

Kai Stewart

SCIENTIST, COMPUTATIONAL BIOLOGY

BioNTech U.S.

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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 — excited to tackle complex problems that can have an outsized impact on human health.

Skills

Programming	Python, Bash, Linux, Mojo (Modular) <ul style="list-style-type: none">• Experience building data-analysis, data pipeline, and optimization packages in Python.• Experimenting with next-generation computational graph compiler in Modular Max Engine.
DevOps & Cloud Computing	Git, Docker, Amazon Web Services, Google Cloud Platform
Single Cell Analysis	10x CellRanger, Scanpy/Muon <ul style="list-style-type: none">• Routinely process single-cell GEX/TCR/BCR and spectral flow data.
Data Pipeline Development	Nextflow, SLURM <ul style="list-style-type: none">• 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	CNN, AlphaFold, ESM-Fold, HuggingFace API <ul style="list-style-type: none">• Experience applying protein folding models to protein design problems.• Experience developing machine vision models for undergraduate particle physics research.
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.
- Engineered 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.

ASSOCIATE SCIENTIST — COMPUTATIONAL BIOLOGY

February 2023 - June 2024

- Developed internal methods and workflows, and applied machine learning tools (i.e., ProteinMPNN, AlphaFold-multimer, ESM-Fold), to drive a de novo protein design project.
- 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 INF γ R 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

Medford, MA

UNDERGRADUATE RESEARCH ASSISTANT

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

Chestnut Hill, MA

UNDERGRADUATE RESEARCH ASSISTANT

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

Medford, MA

B.SC. APPLIED PHYSICS - SUMMA CUM LAUDE

January 2018 - May 2020

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

Bunker Hill Community College

Charlestown, MA

A.A. PHYSICS - Highest Honors

January 2015 - December 2017

Extracurriculars

Tutoring Plus (T+)

Cambridge, MA

ACADEMIC TUTOR

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.