Kai **Stewart**

SCIENTIST, COMPUTATIONAL BIOLOGY

BioNTech U.S.

☐ (617)-528-0353 | ✉ kai.w.stewart@gmail.com | 🔗 kaiwstewart

Summary

Computational biologist with 5+ years experience analyzing single-cell data, building custom bioinformatics and optimization software, and developing data pipelines. Driven by a fascination with how code can transform biological questions into engineering problems by prioritizing DevOps best practices like Git and containerization to produce maintainable code, reproducible analyses, and scalable solutions.

Skills

Programming	Python, Mojo & Max Engine, Bash, Linux
	• Experience building data-analysis, data pipeline, and optimization packages in Python.
	• Experimenting with next-generation computational graph compiler in Mojo.
Single Cell Analysis	10x CellRanger, Scanpy/Muon
	• Routinely process single-cell GEX, CITE, and TCR/BCR data using CellRanger and Scanpy.
Data Pipeline Development	Nextflow, SLURM
	• Implemented massively parallel optimization pipeline using Nextflow and AWS Batch service.
	• Routinely use SLURM to execute CellRanger alignment jobs on AWS-based HPC cluster.
Machine Learning	Experience implementing HuggingFace (HF) models in containerized data pipelines via HF library APIs.
	• Facebook-AI-Research ESM-Fold & Llama 3.1 for protein folding and log file parsing, resp.
	• OpenAI Whisper for audio transcription.
DevOps & Cloud Computing	Git, Docker, Amazon Web Services, Google Cloud Platform
Languages	English (Fluent), German (Fluent)

Work Experience

BioNTech
Cambridge, MA

SCIENTIST, COMPUTATIONAL BIOLOGY — *June 2024 - Present*

- Support cross-functional teams, as well as clinical trials, through regular processing and analysis of single-cell data (GEX, CITE, TCR/BCR, spectral flow), aiding hypothesis generation, informing clinical trial manufacturing decisions, and helping to validate drug and vaccine candidates and experimental protocols.

ASSOCIATE SCIENTIST, COMPUTATIONAL BIOLOGY — *February 2023 - June 2024*

- Developed internal methods and workflows, and applied machine learning tools (i.e., ProteinMPNN, AlphaFold-multimer), to drive a de novo protein design project.
- Created a (now patented) modular and scalable peptide-string optimization algorithm to support projects ranging from oncology to infectious disease by streamlining design input processing and tailoring outputs for group- and project-specific needs.
- Engineered a fault-tolerant single-cell data processing pipeline for an AWS SLURM-based HPC, automating parallel deployment of the 10x CELL-RANGER algorithm, results analysis and data storage, saving the computational biology team significant time each month.
- Directed collaborative development of in-house data storage and visualization application by coordinating efforts between a software engineering team and the computational biology team.
- Fostered and implemented coding and collaboration standards, leading a GITHUB workshop to introduce colleagues to version control, drive team-wide professional development and improve group-wide code quality.

Getz Lab, Broad Institute of MIT and Harvard
Cambridge, MA

ASSOCIATE COMPUTATIONAL BIOLOGIST II — *July 2021 - January 2023*

- Collaborated with Dana-Farber Cancer Institute researchers to analyze bulk RNA and whole-exome sequencing data, generating insights into CAR-T cell therapy resistance mechanisms in DLBCL.
- Enhanced DLBCL study power by building a Docker-based data processing tool, enabling efficient handling of terabyte-scale genomic data.
- Partnered with Massachusetts General Hospital researchers on multi-patient single-cell data analysis, uncovering pre-cancerous cellular expression programs in breast tissue harboring BRCA1/2 mutations.
- Streamlined analysis of formalin-fixed paraffin-embedded (FFPE) whole-exome sequencing data with a custom pipeline for data denoising and copy number event calling.

ASSOCIATE COMPUTATIONAL BIOLOGIST I — *June 2020 - July 2021*

- Leveraged Cancer Genome Computational Analysis tools (GISTIC, MuTECT, ABSOLUTE) for comprehensive characterization of whole-exome sequencing data.
- Collaborated with Massachusetts General Hospital researchers on an analysis of a genome-wide CRISPR knockout screen in glioblastoma, pinpointing INFγR signaling pathway disruption as a CAR-T resistance mechanism in solid tumors.
- Researched and implemented state-of-the-art single-cell data analysis algorithms, improving the lab's analytical capabilities.
- Optimized the integration of single-cell and bulk RNA-sequencing data with the creation of a pseudo-bulk analysis framework.

Wongjirad Lab, Tufts University
Undergraduate Research Assistant

Medford, MA
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.

Burch Lab, Boston College
Undergraduate Research Assistant

Chestnut Hill, MA
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.
- Presented research at an end-of-summer symposium attended by researchers from all scientific departments.
- Operated advanced equipment including liquid nitrogen refrigeration systems, helium-neon lasers, and argon atmosphere glove boxes as part of the data collection process.
- Built custom electronics that improved experimental data collection and enabled research progress.

Education

Tufts University
B.Sc. Applied Physics - Summa cum Laude

Medford, MA
January 2018 - May 2020

- Thesis: Deep Convolutional Neural Network Approach to Liquid Argon Time Projection Chamber Image Synthesis
- Member of the Tufts High Energy Particle Neutrino Research Group (νTufts)

Bunker Hill Community College
A.A. Physics - *Highest Honors*

Charlestown, MA
January 2015 - December 2017

Extracurricular Activity

Tutoring Plus (T+)
Academic Tutor

Cambridge, MA
October 2020 - Present

- Volunteer after-school tutor for low-income middle and high school students in the Cambridge public school system.
- Work with students of all ability levels to help them improve their educational experience and their academic performance.