

Jinrui Liu, M.S.E

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Research Summary

- ◆ Study biological mechanisms related to human diseases through computational analysis of high throughput experimental datasets.
- ◆ Develop novel analytical methodologies for datasets from different modalities using statistical modeling and machine learning techniques.

Education

Cornell University, US

Ph.D. in Physiology, Biophysics and Systems Biology - Bioinformatics Expected: 2028

Johns Hopkins University, US

M.S.E in Biomedical Engineering 2020

University of Missouri, US | East China University of Science and Technology, PRC

B.S in Bioengineering (dual-bachelor program), Honors Scholar 2018

Experiences

Weill Cornell Medicine, NY

Graduate Research Associate Aug 2023 – Present

Regeneron Pharmaceuticals, NY

Sr. Associate Scientist – Bioinformatics Jan 2023 – Jul 2023

Bioinformatics Analyst Jul 2020 – Jan 2023

Johns Hopkins University, MD

Bioinformatics Research Assistant May 2019 – Jul 2020

Publications

* Cited by 52 (Last updated: Oct 2023)

- ◆ Natalie V, ... **Jinrui L et al.** "Circulating tumor DNA (ctDNA) dynamics and survival outcomes in patients (pts) with advanced non-small cell lung cancer (aNSCLC) and high (>50%) programmed cell death-ligand 1 (PD-L1) expression, randomized to cemiplimab (cemi) vs chemotherapy (chemo). " *Journal of Clinical Oncology*, May 2023
- ◆ Huan C, ... **Jinrui L et al.** "Two-stage linked component analysis for joint decomposition of multiple biologically related data sets." *Biostatistics*, Mar 2022
- ◆ Wen Z, ... **Jinrui L et al.** "A framework for highly multiplexed dextramer mapping and prediction of T cell receptor sequences to antigen specificity." *Science Advances*, May 2021

- ◆ Huan C, **Jinrui L** *et al.* "Structured Joint Decomposition (SJD): an R package for the identification of shared molecular dynamics across collections of biologically related multi-omics data matrices." *bioRxiv* (under review at *Bioinformatics*)
- ◆ Decker C, ... Liu J *et al.* "Anti-HLA/peptide CAR T cells demonstrate more durable anti-tumor efficacy than engineered TCR T cells due to costimulatory signaling" (under review at *Cancer Immunology Research*)

Patents

- ◆ Ciro C, **Jinrui L** *et al.* "Identification of tissue-specific extragenic safe harbors for gene therapy approaches" *U.S. Patents* (in grace period)

Talks

- ◆ Shreyash S, Huan C, **Jinrui L** *et al.* "Structured joint decomposition identifies reproducible cell states and their developmental progression across human neocortical development which map onto risk for complex brain disease." *CSHL meeting*, Nov 2022
- ◆ Vladimir J, **Jinrui L** *et al.* "Tumor Immune Correlates of Cemiplimab Response in Cutaneous Squamous Cell Cancer." *Regeneron Translational Data Review*, Sep 2022
- ◆ **Jinrui L**, Mustafa B *et al.* "Predicting Response to Cemiplimab in Cutaneous Squamous Cell Carcinoma (CSCC)." *Regeneron Science Poster Day*, Sep 2022

Skills

- ◆ Proficient in data science programming: R, Python, Bash.
- ◆ Experienced in oncology research through analysis of functional genomics datasets.
- ◆ Experienced in method development using machine learning and statistical techniques.

Selected Projects

Cell Therapy Mechanistic Study: TCR- vs. CAR-T cells Regeneron, 2022

- ◆ Performed transcriptomics data analysis to study differences in anti-tumor activities between engineered TCR- and CAR-T cells.

Clinical Data Analysis of Anti-PD1 Therapy in Skin Cancer Regeneron, 2022

- ◆ Led transcriptomic analysis of Cutaneous Squamous Cell Carcinoma (CSCC) patients from anti-PD1 trial, profiling gene expression differences between drug responders and non-responders.

Transgene Site Discovery Regeneron, 2021

- ◆ Developed a novel computational method to identify potential transgene sites for gene therapy.

Bioinformatics Technology Developments Regeneron, 2021-2023

- ◆ Developed multiple computational pipelines to analyze molecular data of different modalities.
- ◆ Performed benchmark analyses of datasets from newly developed experimental methods.

Method of Transcriptomic Data Decomposition Johns Hopkins University, 2020

- ◆ Developed a computational method in R language that identifies similar biological signatures between high-dimensional transcriptomic datasets from different studies.