Kian H. Kelly, Ph.D

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Bioinformatics Scientist

Bioinformatics Scientist (Ph.D.) specializing in development of novel NGS secondary analysis algorithms for germline and somatic variant detection, with a focus on oncology applications. Experienced in designing statistically rigorous variant calling methods for low allele frequency detection, benchmarking against industry standards, and translating research algorithms into production-ready pipelines. Proven ability to collaborate across computational and experimental teams to enable clinically relevant genomic insights. Outside the lab, I serve as a volunteer firefighter with Indian Peaks Fire and Rescue, operating in high-pressure, team-based emergency response environments.

Research Experience and training

BIOINFORMATICS SCIENTIST, WATCHMAKER GENOMICS, CO JUN '25 – NOW

- Designed and developed algorithms for secondary analysis of high-throughput sequencing data, including variant and biomarker detection, aligned with clinical assay development and oncology applications.
- Spearheading efforts to develop a somatic variant caller in Rust.
- Developed a position-specific trinucleotide error model using low-AF observations as noise estimates, then applied binomial hypothesis testing to call somatic variants, achieving ~20x F1 improvement over existing approaches at AF < 0.07, with potential applications in clinical oncology and liquid biopsy.
- Optimized indel calling in germline TAPS Variant Caller (TVC), bringing F1 scores from ~.74 to ~.875 without compromising runtime. Github: https://github.com/watchmaker-genomics/TVC
- Collaboratively developed and integrated modules into a large-scale, production-grade Nextflow pipeline, with CI support, versioned testing, cloud profiles, and a scientist-facing UI. Collaborating via GitHub through pull requests, code reviews, and version-controlled development workflows.
- Evaluated clinical relevance of variant calls using cBioPortal and functional annotation tools to assess utility in oncology settings.
- Collaborated across wet-lab, marketing, customer support, and leadership teams to align goals and define scope.

GRADUATE STUDENT (STAJICH LAB), UNIVERSITY OF CALIFORNIA RIVERSIDE, CA SEP '22 – JUN '25

- Performed large-scale genomic and metagenomic analyses using Python and R, developing computational methods and statistical workflows applicable to NGS data interpretation, helping to unravel ancient evolutionary relationships between plants and fungi and publishing a first author article in New Phytologist (accepted) and a middle author paper in ISMEJ, along with a first author bioRxiv preprint.

- Designed sequencing workflows (Nanopore, Illumina) for fungal genome and metagenome analysis, generating 8 genomes and characterizing 10,000 taxa.

UNDERGRADUATE RESEARCH FELLOW (KAWATE LAB), CORNELL UNIVERSITY, NY MAY ‘21 – AUG ‘21

- Obtained first cryo-electron micrographs of plant membrane protein NPF3, which resulted in the first clear two-dimensional representations of the protein. Used Cryo-EM modeling software employing computer vision.

Preprints and Publications

1. **Kelly, K. H.,** Coleine, C., Coshland, C., & Stajich, J. E. (2026). Novel Glomeromycotina-Moss Associations Identified in California Dryland Biocrusts. *New Phytologist (accepted March 2026)*.
2. Ghotbi, M., Stajich, J. E., Dallas, J., Rurik, A., Cummins, C., Vargas-Gastélum, L., Ghotbi, M., Spatafora, J. W., **Kelly, K.**, Alexander, N. R., Moe, K. C., Syring, K. C., Shadmani, L., Perez-Marron, J., & Walker, D. M. (2025). Absolute abundance unveils Basidiobolus as a cross-domain bridge indirectly bolstering gut microbiome homeostasis. *ISME J*. https://academic.oup.com/ismej/article/19/1/wraf150/8209741
3. **Kelly K.,** Liu X.**,** Croyle J.., Stajich J. (2025) Increased aridity is associated with community shifts toward extreme adapted taxa and reduced diversity in the biocrust mycobiome of Southern California. BioRxiv: https://www.biorxiv.org/content/10.1101/2025.03.05.641731v1.abstract

Skills

Languages: Python, R, Rust, Bash

Bioinformatics: Variant calling (germline & somatic) secondary analysis, NGS analysis (Illumina, Nanopore), genome assembly & annotation, metagenomics, phylogenetics, methylation analysis.

Tools & Platforms: GATK/HaplotypeCaller, Mutect2, Nextflow, GitHub Actions, HPC/cloud computing

Statistics & ML: Binomial hypothesis testing, trinucleotide error modeling, Fisher's exact test, F1/precision-recall benchmarking, hidden Markov models, CNN development.

Wet Lab: NGS library preparation, qPCR, DNA amplification & purification

Training and Teaching Experience

NSF REU Mentor (2023), Microbiology TA (2024), Lead Peer Educator (2019–2022)

Education

University of California Riverside, Plant Pathology/Microbiology — Ph.D. (GPA 3.89)	**SEP ‘22 – NOV ‘25**
Fort Lewis College — B.S. (GPA 3.70)	**SEP ‘18 – MAY ‘22**

Honors and Activities

NSF ExFAB Biofoundry Research Fellow | Chancellor's Distinguished Fellow, UC Riverside | GAAN Fellow, UC Riverside | Volunteer firefighter, Indian Peaks Fire & Rescue