ZHIYUAN HU

MRC Weatherall Institute of Molecular Medicine ◇ Oxford, UK
zhiyhu.github.io

EDUCATION

University of Oxford, United Kingdom *2015 - 2020*
D.Phil in Clinical Medicine
Thesis title: *Functional genomics studies of cancer and cells of origin: from pan-cancer to single-cell*
Supervisors: Dr Christopher Yau and Prof Ahmed Ahmed

Peking University, China *2011 - 2015*
B.S. in Biological Science
Undergraduate Honors Program in Biology; GPA ranking: 1st/108

WORK EXPERIENCE

Postdoctoral Research Assistant *March - Dec 2020*
MRC Weatherall Institute of Molecular Medicine/Nuffield Department of Women's & Reproductive Health, University of Oxford
Supervisor: Prof Ahmed Ahmed

- Analysed the prognostic prediction power of a gene panel (OxC) in an independent patient cohort
- Developed a computational workflow for neoantigen prediction in ovarian cancer
- Stayed to finish off my DPhil projects

Summer Research Internship *July - Aug 2014*
Nuffield Department of Medicine, University of Oxford
Supervisors: Prof Christopher Yau and Dr Quin Wills

- Analysed the effect of metformin on cancer single-cell transcriptome

PUBLICATIONS

Z. Hu†, P. Cunnea†, Z. Zhong, H. Lu, O. Osagie, L. Campo, M. Artibani, K. Nixon, J. Ploski, L. Santana Gonzalez, A. Alsaadi, N. Wietek, S. Damato, S. Dhar, S. P. Blagden, C. Yau, J. Hester, A. Albukhari, E. O. Aboagye, C. Fotopoulou*, A. A. Ahmed*. The Oxford Classic links epithelial-mesenchymal transition to immunosuppression in poor prognosis ovarian cancers. *Clinical Cancer Research* (in press).

Y. Liu†, **Z. Hu**†, J. Cheng, P. Siejka-Zieliska, J. Chen, M. Inoue, A. A. Ahmed, C.-X. Song. Subtraction-free and bisulfite-free specific sequencing of 5-methylcytosine and its oxidized derivatives at base resolution. *Nature Communications* (in press).

Z. Hu, M. Artibani, A. Alsaadi, N. Wietek, M. Morotti, T. Shi, Z. Zhong, L. Santana Gonzalez, S. El-Sahhar, M. KaramiNejadRanjbar, G. Mallett, Y. Feng, K. Masuda, Y. Zheng, K. Chong, S. Damato, S. Dhar, L. Campo, R. Garruto Campanile, V. Rai, D. Maldonado-Perez, S. Jones, V. Cerundolo, T. Sauka-Spengler, C. Yau*, A. A. Ahmed*. The repertoire of serous ovarian cancer non-genetic heterogeneity revealed by single-cell sequencing of normal fallopian tube epithelial cells. *Cancer Cell*, 37(2), 226242.e7 (2020).

R. Ma*, K. P. Capobianco, N. T. Buchanan, **Z. Hu**, J. M. Oakman*. Etiologic and Treatment Conceptualizations of Disordered Eating Symptoms among Mainland Chinese Therapists. *International Journal of Eating Disorders* (2019).

M. P. Menden, D. Wang, M. J. Mason, B. Szalai, K. C. Bulusu, Y. Guan, T. Yu, J. Kang, M. Jeon, R. Wolfinger, T. Nguyen, M. Zaslavskiy, **AstraZeneca-Sanger Drug Combination DREAM Consortium**, I. Sock Jang, Z. Ghazoui, M. Eren Ahsen, R. Vogel, E. Chaibub Neto, T. Norman, E. K. Y. Tang, M. J. Garnett, G. Y. Di Veroli, S. Fawell, G. Stolovitzky, J. Guinney*, J. R. Dry* J. Saez-Rodriguez*. Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. *Nature Communications* **10**, 2674 (2019).

T. Motohara, K. Masuda, M. Morotti, Y. Zheng, S. El-Sahhar, K. Chong, N. Wietek, A. Alsaadi, M. Karaminejadranjbar, **Z. Hu**, M. Artibani, L. Santana Gonzalez, H. Katabuchi, H. Saya and A. Ahmed. An evolving story of the metastatic voyage of ovarian cancer cells: cellular and molecular orchestration of the adipose-rich metastatic microenvironment. *Oncogene*, 38, 2885−2898 (2019).

Z. Hu, C. Yau* and A. Ahmed*. A pan-cancer genome-wide analysis reveals tumour dependencies by induction of non-sense mediated decay. *Nature Communications* **8**, 15943 (2017).

CONFERENCE ABSTRACT

Z. Hu, A. Alsaadi, N. Wietek, L. Santana Gonzlez, C. Yau* and A. Ahmed*. Deep single-cell RNA-seq of the putative cell of origin revealed a novel molecular subtype of high-grade serous ovarian cancer with poor prognosis [abstract]. In: *Proceedings of the American Association for Cancer Research Annual Meeting 2019*; 2019 Mar 29-Apr 3; Atlanta, GA. Philadelphia (PA): AACR; Cancer Res 2019;79(13 Suppl):Abstract nr 467.

PATENT

International Patent No. WO 2020/174211 A1. Ovarian Cancer Biomarkers. Inventors: AHMED, Ahmed Ashour, **HU, Zhiyuan**, YAU, Christopher

SOFTWARE

Z. Hu, C. Yau and A. Ahmed (2017). masonmd: making sense of nonsense mediated decay. MIT License. doi: 10.5281/zenodo.546698

- *This is an R package to predict a type of loss-of-function mutations in pan-cancer genomes. It can be used to de novo predict the functional consequence of mutations in cancer.*

SCHOLARSHIPS, AWARDS & GRANTS

NIHR Oxford Biomedical Research Centre Small Grants in Health Sciences (£24,395)	*2020*
WHG Public Engagement Seed Award, University of Oxford (£1,000)	*2019*
AACR-Margaret Foti Scholar-in-Training Award, AACR ($2,000)	*2019*
Travel and Research Fund, St Cross College, University of Oxford (£500)	*2019*
Poster Prize, CRUK Oxford Centre 2018 Symposium	*2018*
NDM Graduate Student Prize, University of Oxford	*2017*
Shen Tong Outstanding Undergraduate Award, Peking University (CNY 20000)	*2015*
China National Scholarship (CNY 8000)	*2014*
Li & Fung Scholarship, Victor and William Fung Foundation	*2014*
Arawana Scholarship, Yihai Kerry, Wilmar China (CNY 12000)	*2013*
Robin Li Scholarship, Robin Li Foundation (CNY 5000)	*2012*

SKILLS

Computational skills

- Proficient in: R (daily usage), Shell (regular usage), Git/GitHub (daily usage), Python (Snakemake included, regular usage), analysis of NGS data and single-cell RNA-Seq data and statistical/machine learning
- Familiar with: C (used extensively during undergrad), MATLAB (used for a course project) and Rcpp (being improved)
- Familiar with neural networks and Bayesian inference

Web lab skills

- Tissue processing: human/mouse sample dissociation, primary cell preservation, primary cell culture and etc.
- Next-generation sequencing: RNA-Seq library preparation, single-cell RNA-Seq (Smart-Seq2 and 10x), Illumina sequencing and etc.
- Cell biology techniques: fluorescent staining, flow cytometry/FACS, confocal microscope and image processing (Fiji, Qupath), cell culture and etc.
- Molecular techniques: DNA/RNA extraction, RT, PCR, qPCR, electrophoresis, Sanger sequence, NanoString assay and etc.

Other relevant skills

- Language: English (fluent) and Mandarin Chinese (native)
- Proficient in LaTeX, Adobe Illustrator, iMovie etc.

SUPERVISORY EXPERIENCE

Supervised and trained an undergrad intern for computational projects	*June - Aug 2020*
Supervised and trained a predoctoral RA for wet-lab work	*March - Oct 2020*
Supervising and training an undergrad intern for wet-lab work and data analysis	*July - Aug 2019*
Held a volunteer position as a junior advisor at St Cross College	*2017 - 2018*
Supervised and trained undergrad intern for computational projects	*July - Aug 2017*

UNDERGRAD RESEARCH EXPERIENCE

Center for Quantitative Biology, Peking University *2013 - 2015*
Project: Computational genomics study of horizontal gene transfer in microbial microevolution
Advisor: Prof. Huaiqiu Zhu

- Classified the transferred genes based on the Cluster of Orthologous Groups of proteins (COG) database.
- Classified genes by their translation initiation mechanisms to study the characteristic translation regulation of horizontally transferred genes.
- Developed new methods to detect horizontally transferred genes and analysed the rate of horizontal gene transfer on the phylogenetic tree.