 15(4).
- ❖ **Ou, J.H.**, Liao, C.T. (2019). Training set determination for genomic selection. *Theoretical and Applied Genetics*, 132(10). (Also being used as my master's thesis)
- ❖ Lin, P.C., Tsai, Y.C., Hsu, S.K., **Ou, J.H.**, Liao, C.T., Tung, C.W. (2018). Identification of nature variants affecting chlorophyll content dynamics during rice seedling development. *Plant breeding*, 137(3).

PRESENTATIONS

- | | |
|--|------------|
| ❖ Presentation for the Slice of Science activity | 2024/04/09 |
| ❖ Presentation for the genomic seminar series | 2024/02/23 |
| ❖ Presentation for the genomic seminar series | 2023/04/14 |
| ❖ Presentation for the Swedish Bioinformatics Workshop | 2022/07/28 |
| ❖ Half-time presentation | 2022/04/12 |
| ❖ Presentation for the genomic seminar series | 2021/08/27 |
| ❖ Collaboration workshop with CAU | 2020/11/24 |