Austin Crinklaw

CONTACT
INFORMATION

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github.com/acrinklaw

EDUCATION

University of California, San Diego

BSc. in Biology: Specialization Bioinformatics (September 2018)

RESEARCH
EXPERIENCE

La Jolla Institute for Immunology

Research Technician, Peters Lab (2018 – Present)

- Developed an RNA-Seq pipeline for allele-specific HLA expression using a combination of MultiQC, Kallisto, STAR, and HTSeq. Maintained in a snakemake pipeline designed for HPC cluster.
- Implemented and optimized a mathematical method for determining T-cell receptor similarity and epitope specificity. Prototyped in Python, optimized in C++. Responsible for manuscript and tool implementation both back-end and web server front-end (Django framework).
- Created a Python package that classifies unknown protein sequences into T-cell receptor, Antibody, or MHC molecule using a combination of Hidden Markov Models and curated BLAST databases.
- Developed and maintained automated scripts for data validation for the Immune Epitope Database and MHC Restriction Ontology using Python.

SKILLS

Programming Languages/Frameworks:

- Strong Python skills, but heavy interest in statically-typed compiled languages, particularly Rust and C/C++. Familiar with R, primarily for visualization.
- Extremely comfortable on Linux and with Linux CLI tools. Experienced working in HPC environments using TORQUE queuing system. Familiar with both Snakemake and Nextflow for pipelines.
- Focus on proper development, clean documentation, best practices including CI, testing, optimization. Interested in modern DevOps (Git, Docker, CI, AWS, etc).
- Proficient with a wide array of bioinformatics tools for data analysis. Heavy focus on bulk RNA-Seq analysis with occasional single-cell.

SOFTWARE

TCRMatch: Alignment free determination of the similarity between T-cell receptors
https://github.com/iedb/TCRmatch

ARC: Classifies unknown protein sequences as T-cell receptor, Antibody, or MHC
https://github.com/iedb/ARC

SELECT
PUBLICATIONS

Papers/Articles

Chronister W, **Crinklaw A***, Mahajan S, Vita R, Kosaloglu Yalcin Z, Greenbaum J, Jessen L, Nielsen M, Christley S, Cowell L, Sette A, Bjoern P (2021). "TCRMatch: Predicting T-Cell Receptor Specificity Based on Sequence Similarity to Previously Characterized Receptors."
Frontiers in Immunology. doi:10.3389/fimmu.2021.640725
*Co-first author and lead programmer