

XU ZHANG

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EDUCATION

M.Phil. in Computer Science , The University of Hong Kong	2021 - Present
B.S. in Biology Science (Animal Orientation) , Shanxi Agricultural University	2013 - 2017
• Rank: 3/30	• Graduation Thesis: 1/30

PROFESSIONAL EXPERIENCES

MPhil Student	2021 - Present
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Supervisor: Prof. HF Ting and Prof. TW Lam, The University of Hong Kong

Automated model selection and optimization for identifying multi-gene prognostic signatures

Contributions: Pioneered automated machine learning for model selection and optimization in identifying multi-gene prognostic signatures, and developed a web application for estimating breast cancer risk

Developed a system to identify multi-gene prognostic biomarkers

Contributions: Engineered a web application to identify potential multi-gene prognostic signatures by integrating a chatbot for addressing user queries, a module for identifying multi-gene prognostic biomarkers, and a module for automatically generating tailored reports

Identified a prognostic signature related to genome instability for lung adenocarcinoma patients

Contributions: Pioneered a prognostic signature related to genome instability by analyzing genomic, transcriptomic, and clinical data of 397 lung adenocarcinoma patients in TCGA database, including using univariate Cox regression analysis to screen genes, multivariate Cox regression analysis to construct the risk model, Kaplan-Meier survival analysis and log-rank tests to evaluate the prognostic signature

Research Assistant

2019 - 2021

Supervisor: Prof. Chu-Xia Deng, University of Macau

Investigated divergent drug responses in breast, liver, and colon cancers

Contributions: Led the genomic and transcriptomic data analysis of more than 100 breast cancer samples, including calling single-nucleotide variant (SNV) and copy number variation (CNV) from tumors as well as tumor-derived organoids, and identified differentially expressed genes (DEGs) between drug-sensitive and drug-resistant groups of tumor-derived organoids to predict drug-resistant tumors

Investigated the mechanism of PARPi resistance in BRCA1-deficient mouse models using single-cell analysis

Contributions: Led the analysis of scRNA-seq (10X) data to explore alterations in tumors and their microenvironment following PARPi resistance, focusing on identifying subclusters and biomarkers.

Explored the intra-tumor heterogeneity and temporal tumor evolution in breast cancer

Contributions: Inferred intra-tumor heterogeneity and tumor evolution tree by analyzing single-cell genomic data

Bioinformatics Engineer

2017 - 2019

Research and Development Department, GENE Co. Ltd

Developed and maintained tumor analysis toolkits

Contributions: Developed and maintained pipelines of high-throughput sequencing data analysis for tumor samples with and without matched normal samples

Developed graphical user interfaces (GUIs) for tumor analysis

Contributions: Adapted tumor analysis tools for the cloud platform to provide services for customers lacking programming experience

Created local databases for internal staff to match mutations with drug responses

Contributions: Optimized database by web scrapping and automated generating report

Visiting Student

2016 - 2017

Supervisor: Prof. Ying Xu, University of Georgia

Investigated the differences in OGT and OGA between tumor cells and normal cells

Contributions: Mined TCGA's genomic and transcriptomic data, as well as visualized analysis results

Project Leader of UTIEP

2014 - 2016

Supervisor: Prof. Guoqing Cao, Shanxi Agricultural University

Established fibroblast cell lines from Guangling Donkey

Contributions: Designed experiments, cultured cells, collected data and wrote the paper

PUBLICATIONS

Primary Author Publications:

- **Xu Zhang**, Lei Chen. MulMarker: a comprehensive framework for identifying multi-gene prognostic signatures. **2023 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)**, IEEE Computer Society, 2023
- **Xu Zhang**, Tak-Wah Lam, and Hing-Fung Ting. Genome instability-derived genes as a novel prognostic signature for lung adenocarcinoma. **Frontiers in Cell and Developmental Biology (IF: 6.08)**, 2023, 11
- Ping Chen, **Xu Zhang**, Renbo Ding, et al. Development of tailored therapy for advanced breast cancer based on patient-derived organoids and precision oncology. **Advanced Science (IF: 17.52)**, 2021, 8(22)
- **Xu Zhang**, Baoyu Le, Zhimin Chen, et al. Establishment and Biological Characteristics Analysis of Fibroblast Cell Line of Guangling Donkey. **China Animal Husbandry & Veterinary Medicine**, 2018, 45(3)

Contributing Author Publications:

- Jianjie Li, Xiaodong Shu, Jun Xu, Sek Man Su, Un In Chan, Lihua Mo, Jianlin Liu, Xin Zhang, Ragini Adhav, Kai Miao, Yuqing Wang, Tingting An, **Xu Zhang**, and NgaTeng IU, Chu-Xia Deng, Xiaoling Xu. S100A9-CXCL12 Axis in BRCA1 Deficiency Orchestrates the Immunosuppressive Microenvironment to Promote Breast Cancer Formation. **Nature Communications (IF: 17.69)**, 2022, 13(1)
- Heng Sun, Jianming Zeng, Zengqiang Miao, Johnny Kuan Cheok Lei, Chen Huang, Lingling Hu, Sek Man Su, Un In Chan, Kai Miao, **Xu Zhang**, Aiping Zhang, Sen Guo, Ya Meng, Chris Koon Ho Wong, Xiaohua Douglas, Xiaoling Xu, Chu-Xia Deng. Dissecting the heterogeneity and tumorigenesis of BRCA1 deficient mammary tumors via single cell RNA sequencing. **Theranostics (IF: 11.56)**, 2021, 11(20)
- Licen Li, Jiaolin Bao, Haitao Wang, Cheng Peng, Haipeng Lei, Jianming Zeng, Wenhui Hao, **Xu Zhang**, Xiaoling Xu, Chundong Yu, Chu-Xia Deng and Qiang Chen. Upregulation of amplified in breast cancer 1 contributes to pancreatic ductal adenocarcinoma progression and vulnerability to blockage of hedgehog activation. **Theranostics (IF: 11.56)**, 2021, 11(4)
- Fangyuan Shao, Xueying Lyu, Kai Miao, Haitao Wang, Qiang Chen, Hao Xiao, Renbo Ding, Ping Chen, Fuqiang Xing, **Xu Zhang**, Guang-Hui Luo, Wenli Zhu, Li-Gong Lu, Gregory Cheng, Ng Wai Lon, Scott E. Martin, Guanyu Wang, Guokai Chen, Chu-Xia Deng. Enhanced protein damage clearance induces broad drug resistance in multi-type of cancers revealed by an evolution drug resistant model and genome-wide siRNA screening. **Advanced Science (IF: 17.52)**, 2020, 7(23)
- Jianlin Liu, Ragini Adhav, Kai Miao, Sek Man Su, Lihua Mo, Un In Chan, Xin Zhang, Jun Xu, Jianjie Li, Xiaodong Shu, Jianming Zeng, **Xu Zhang**, Xueying Lyu; Lakhansing Pardeshi, Kaeling Tan, Heng Sun; Koon Ho Wong, Chu-Xia Deng; Xiaoling Xu. Characterization of BRCA1-deficient premalignant tissues and cancers by bulk and single-cell exome sequencing identifies Plekha5 as a tumor metastasis suppressor. **Nature Communications (IF: 17.69)**, 2020, 11(1)
- Liang Sen, Sen Yang, Dayang Liang, Jiechao Ma, Yuan Tian, Jing Zhao, **Xu Zhang**, Ying Xu, and Yan Wang. A Novel Matched-pairs feature selection method considering with tumor purity for differential gene expression analyses. **Mathematical Biosciences (IF: 3.935)**, 2019, 311

PRESENTATION

- **MulMarker: a comprehensive framework for identifying multi-gene prognostic signatures.**
IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Istanbul, Turkey, December 2023

TEACHING

Teaching Assistant at COMP7409: Machine Learning in Trading and Finance (Class Size: 150) 2023

- Facilitated discussion sessions and conducted office hours to actively engage students in course
- Mentored and supervised students for their projects

HONORS & AWARDS

Postgraduate Scholarships , The University of Hong Kong	2021 - 2023
Outstanding Graduates , Shanxi Agricultural University	2017
Academic Excellence Scholarship (triple) , Shanxi Agricultural University	2014 - 2016
Merit Student , Shanxi Agricultural University	2015
First Prize , the Fourth CP RBC Cup Competition of Shanxi Province	2014
Third prize (team leader) , Shanxi Agricultural University Debating Competition	2013

ADDITIONAL INFORMATION

Languages: Chinese Mandarin (Native), English (Fluent)

Skills: Linux Operating System, R, Python, C/C++, JavaScript, TensorFlow, PyTorch