

Drew T.

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Bioinformatician

Bioinformatician with 3+ years of experience in NGS data analysis, Snakemake pipeline development, and HPC cluster usage. Skilled in reproducible research, variant calling, and benchmarking. Passionate about applying these skills in an industry setting post-graduation in September 2025.

WORK EXPERIENCE

Center for Genomic Medicine at Rigshospitalet | Copenhagen, DK | 03/2023 - Present

Student Assistant | Internship

- » Developed a reproducible benchmarking pipeline in Snakemake to evaluate 15 variant callers; visualized results with R for publication-quality comparisons.
- » Utilized HPC cluster with qsub for efficient job scheduling and data analysis, integrating with Snakemake workflows and dependency flows
- » Created a robust data analysis Snakemake workflow integrating scripts in Python, Bash, and R for PRS analysis
- » Added a new variant caller to a production-level Snakemake pipeline used for processing FASTQ files into clinical-grade reports.

Whitney Marine Lab-University of Florida | St Augustine, Florida, United States | 06/2021 - 08/2021

NSF REU Intern

- » Programmed and executed copy number (CNV) and single nucleotide variation (SNV) analysis on 21 paired tumor-normal Green sea turtle whole genome sequences using R and CLI tools
- » Executed bioinformatics CLI commands such as bcftools on a SLURM-based timeshare (UNIX)
- » Organized and presented research results in poster and presentation format at lab meetings and four academic conferences

UC Santa Cruz Genomics Institute | Santa Cruz, California, United States | 01/2020 - 06/2021

Undergraduate Student Researcher at Treehouse Childhood Cancer Initiative

- » Enhanced and used a previously published pipeline, ProTECT, in Python, adding and validating the capacity to generate neoepitope analysis from RNA-seq without DNA-seq data.
- » Reproducible analysis of RNA-Seq expression in R using ggplot and tidyverse
- » Maintained clear daily documentation and concise progress summaries to support seamless collaboration and efficient handover of work.

University of Washington School of Oceanography | Seattle, Washington | 06/2018 - 06/2019

Intern

- » Programmed machine learning algorithms in MATLAB to help identify pictures of plankton in-flow, on plankton cultures

SKILLS

Programming: R, Python, C

Tools: Snakemake, bcftools, Git, SLURM/qsub, bwa, conda, PyMol

Languages: English (Native), Danish (Beginner)

EDUCATION

Master of Science (MSc) in Bioinformatics

University of Copenhagen
09/2023 - 09/2025

Relevant coursework:

Advanced Algorithms and Data Structures, Statistics for Bioinformatics and eScience, Machine Learning A, Biological Sequence Analysis, Advanced Bioinformatics for NGS

Bachelor of Science (BSc) in Bioinformatics and Marine Biology

University of California, Santa Cruz
06/2023

Relevant coursework:

Research Programming in the Life Sciences, Bioinformatics Models and Algorithms, Introduction to Database Management Systems, Data Viz, Technical Writing

**AIMM - Marine Environment Research Association | Portugal |
10/2018 - 10/2018**

Intern at AIMM

- » Assisted with dolphin biopsy, plankton collection, and data entry in Excel of field sightings

CERTIFICATIONS

Student Success Mentor Training | 09/2020 - Present

Mentor Collective

AWARDS & SCHOLARSHIPS

Student Award Winner - FP Research Symposium | 10/2021

Best Poster - REU Whitney Lab | 08/2021

Dean's Honors - UC Santa Cruz

VOLUNTEERING & LEADERSHIP

ClinGen | 04/2025 - Present

Baseline Annotator

Annotating biomedical literature in a standardized form to support the work of ClinGen Expert Panels in evaluating variant pathogenicity, gene-disease validity, and more.

Mentor Collective | 09/2021 - 12/2023

Student Mentor

I connect with 5 mentees individually at least once a month to help provide access to resources and give peer advice on the college experiences

The Sea Turtle Hospital | 07/2021 - 08/2021

Husbandry Volunteer

UCSC Long Marine Lab | 10/2019 - 03/2020

Survey Slugs

PUBLICATIONS

The Case for Using Mapped Exonic Non-Duplicate Reads When Reporting RNA-Sequencing Depth: Examples from Pediatric Cancer Datasets |

03/2021

GigaScience

- » Beale, Holly C., Roger, Jacquelyn M., Cattle, Matthew A., McKay, Liam T., Thompson, Drew K. A., Learned, Katrina, Lyle, A. Geoffrey, Kephart, Ellen T., Currie, Rob, Lam, Du Linh, Sanders, Lauren, Pfeil, Jacob, Vivian, John, Bjork, Isabel, Salama, Sofie R., Haussler, David, and Vaske, Olena M.
- » DOI: 10/gjgkvv.