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INTERESTS

My research focuses on understanding the multi-omic landscape (genomics, epigenomics, transcriptomics, *etc.)* and immune responses in human diseases (cancer, aging, and infectious diseases, *etc.*), and identifying robust gene signatures and targets for disease diagnostics, prognostics, and therapeutics.

PROFESSIONAL EXPERIENCE

2020-Present   Stanford University

Postdoctoral researcher in Khatri lab (khatrilab.stanford.edu). Currently working on multi-cohort pan-viral analysis of blood transcriptome to identify gene modules associated with severity of viral infection including SARS-CoV-2 and single-cell RNASeq profiling of infectious diseases.

2017-2020   Stanford University

Postdoctoral researcher in Gevaert lab. Worked on transcriptome analysis and data integration in biomedical research.

- **Benchmarking RNA sequencing analysis pipeline.** Evaluated several key aspects in RNA sequencing analysis, including nine common workflows, protocols for library preparation (un-stranded vs. strand-specific), and transcriptome annotation.
- **Long noncoding RNAs (lncRNAs)**. Profiled the expression pattern of lncRNAs in cancer samples and integrating with other omics data such as DNA methylation to identify regulatory lncRNAs in cancer.
- **Integration of imaging and molecular data**. Applied machine learning methods to link DNA methylation patterns to imaging features in cancer samples.
- **Missing data imputation**. Helped in evaluating the methods for imputing missing values in genomic data, including KNN, SVD, and variational auto-encoder (VAE).

2012-2016   The University of Hong Kong

Ph.D thesis: Identification of genetic susceptibility genes and characterization of somatic mutations in nasopharyngeal carcinoma (available at hdl.handle.net/10722/270220)

Ph.D. candidate in the lab of Prof. Maria Li Lung, Department of Clinical Oncology, Faculty of Medicine, studying the genetic and genomic basis of nasopharyngeal carcinoma (NPC). Established the pipeline for analysis of multiple next-generation sequencing datasets, including whole-exome sequencing (WES), targeted sequencing and RNASeq. Worked collaboratively on several projects.

- **Genetic susceptibility study of NPC**. WES and targeted sequencing were used to examine blood samples of cancer cases and controls to identify genes or pathways associated with disease risk.
- **Characterization of somatic mutations of NPC tumors**. Paired tumor and blood samples were sequenced to characterize the mutation landscape and signatures in NPC tumors and to identify significantly mutated genes and pathways.
- **Expression profiling of NPC tumors.** Paired tumor and non-tumor samples were examined with RNASeq to characterize the expression profiles, alternative splicing, and fusion events in tumors.
- **DNA methylome profiling of NPC tumors**. Helped in the analysis of DNA methylome data using HumanMethylation450 BeadArray to study the methylation patterns in NPC tumors.

2010-2012   Peking University

Worked at the State Key Laboratory of Protein and Plant Gene Research, studying plant pathogens and host defense responses, particularly the role of small RNAs and host microRNAs in the defense response of *Oryza sativa* against two rice viruses. Conducted both bench-top experiments and data analysis.

- Constructed small RNA libraries from rice infected by viruses for Solexa/Illumina high throughput sequencing
- Analyzed the small RNASeq data to investigate the profile of small RNAs and host microRNAs

EDUCATION

Ph.D.	2012-2016	**Cancer Genomics**
		The University of Hong Kong, Hong Kong, China
		Supervisor: Prof. Maria Li Lung
		Thesis title: Identification of Genetic Susceptibility Genes and Characterization of Somatic Mutations in Nasopharyngeal Carcinoma (hub.hku.hk/handle/10722/270220)
B.E.	2006-2010	**Biomedical Engineering**, Xi'an Jiaotong University, China
		Graduated with Distinguished Graduate Student Award

SKILLS

- Hands-on experiences in bioinformatics toolkits and pipelines. Familiar with cloud computing platforms, Docker, and building web apps using Shiny.

- Experienced in working with large scale sequencing datasets, including the Cancer Genome Atlas (TCGA), The Genotype-Tissue Expression (GTEx), and NCBI SRA/GEO

- Intensive analysis and interpretation skills of multiple next-generation sequencing datasets:
    - DNA sequencing
        - Whole-exome sequencing
        - Whole-genome sequencing
    - RNA sequencing
        - RNA-Seq
        - Small RNA-seq
        - Single-cell RNA-Seq
    - Epi-genomics
        - HumanMethylation450 array

- o Bisulfite sequencing
- o ChIP-Seq

- Familiar with statistical methods, high-dimensional data analysis, and machine learning algorithms.

- Profound knowledge in cancer genomics and immunology.

- Excellent data visualization skills
  - o Poster made with R only: https://f1000research.com/posters/9-1410
  - o github.com/zhengh42/ArtisticVisualization

- **Programming languages**
  R   Professional working proficiency
  Linux/Bash   Professional working proficiency
  Perl   Professional working proficiency
  Python   Professional working proficiency
  MATLAB   Limited working proficiency

- **Experimental skills**
  DNA/RNA extraction
  PCR and quantitative PCR

- **Languages**
  Chinese   Native
  English   Full professional proficiency
  Cantonese Full professional proficiency
  German   Elementary proficiency

PUBLICATIONS

1. Buturovic L*, **Zheng H***, Tang B, *et al*. A 6-mRNA host response whole-blood classifier trained using patients with non-COVID-19 viral infections accurately predicts severity of COVID-19. medRxiv. 2021 Jan 6, *contributed equally

2. **Zheng H***, Rao AM*, Dermadi D*, Toh J*, Jones LM*, Donado M*, *et al.*, Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity irrespective of virus. *Immunity (accepted)* *contributed equally

3. Qiu YL, **Zheng H**, Devos A, Selby H, Gevaert O. A meta-learning approach for genomic survival analysis. *Nat Commun*. 2020 Dec 11;11(1):6350.

4. Qiu YL, **Zheng H**, Gevaert O. Genomic data imputation with variational auto-encoders. *GigaScience*. 2020 Aug 1;9(8).

5. **Zheng H**, Momeni A, Cedoz P-L, Vogel H, Gevaert O. Whole slide images reflect DNA methylation patterns of human tumors. *NPJ Genomic Med*. 2020;5:11.

6. **Zheng H**, Brennan K, Hernaez M, Gevaert O. Benchmark of long non-coding RNA quantification for RNA sequencing of cancer samples. *GigaScience*. 2019 01;8(12).

7. Lin W, Yip YL, Jia L, Deng W, **Zheng H**, Dai W, *et al*. Establishment and characterization of new tumor xenografts and cancer cell lines from EBV-positive nasopharyngeal carcinoma. *Nat Commun*. 2018 Nov 7;9(1):4663.

8. Bakr S, Gevaert O, Echegaray S, Ayers K, Zhou M, Shafiq M, **Zheng H**, *et al*. A radiogenomic dataset of non-small cell lung cancer. *Sci Data*. 2018 Oct 16;5(1):1–9.

9. Dai W, Ko JMY, Choi SSA, Yu Z, Ning L**, Zheng H**, *et al.* Whole-exome sequencing reveals critical genes underlying metastasis in oesophageal squamous cell carcinoma. *J Pathol.* 2017 Aug;242(4):500–10.

10. **Zheng H**[*], Dai W[*], Cheung AKL[*], Ko JMY, Kan R, Wong BWY, *et al.* Whole-exome sequencing identifies multiple loss-of-function mutations of NF-ϰB pathway regulators in nasopharyngeal carcinoma. *Proc Natl Acad Sci U S A.* 2016 Oct 4;113(40):11283–8. [*]contributed equally

11. Dai W[*], **Zheng H**[*], Cheung AKL, Tang CS, Ko JMY, Wong BWY, *et al.* Whole-exome sequencing identifies MST1R as a genetic susceptibility gene in nasopharyngeal carcinoma. *Proc Natl Acad Sci U S A.* 2016 Mar 22;113(12):3317–22. [*]contributed equally

12. Dai W, **Zheng H**, Cheung AKL, Lung ML. Genetic and epigenetic landscape of nasopharyngeal carcinoma. *Chin Clin Oncol.* 2016 Apr;5(2):16.

13. Dai W, Cheung AKL, Ko JMY, Cheng Y, **Zheng H**, Ngan RKC, *et al.* Comparative methylome analysis in solid tumors reveals aberrant methylation at chromosome 6p in nasopharyngeal carcinoma. *Cancer Med.* 2015 Jul;4(7):1079–90.

14. Wu J, Yang Z, Wang Y, Zheng L, Ye R, Ji Y, Zhao S, Ji S, Liu R, Xu L, **Zheng H,** *et al.* Viral-inducible Argonaute18 confers broad-spectrum virus resistance in rice by sequestering a host microRNA. *eLife.* 2015 Feb 17;4.

15. Jiang L, Qian D**, Zheng H**, Meng L-Y, Chen J, Le W-J, *et al.* RNA-dependent RNA polymerase 6 of rice (Oryza sativa) plays role in host defense against negative-strand RNA virus, Rice stripe virus. *Virus Res.* 2012 Feb;163(2):512–9.

16. Du P, Wu J, Zhang J, Zhao S, **Zheng H**, Gao G, *et al.* Viral infection induces expression of novel phased microRNAs from conserved cellular microRNA precursors. *PLoS Pathog.* 2011 Aug;7(8):e1002176.

PRESENTATIONS AND CONFERENCES

International

2021   Poster presentation at Pacific Symposium on Biocomputing (PSB), Jan. 5-7, Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity irrespective of virus

2018   Poster presentation at AACR Annual Meeting, Chicago, April 14-18, Benchmark of lncRNA Quantification for RNA-Seq of Cancer Samples

2016   Invited talk, Nasopharyngeal Carcinoma Gordon Research Conference, Hong Kong, June 26 - July 1, Identification of genetic susceptibility genes in nasopharyngeal carcinoma by next-generation sequencing

2016   Poster presentation at AACR Annual Meeting, New Orleans, April 16-20, Whole-exome sequencing identifies NF-ϰB pathway regulators frequently mutated in nasopharyngeal carcinoma

2015   Poster presentation at AACR Annual Meeting, Philadelphia, April 18-22, Unraveling the genetic basis of nasopharyngeal carcinoma using next-generation sequencing approaches

Local

2018   Presentation at Stanford NCI CTD[2] Site Visit, May 10, Differential methylation analysis of bisulfite sequencing data

2016   Presentation at NPC AoE General Meeting, The University of Hong Kong, August 27, Whole-exome sequencing of NPC xenografts and human tumors

2016   Presentation at departmental postgraduate seminar, August 20, Genetic and genomic characterization of nasopharyngeal carcinoma, received best presentation award

2015   Presentation at Joint NPC AoE and TBRS Thematic meeting, The University of Hong Kong, September 5, Whole-Exome sequencing analysis identifies the landscape of somatic mutations in NPC

2014   Poster presentation at 19th Research Postgraduate Symposium, Li Ka Shing Faculty of Medicine, The University of Hong Kong, December 10-11, Whole-exome sequencing of nasopharyngeal carcinoma

2014   Presentation at NPC AoE Genetics and Genomics Thematic Meeting, The University of Hong Kong, September 29, Whole-exome sequencing of NPC

2013   Presentation at NPC AoE General Meeting, The University of Hong Kong, August 31, Whole-exome sequencing of nasopharyngeal cancer

PROFESSIONAL MEMBERSHIPS

2014-present   Associate member of American Association for Cancer Research (AACR)

AWARDS AND HONORS

2017   Summer Institutes Scholarship, Department of Biostatistics, University of Washington
2016   Y S and Christabel Lung Postgraduate Scholarship, The University of Hong Kong
2012-2016   Postgraduate Scholarship, The University of Hong Kong
2011   Excellent Academic Performance Scholarship, Peking University
2011   Dupont Scholarship, Peking University
2007-2010   Cyrus Tang Scholarship
2010   Distinguished Graduate Student Award, Xi'an Jiaotong University
2007-2009   Distinguished Student Xi'an Jiaotong University
2008-2010   Siyuan Scholarship, Xi'an Jiaotong University

TEACHING AND MENTORING

2019   Mentor, Stanford Canary CREST Program; Mentee: Megan Li; Project: Gene Regulatory Module Network Analysis of Cancer from Bulk and Single-cell RNA Sequencing

2018   Mentor, Stanford Canary CREST Program; Mentee: Irmina Benson; Project: Learning bioinformatics and Differential Gene Expression Analysis of RNA-Seq data

2018   Instructor, Principles of Cancer Systems Biology (CBIO 243), DNA methylation analysis, Stanford University

2011   Teaching assistant, New Thinkings of Life Science, School of Life Sciences, Peking University

2011   Teaching assistant, Molecular Virology, School of Life Sciences, Peking University

NON-ACADEMIC WORK

Consulting

2016-2017
Bioinformatics consultant, Prenetics Limited, Hong Kong, China

- Developed next-generation sequencing analysis pipeline for detection and annotation of disease-related genetic alterations
- My work laid the foundation for the company's product 'Inherited Cancer Screen' and other future screening service products.

Science communication

2010-2019	Science writer of Scientific Guokr and Caixin Global
2014	Organized One Youth Talk at HK, The University of Hong Kong, October 5
2014	Invited talk, One Youth Talk at HK, City University of Hong Kong, April 13, DNA sequencing, genetic testing and risk prediction