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EDUCATION

Shanghai Jiao Tong University | Immunology (Master)

2019.09 - 2022.07

Xinjiang Medical University | Medical laboratory technology (Bachelor)

2015.09 - 2019.06

RESEARCH EXPERIENCE

uniPort: a unified framework for single-cell data integration with optimal transport.

Academy of Mathematics and Systems Sciences, Chinese Academy of Sciences

2021.12 - Present

- Built a unified single-cell data integration framework that combined a coupled Variational Autoencoder (coupled-VAE) and Minibatch Unbalanced Optimal Transport.
- Constructed a reference atlas through coupled-VAE for online prediction, which has been strongly proved through predicting unmeasured genes in MERFISH data with matched single-cell RNA (scRNA) sequencing data.
- Output a global transport plan which could deconvolute compounded barcoding-based spatial transcriptome data in a broad application spectrum of resolution maps.

Single-cell RNA sequencing profiling heterogenous immune networks in progressive lung adenocarcinoma.

Shanghai Pulmonary Hospital, Tongji University School of Medicine

2021.11 - Present

- Collected massive public scRNA sequencing data from multistage lung adenocarcinoma samples. Aligned and assembled them, then obtained programs of gene expression.
- Merged the harmonized expression matrixes after respectively normalizing and stabilizing variance of sequencing depth based on negative binomial. Then sorted highly variable genes with biological function to assist dimension reduction using Principal Component Analysis. Clusters were identified by Shared Nearest Neighbor at an appropriate resolution. Finally, cell identities were confirmed based on their conventional biomarkers.
- Purified malignant cells accounting for analysis of Copy Number Variations, were re-clustered to reveal the interaction networks between tumor and immune cells, especially macrophages. Meanwhile, explore their potential impact on the evolution of malignant cells through trajectory analysis.

Multi-omics data profiling the role of B cell subsets in the immune microenvironment of colorectal cancer.

Shanghai Institute of Immunology, Shanghai Jiao Tong University School of Medicine

2021.09 - Present

- Performed standard scRNA analysis on paired normal and colorectal cancer tissues, rendering an atlas of B cell subclusters. Then pathway enrichment analysis led to focus on the transformation of germinal center B cells.
- Applied GRNBoost to construct co-expression modules between targets and transcriptome factor (TF). Then RcisTarget was used to enrich TF-motifs and refined the regulons comprised of paired TF and target genes. Finally, AUCell was applied to quantify regulon activity.
- Paired VDJ datasets of B cell subclusters were used to estimate clonality, transition, and somatic hypermutation level.
- Identified Tertiary Lymphoid Structures in spatial transcriptome data, a rising strong predictor for immunotherapy via co-localizing signals of T and B cells.

Mechanism of FGL1 regulation of tissue-resident memory CD103⁺CD69⁺CD8⁺T cell function in liver cancer.

Renji Hospital, Shanghai Jiao Tong University School of Medicine

2021.08 - Present

- Confirmed the protein CD103 as a protective factor in liver cancer through Kaplan-Meier survival analysis and Cox Proportional Hazards Model. While FGL1 was identified as the adverse prognostic factor following the methods above.
- Demonstrated the linear relationship between expression of CD103 and FGL1 using Pearson's correlation coefficients.

Prognosis value of iron ferroptosis genes in clear cell renal cell carcinoma.

Renji Hospital, Shanghai Jiao Tong University School of Medicine

2021.06 - Present

- Achieved public mRNA expression profiles from The Cancer Genome Atlas to analyze the differential expression and functional enrichment, leading to the discovery of seven ferroptosis-related differentially expressed genes.
- The prognostic value of seven genes was demonstrated by Kaplan-Meier and univariate Cox analysis.

Single-cell profiling the crosstalk mechanism between Schwann and fibroblast in neurofibromatosis type one.

Shanghai Ninth People's Hospital, Shanghai Jiao Tong University School of Medicine

2021.02 - Present

- Constructed a transcriptome atlas of neurofibromatosis type one (NF1). Further, refined the heterogeneity of subgroups in Schwann and fibroblast cells. NicheNet and CellChat were performed to profile the communicating molecules.
- Both data-driven and experimental results demonstrated that Schwann cells regulate the proliferation and collage-

secreting of fibroblasts through PTN molecule, implicating a novel therapy direction for NF1 and ongoing mining for downstream pathways.

Meta-transcriptomic analysis reveals the gene expression and novel conserved sub-genomic RNAs in SARS-CoV-2 and MERS-CoV.

Shanghai Institute of Immunology, Shanghai Jiao Tong University School of Medicine 2020.03 - 2020.06

- Collected bulk sequencing data from NCBI Short Reads Archive, following the alignment using bwa, SNPs call using bcftools, and annotation with vcf-annotator.
- Breakpoints were identified from alignments with soft or hard clips, rendering the profiling of typical sub-genomic RNAs.

Mechanism of PolB regulation in AID targeting in antibody somatic hypermutation

Shanghai Institute of Immunology, Shanghai Jiao Tong University School of Medicine 2019.09 - 2020.02

- To figure out whether the short distance between the flag and lyase domain impacts PolB function, wild type and 3KR (knocked out three sites near lyase domain) PolB plasmids were constructed for the virus package.
- Resuscitated and infected 293T cell lines for subclone and proliferation of plasmids. Transfected virus package in CH12 cell lines. Western blot was used to test PolB expression, also next-generation sequencing to analyze somatic hypermutation levels of B cells.

TGF- β /Smad signaling pathway in mediating calcified hepatic echinococcus in mice.

First Affiliated Hospital of Xinjiang Medical University 2017.05 - 2018.11

- Responsible for the national project of college students, leading the model preparation and experimental implementation.
- Imagological diagnosis confirmed calcified hepatic echinococcus mice have extracted liver samples for RT-PCR and immunohistochemistry to quantify the expression of SMAD3/4 and TGF- β , demonstrating the promoting effect of this pathway in calcification.

PUBLICATIONS

- Hao Song, Chao Lou, Jie Ma, **Qiyu Gong**, ... Meng Xiao*. Single-Cell Transcriptome Analysis Reveals Changes of Tumor Immune Microenvironment in Oral Squamous Cell Carcinoma after Chemotherapy. *Front. Cell Dev. Biol.*

Manuscripts

- Kai Cao*, **Qiyu Gong***, Yiguang Hong, Lin Wan. uniPort: a unified framework for single-cell data integration with optimal transport. *bioRxiv*. Doi: <https://doi.org/10.1101/2022.02.14.480323>. *Under review.* (co-first author)
- Zhuowei Tian#, Zhong Du#, **Qiyu Gong**#, ... Yanan Wang1,2*. Single-cell transcriptome analysis reveals the role of Schwann cell-derived PTN in collagen deposition of plexiform neurofibroma. *Under review.* (co-first author.)
- Lin Lyu, Ru Feng, Mingnan Zhang, **Qiyu Gong**, Yinjing Liao, Yanjiao Zhou, Xiaokui Guo, Bing Su, Yair Dorsett, Lei Chen. Meta-transcriptomic analysis reveals the gene expression and novel conserved sub-genomic RNAs in SARS-CoV-2 and MERS-CoV. *bioRxiv*. Doi: <https://doi.org/10.1101/2020.04.16.043224>.

AWARDS

Merit Student of Shanghai Jiao Tong University	2019 - 2020
Advanced Individual of Xinjiang Medical University	2018 - 2019
Individual Scholarship of Xinjiang Medical University (twice)	2015 - 2017

SKILL AND LANGUAGE

Experimental skills

Flow cytometry, PCR, WB, ELISA, ISH, and basic cellular experiment skills

Software

R, Python, shell, and Latex (all more than two years.)

Certificate

Medical laboratory scientist

Language

Mandarin, English

INTERNSHIP EXPERIENCE

Haitong Securities Co. Pharmaceutical Group	2021.07 - 2022.01
Industrial Securities Co. Pharmaceutical Group	2021.11 - 2022.01
Xinjiang Provincial Cancer Hospital	2018.06 - 2019.05