# **JEN-HSIANG OU**

I'm a postdoctoral researcher at the Department of Medical Genetics, National Taiwan University Hospital. My research focuses on structural variations, like repeat sequences, and DNA methylation in relation to diseases. I work with both next-generation and long-read sequencing technologies to study the genetic basis of rare diseases. Having completed my doctoral studies at Uppsala University and earned a master's degree in Biostatistics from National Taiwan University, my goal is to better understand genetic variation and its role in disease, contributing to advancements in medical research.

# **Personal Information**

歐任翔 Jen-Hsiang (Mark) Ou, Ph.D. Postdoc researcher, Department of Medical Genetics, National Taiwan University Hospital Position: Phone: [Work] (02) 2312-3456 ext.271904 | [Personal] +886-(0)910-397161 [Wrok] jhou@ntuh.gov.tw | [Personal] oumark.me@outlook.com E-mail: Address:

## **EDUCATION**\_

## PhD candidate in Computational Genetics

- 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

- 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

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

# **Experiences & Achievements**

ISAG Conference bursary winner	2023
<ul> <li>International Society for Animal Genetics Conference (ISAG2023)</li> </ul>	
Organizer and Host of the Department day	2023
<ul> <li>IMBIM-day 2023. A full-day scientific workshop and banquet</li> </ul>	
TA of Comparative Genomics for Biomedicine Course	2020-2024
Master-level course at Uppsala University	
Teacher of Bioinformatic Course	2020-2024
<ul> <li>Master-level course at Uppsala University</li> <li>Responsible for the GWAS module, giving main lectures, serving as an examiner, and practicing TA</li> </ul>	
Research assistant	2019
<ul> <li>Uppsala Biomedical Centre, Uppsala University, Sweden</li> <li>NGS data alignment, quality control, server maintenance, teaching, and software development</li> </ul>	
Research assistant	2018-2019
<ul> <li>National Taiwan University, Taiwan</li> <li>Software developed for simulation studies, server maintenance, and manuscript writing</li> </ul>	
TA & 3 times excellent teaching assistants	2016-2018
<ul> <li>National Taiwan University, Taiwan</li> <li>TA for statistics labs. Teaching the R programming language and practical application of statistics</li> </ul>	
Languages & Skills	

#### 2020-2024

2016-2018

### 2012-2016

- 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**

- **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.**, 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.** (2024). geno2r: Functions for reading genotype data in R. *R package version* 1.6.2. https://www.oumark.net/geno2r/.
- **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).