

# Kai Stewart

 kseuro |  kaiwstewart |  kai.w.stewart@gmail.com |  617.528.0353

## SUMMARY

---

Curious and motivated computational biologist with experience analyzing genomic and transcriptomic data. I enjoy the challenge of integrating multi-modal data, including single-cell, bulk RNA, and genomic data, to help drive questions and insights into mechanisms of disease drug resistance and relapse. I thrive in collaborative research environments that include scientists of diverse disciplines, and am fascinated by the possibilities that exist at the interface of computing and life sciences.

## WORK EXPERIENCE

---

### **Associate Computational Biologist II - Getz Lab, Broad Institute** July 2021 - Present

- Performed analysis of joint bulk RNA and whole exome sequencing data of diffuse large B-cell lymphomas (DLBCL) refractory to CAR-T cell therapy and identified mechanisms of treatment resistance and relapse, in collaboration with researchers at Dana-Farber Cancer Institute
- Built Docker based data processing tool for incorporation of terabyte scale genomic data into analysis of DLBCL whole exomes in order to boost study's statistical power
- Performed large scale analysis of 10x single-cell data of germline heterozygous BRCA1/2 mutated breast epithelial tissue and immune cells to identify pre-cancerous cellular expression programs, in collaboration with researchers at Massachusetts General Hospital
- Designed and implemented custom data processing pipeline to denoise formalin fixed paraffin embedded whole exome sequencing data and call copy number events
- Designed and implemented single-cell data pseudo-bulk analysis tool designed for fast, multi-tiered differential expression analysis

### **Associate Computational Biologist I - Getz Lab, Broad Institute** June 2020 - July 2021

- Characterized whole exome sequencing data using Cancer Genome Computational Analysis pipeline tools including GISTIC, MuTECT, AllelicCapSeg, and ABSOLUTE
- Performed data analysis of genome-wide CRISPR knockout screen in glioblastoma using MAGeCK algorithm to identify loss of  $\text{INF}\gamma\text{R}$  signaling pathway as a mechanism of CAR-T resistance in solid tumors
- Researched current methods in single-cell data analysis and implemented published algorithms and tools for the analysis of 10x single-cell data
- Designed a chronology based workflow and results tracking system for projects to provide both high-level and detailed information on every aspect of an analysis

### **Undergraduate Research Assistant - Wongjirad Lab, Tufts University** June 2018 - May 2020

- Researched, developed, and tested deep learning models on particle detector data, including convolutional neural networks, Wasserstein-generative-adversarial neural networks, and auto-encoders, as part of the MicroBooNE collaboration with FermiLab National Laboratory
- Presented model accuracy and prediction results at FermiLab Neutrino conference in Batavia, IL
- Extended deep learning research into honors physics thesis: “A Deep Convolutional Neural Network Approach to Liquid Argon Time Projection Chamber Image Synthesis”; nominated for 2019 Goldwater Scholarship on the basis of research quality

### **Undergraduate Research Assistant - Burch Lab, Boston College** June 2017 - August 2017

- Conducted National Science Foundation funded research in solid state physics in the context of topological semiconductors and presented research findings at NSF research symposium at Boston College
- Operated advanced equipment including liquid nitrogen refrigeration systems, helium-neon lasers, and argon atmosphere glove boxes
- Built custom electronics that improved experiment data collection

## EDUCATION

---

2018 - 2020 B.Sc. Applied Physics **Tufts University** *Summa cum Laude; Highest Thesis Honors*  
2015 - 2017 A.A. Physics **Bunker Hill Community College** *Highest Honors*

## PUBLICATIONS

---

Larson, R.C. et al. (Apr. 2022). “CAR T cell killing requires the IFN $\gamma$ R pathway in solid but not liquid tumours”. In: *Nature* 604, pp. 563–570. URL: <https://www.nature.com/articles/s41586-022-04585-5>.

## SKILLS

---

Programming	PYTHON, BASH, DOCKER, L <sup>A</sup> T <sub>E</sub> X, GIT, LINUX / UNIX, GOOGLE CLOUD PLATFORM
Machine Learning	Experience implementing: CNN, GAN, AE using PYTORCH
Bioinformatics	Whole genome analysis, whole exome analysis, bulk RNAseq analysis, 10x single-cell-seq analysis, SamTools, Scanpy, CellBender, Limma-Voom
Spoken Languages	English: <i>Fluent</i> , German: <i>Fluent</i>

Last updated: November 23, 2022