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INTERESTS

Genetics and genomics; Multi-omics multi-scale data integration; Non-coding RNAs; Viruses; Data visualization; Precision medicine

PROFESSIONAL EXPERIENCE

2017-present Stanford University

Postdoctoral researcher in the lab of Olivier Gevaert, Stanford Center for Biomedical Informatics Research, School of Medicine, Stanford University. My research focuses on non-coding RNAs and DNA methylation profiling in cancer, as well as data integration in biomedical research.

- **Benchmarking RNA sequencing analysis pipeline.** Evaluating 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).** Profiling 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.** Applying machine learning methods to predict DNA methylation patterns in cancers from whole slide images.
- **DNA methylation profiling in cancers.** Developing a framework to model DNA methylation from bisulfite sequencing of cancer samples, identifying genes or non-coding regions that are epigenetically-regulated in cancers and revealing epigenetically distinct cancer subtypes.
- **Module network analysis of single-cell RNA sequencing datasets.** Developing a module network analysis framework to capture major biological pathways driving cell type evolution and tumor subtype classification from single-cell RNA sequencing datasets.
- **Viruses in human diseases.** Investigating viruses associated signatures from RNA sequencing samples across human diseases, in particular, human herpesviruses and their role in pathogenesis.

2012-2016 The University of Hong Kong

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
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 and Docker applications.
- Experienced in working with large scale sequencing datasets, including the Cancer Genome Atlas (TCGA) and The Genotype-Tissue Expression (GTEx).
- 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
 - Bisulfite sequencing

- ChIP-Seq

- Familiar with statistical methods, high-dimensional data analysis, and machine learning algorithms.
- Excellent data visualization skills using R (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

PRESENTATIONS AND CONFERENCES

International

- 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- κ B 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 CTD₂ 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)

PUBLICATIONS

Original Articles

1. **Zheng H**, Momeni A, Cedoz P, Vogel H, Gevaert O, Whole slide images reflect DNA methylation patterns of human tumors, under revision
2. Qiu Y, **Zheng H**, Devos A, Gevaert O, A meta-learning approach for genomic survival analysis, under review
3. **Zheng H**, Brennan K, Hernaez M, Gevaert O, Benchmark of long non-coding RNA quantification for RNA sequencing of cancer samples, *GigaScience*, Volume 8, Issue 12, 2019 Dec.
4. Qiu Y, **Zheng H**, Gevaert O, A deep learning framework for imputing missing values in genomic data, *bioRxiv preprint*, doi: <https://doi.org/10.1101/406066>
5. 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
6. Bakr S, Gevaert O, Echegaray S, Ayers K, Zhou M, Shafiq M, **Zheng H**, Benson J, Zhang W, Leung A, Kadoch M, Shrager J, Quon A, Rubin D, Plevritis S, Napel S, A Radiogenomic Dataset of Non-Small Cell Lung Cancer, *Sci Data*. 2018 Oct 16;5:180202
7. Dai W, Ko JMY, Choi SSA, Yu Z, Ning L, **Zheng H**, et al. Whole-exome sequencing reveals critical genes underlying metastasis in esophageal squamous cell carcinoma. *J Pathol*. 2017 Aug;242(4):500-510
8. **Zheng H***, Dai W*, Cheung AKL*, Ko JMY, et.al. Whole-exome sequencing identifies multiple loss-of-function mutations of NF- κ B pathway regulators in nasopharyngeal carcinoma, *Proc Natl Acad Sci U S A*. 2016, 113(40):11283–11288 *contributed equally
9. 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, 113(12):3317-3322. *contributed equally
10. Dai W, Cheung AKL, Ko JM, Cheng Y, **Zheng H**, Ngan RK, Ng WT, Lee AW, Yau CC, Lee VH et al: Comparative methylome analysis in solid tumors reveals aberrant methylation at chromosome 6p in nasopharyngeal carcinoma. *Cancer Med*. 2015, 4(7):1079-1090.
11. 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, 4.

12. Jiang L, Qian D, **Zheng H**, Meng LY, Chen J, Le WJ, Zhou T, Zhou YJ, Wei CH, Li Y: 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, 163(2):512-519.
13. Du P, Wu J, Zhang J, Zhao S, **Zheng H**, Gao G, Wei L, Li Y: Viral infection induces expression of novel phased microRNAs from conserved cellular microRNA precursors. *PLoS Pathog.* 2011, 7(8):e1002176.

Reviews

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

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	Siyan 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

Oct. 2016 - Jan. 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-present 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

Other

- 2017-present Board member, Chinese Life-science Postdocs and Students (CLIPSS), Stanford University