



E-mail: linyang@ds.dfci.harvard.edu

RESEARCH EXPERIENCE (MAJOR PROJECTS)

08/2020 - Present

RNA-Seq Immune Analysis Pipeline

Advisor: X. Shirley Liu | Dana-Farber Cancer Institute Franziska Michor | Dana-Farber Cancer Institute

- Integrated bulk-RNA-related computational tools into a snakemake pipeline.
- Developed visualization modules to facilitate comparison.
- Processed and analyzed bulk RNA-seq data from the CIMAC-CIDC immunotherapy clinical trial.

CIMAC-CIDC: https://cimac-network.org

Github: https://github.com/liulab-dfci/RIMA pipeline

Tutorial: https://liulab-dfci.github.io/RIMA

06/2021 - Present

Association between EMT and Immune Evasion

Advisor: X. Shirley Liu | Dana-Farber Cancer Institute Kai Wucherpfennig | Dana-Farber Cancer Institute

- Conducted analysis of CRISPR screening data in collaboration with experimental researchers.
- Utilized public CRISPR data to help identify key genes related to EMT and immune evasion.

08/2021 - 10/2021

Hippo Signaling Pathway Regulates Cancer Cell-intrinsic MHCII Expression

Advisor: X. Shirley Liu | Dana-Farber Cancer Institute

- Elucidated a tumor-specific MHCII gene signature from single-cell RNA-seq data to support work related to MHCII expression.
- Applied and modified the model to predict tumor-specific MHCII levels from bulk RNA-seq.

Status: submitted to the Genome Medicine

03/2021 - 09/2021

Syngeneic Mouse Tumor Database (TISMO)

Advisor: X. Shirley Liu | Dana-Farber Cancer Institute

- Collected and processed 605 *in vitro* and 1518 *in vivo* RNA-seq samples from 49 syngeneic cancer cell lines.
- Built TISMO website interface and developed visualization functions.

TISMO website: http://tismo.cistrome.org

08/2019 - 03/2020

Potential Epigenetic Factors Regulating Mouse ESC Development

Advisor: Wei Li | Children's National Hospital Jin Zhang | Zhejiang University, China

- Analyzed Single-cell CRISPR screens to study epigenetic factors that regulates mouse ESC self-renewal.
- Applied trajectory analysis to study mouse ESC differentiation.



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03/2019 - 01/2020

Novel Bioinformatics Methodology for Single-Cell CRISPR Screening

Advisor: Wei Li | Children's National Hospital

- Applied and modified Robust Rank Aggregation (RRA) and the linear regression (LR) approach to detect gene expression regulatory relationship from cells with perturbations.
- Validated the methods using public CROP-seq data.
- Developed visualization functions.

Github: https://github.com/weililab/scMAGeCK

07/2016 - 07/2017

Mechanisms of Bacterial Nitrogen-fixation

Advisor: Sanfeng Chen | China Agricultural University, China

- Reconstructed the pET-28b plasmid with the synthetic *nif* gene.
- Screened successfully introduced strains.
- Performed Nitrogen-fixing related protein induction, extraction, isolation, and western blot for protein validation.

EMPLOYMENT

08/2020 - Present

Computational Biologist I

Department of Data Science Dana-Farber Cancer Institute

450 Brookline Avenue, Boston, MA 02215

05/2019 - 08/2019

Research Assistant

Center for Genetic Medicine Research Children's National Medical Center

111 Michigan Ave NW, Washington, DC, 20010

EDUCATION

08/2018 - 05/2020

George Washington University | Bioinformatics (Master)

Major: Bioinformatics, Next Generation Sequencing, Big data, Biochemistry,

Medical Genome

Tools: Python, Linux, R, Seurat, Cell Ranger

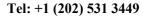
09/2013 - 07/2017

China Agricultural University | Biological Science (Bachelor)

Major: Biochemistry, Molecular Biology, Genetics

Tools: C Programming Languages

Lab: Biochemistry Laboratory, Cell Biology Laboratory





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PUBLICATIONS (* FIRST/CO-FIRST AUTHOR)

• TISMO: syngeneic mouse tumor database to model tumor immunity and immunotherapy response

Nucleic Acids Res. 2021. Sep 17; PMID: 34534350; doi.org/10.1093/nar/gkab804 Zeng Z*, Wong CJ*, Yang L*, et al.

• scMAGeCK links genotypes with multiple phenotypes in single-cell CRISPR screens

Genome Biol **21**, 19 (2020); PMID: 31980032; 10.1186/s13059-020-1928-4 **Yang**, L*., Zhu, Y*., Yu, H. et al.

• CRISPR Screening "Big Data" Informs Novel Therapeutic Solutions

Cris. J., Jun 2, 2019; PMID: 31225758; 10.1089/crispr.2019.29062.sch Chen, S*., Yang, L*. & Li, W.

SUBMITTED AND PREPRINT MANUSCRIPTS (* FIRST/CO-FIRST AUTHOR)

2021

Tutorial: integrative computational analysis of tumor immunity of bulk RNA-seq data using RIMA Submitted to *Nature protocols*

Yang L*, Wang J*, Altreuter J*, Jhaveri A*, Wong CJ, et al.

Machine learning on syngeneic mouse tumor profiles to model clinical immunotherapy response Submitted to *Science Advances*

Zeng Z, Gu S, Wong CJ, Ouardaoui N, Yang L, et al.

Hippo signaling pathway regulates cancer cell-intrinsic MHCII expression

Submitted to *ImmunoTherapy of Cancer* Zeng Z, Gu S, Ouardaoui N, Tymm C, **Yang L**, et al.

Durvalumab, tremelimumab alone or in combination with low-dose or hypofractionated targeted radiotherapy in metastatic non-small cell lung cancer refractory to prior PD(L)-1 therapy: a multicentre, open-label, randomized, phase 2 trial

Accepted by *Lancet oncology*

Jonathan D Schoenfeld, Anita Giobbie-Hurder, Srinika Ranasinghe, Katrina Z Kao, Ana Lako, Junko Tsuji, Yang Liu, Ryan C Brennick, Ryan D Gentzler, Carrie Lee, Joleen Hubbard, Susanne M Arnold, James L Abbruzzese, Salma K Jabbour, Nataliya V. Uboha, Kevin Stephans, Jennifer M Johnson, Haesong Park, Liza C Villaruz, Elad Sharon, Howard Streicher, Mansoor Ahmed, Hayley Lyon, Carrie Cibuskis, Niall Lennon, Aashna Jhaveri, **Lin Yang**, Jennifer Altreuter, et al.

SKILLS

Languages: R, Python

Technologies: Git, Snakemake

Bioinformatics: Bulk and Single-Cell RNA-seq, Spatial transcriptomics, CRISPR screening