

Kai Stewart

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SUMMARY

Computational biologist driven by a fascination with how code can create solutions that compound on each other to transform biological problems into engineering problems. My work focuses on the development of streamlined bioinformatics pipelines, building optimization software, and single-cell data analysis. I prioritize best practices like Git and containerization to produce maintainable code and reproducible analyses

WORK EXPERIENCE

Scientist, Computational Biology - BioNTech U.S.

June 2024 - Present

Associate Scientist, Computational Biology — BioNTech U.S.

February 2023 - June 2024

- Developed internal methods and workflows, and applied machine learning tools (like ProteinMPNN and AlphaFold), to drive de novo protein design projects, emphasizing efficiency, reproducibility and pipeline flexibility.
- Created a modular and scalable peptide-string optimization algorithm to support projects ranging from oncology to infectious disease by streamlining peptide-string design processing and tailoring outputs for group and project specific needs.
- Engineered an error-tolerant single-cell data processing pipeline for an AWS SLURM-based HPC, automating parallel deployment of the 10X CELLRANGER algorithm, results analysis and data storage. This saves the computational biology team significant time each month.
- Actively collaborate with internal and external software engineers to steer the development of data analysis portals and point-and-click databases, dramatically reducing iteration time for experimental colleagues and enabling company-wide data sharing.
- Fostered and implemented coding and collaboration standards, leading a GITHUB workshop to introduce colleagues to version control, drive team-wide professional development, improve group-wide code quality and reproducibility.
- Support cross-functional teams, as well as clinical trials, through regular processing and analysis of single-cell data (GEX, CITE, TCR, spectral flow), aiding hypothesis generation, informing clinical trial manufacturing decisions, and helping to validate drug and vaccine candidates.

Associate Computational Biologist II - Getz Lab, Broad Institute

July 2021 - January 2022

- 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 large-scale 10x single-cell data analysis, uncovering pre-cancerous cellular expression programs in BRCA1/2 mutated breast tissue.
- Streamlined analysis of formalin-fixed paraffin-embedded whole-exome sequencing data with a custom pipeline for denoising and copy number event calling.

Associate Computational Biologist I - Getz Lab, Broad Institute

June 2020 - July 2021

- Leveraged Cancer Genome Computational Analysis tools (GISTIC, MuTECT, ABSOLUTE) for comprehensive characterization of whole-exome sequencing data.
- Collaborated on analysis of a genome-wide CRISPR knockout screen in glioblastoma, pinpointing $\text{INF}\gamma\text{R}$ 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.

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 as part of the data collection process.
- Built custom electronics that improved experimental data collection.

EDUCATION

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

SKILLS

Programming & Development:	Python, MojoLang, Bash, Docker, Git, Linux
Cloud Computing:	Google Cloud Platform, Amazon Web Services
Bioinformatics:	Single-cell RNAseq analysis, data pipeline development, machine learning-driven protein design
Collaboration & Best Practices:	Proficient with version control, containerization, and unit testing
Machine Learning:	Experience with FastFold, AlphaFold-multimer
Languages:	English (Fluent), German (Fluent)