

# JEN-HSIANG OU

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## PERSONAL PROFILE

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I am currently a PhD candidate in Computational Genetics at Uppsala University, and I am 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 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

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### PhD candidate in Computational Genetics 2021-Current

- Department of Medical Biochemistry and Microbiology, Faculty of Medicine, Uppsala University, Sweden
- Thesis: Exploring the Genetic Landscape of Chicken Populations: Admixture, Growth QTLs, and Long-Term Selection Dynamics  
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.

### MSc in Biostatistics 2018-2019

- Department of Agronomy, College of Bioresources and Agriculture, National Taiwan University, Taiwan
- Thesis: Training Set Determination for Genomic Selection (doi:10.1007/s00122-019-03387-0)  
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.

### BSc in Agronomy 2016-2018

- Department of Agronomy, College of Bioresources and Agriculture, National Taiwan University, Taiwan

## EXPERIENCES & ACHIEVEMENTS

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### ISAG Conference bursary winner 2023

- International Society for Animal Genetics Conference (ISAG2023)

### Organizer and Host of the Department day 2023

- IMBIM-day 2023. A full-day scientific workshop and banquet

### TA of Comparative Genomics for Biomedicine Course 2021-2024

- Master-level course at Uppsala University

### Teacher of Bioinformatic Course 2021-2024

- Master-level course at Uppsala University
- Responsible for the GWAS module, giving main lectures, serving as an examiner, and practicing TA

### Research assistant 2020-2021

- Uppsala Biomedical Centre, Uppsala University, Sweden
- NGS data alignment, quality control, server maintenance, teaching, and software development

### Research assistant 2019-2020

- National Taiwan University, Taiwan
- Software developed for simulation studies, server maintenance, and manuscript writing

### TA & 3 times excellent teaching assistants 2018-2019

- National Taiwan University, Taiwan
- TA for statistics labs. Teaching the R programming language and practical application of statistics

## LANGUAGES & SKILLS

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- Mandarin (Native)
- English (Fluent)
- R (Advanced)
- LaTeX/Debian (Advanced)
- Linux (Advanced)
- Bioinformatic tools (GATK, Plink, vcftools, etc.)
- Python (Intermediate)
- C++ (Elementary)
- HTML + CSS (Elementary)

## PUBLICATIONS

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- **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*, 19(5):e0295109.
- **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).
- 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).