KEVIN J. ANDERSON

Durham, NC ✉ kev13rac@gmail.com 📱 (804) 389-1172 💼 /in/kevin-anderson11 🐙 /kev08rac

SKILLS

Assay Experience: Illumina RNA-seq, Ion Torrent, Single-Cell RNA/TCR/BCR/Cell-Surface Protein, Spatial Gene Expression Profiling, GWAS

Programming languages: R, Python, Unix, Java, SQL

Other relavent experience: Docker, Nextflow, High-Performance Computing, GitFlow, Kubernetes, PLINK

EDUCATION

University of Pittsburgh • Pittsburgh, PA   Graduated: April 2022
Masters of Science • *Bioinformatics*
  Coursework: NGS Pipelines/Visualization, Molecular Basis of Disease, Population & Statistical Genetics

University of Pittsburgh • Pittsburgh, PA   Graduated: April 2020
Bachelors of Science • *Bioinformatics & History Minor*

EXPERIENCE

Bioinformaticist – IQVIA Labs / Q^2 Solutions   May 2022 – August 2024
Durham, NC   Internship: June 2021 – September 2021
- Tested large scale genomics NGS datasets for accuracy, precision, and other metrics to validate over five CAP-CLIA and non CAP-CLIA clinical assays spanning multiple omics technologies
- Deployed efficient data pipelines using Docker and NextFlow
- Presented customized data analyses to pharmaceutical clients in order to support their clinical trial needs
- Lead developer on an agile software project team to implement a Kubernetes hosted web application that facilitates the creation of customized configuration files for two assay validation pipelines using RShiny

Bioinformatics Analyst – UPMC Children's Hospital   July 2019 – May 2020
Pittsburgh, PA
- Processed bulk RNA-seq samples from more than 1000 patients to analyze their immune profiles, and characterize the TCR repertoire
- Deployed customized analysis pipelines and workflows using R and Unix

Bioinformatics Intern – National Cancer Institute   June 2015 – July 2016
Frederick, MD
- Parallelized a GWAS R package specializing in linkage Mapping by Admixture Linkage Disequilibrium
- Presented a poster on parallel computing and the R package at the Institute's research festival

PUBLICATIONS

- Carlson JC, Krishnan M, Liu S, **Anderson KJ**, Zhang JZ, Yapp TJ, Chiyka EA, Dikec DA, Cheng H, Naseri T, Reupena MS, Viali S, Deka R, Hawley NL, McGarvey ST, Weeks DE, Minster RL. Improving imputation quality in Samoans through the integration of population-specific sequences into existing reference panels. (Submitted to the American Journal of Human Genetics, October 2023) medRxiv 2023.10.31.23297835

PROJECTS

Population-Specific Reference Panel for Improved Imputation – Pitt GSPH   August 2021 – April 2022
Pittsburgh, PA
- Contributed to a Genome-Wide Association Study (GWAS)/Whole-Genome Sequencing (WGS) study to publish reliable imputation panels for Samoan Pacific Islanders who are underrepresented in genotyping studies and publicly available imputation panels
- Developed a data dashboard using RShiny to visualize GWAS statistics from multiple large datasets and imputation statistics from 1000Genomes, TOPMed, and the study-specific reference panels
- Determined the minimum number of participants to sequence and include in imputation reference panels needed to obtain accurate imputation quality required for future genetic studies on this population

EctothermER: Frogs Under the Weather – Pitt Bio Outreach Program   January 2020 – April 2020
Pittsburgh, PA
- Collaborated with the University of Pittsburgh Department of Biological Science's Outreach Program on an agile software team to help facilitate real scientific experiments and analysis to middle/high school classrooms all around the country
- Developed a website that is the central hub for teachers to access all the handbook materials and relevant information needed for the module, as well as a place for schools to input and visualize data collected from their location using RShiny