

## Kathryn Kananen

**Summary:** 5 years working experience, 2 post education, in bioinformatics and computational biology. My research interests include population genetics with a focus on structural variation, specifically transposable elements, in biomedical research and their relationship with treatments. Strong genetics background with a love for designing, solving biological problems, and exploring all parts of the research process. Combined with skills for workflow development, knowledge of computational tools, and ways to make new tools, I look forward to solving and improving medical treatments.

### Experience

#### OSTOR-ASTOR Project

2020-2022

- Lead developer on harmonization pipeline development.
  - RNASeq, WES, variant calling, annotation, Snakemake, pip, template management systems, docker, environment control,
  - Minor role in Keycloak and Kubernetes and setup
- Lead developer on visualization development and data management of ORIEN Avatar Project.
  - Pancancer genetic quality control, clinical data quality control and ingest, sequences quality control and ingest, cBioPortal development.
- Tool Development – Recontig.
- Research and analysis consults.
  - working with Nanopore reads, used EBV genome assembly with Nanopore.
- Daily work on remote cluster.

#### Hufford Labs

2015-2019

- Bioinformatics in maize populations.
  - Population structure, dynamic scripting, using computational tools for analysis.
- Programmed in Python, R, and Bash.
- Bi-Weekly presentations.
- Work with HPC system.
- Field and lab work.
  - DNA isolations, pollinations, phenotype measurements, etc.

### Education

#### MSc Applied Bioinformatics

Cranfield University

2019-2020

- *Group thesis* - Bulk Segregant Analysis software creation (Java)
- *Ind. Thesis* - R package expansion - VarGen
- Graduated with GPA 4.0

#### B.S. in Bioinformatics and Computational Biology

Iowa State University

2015-2019

#### Activities of interest

OVCN – Columbus

2022-Present

Study Abroad – Japan

2017-2018

Speaker's Bureau

2015 - 2018

Emerging Leadership Award

2016

## Other Qualifications

- Knowledge of multiple programming languages Python (6yrs), Bash (3.5yrs), R (2yr), and Java (1.5yrs).
- Works in Unix environment natively; works on Linux daily.
- Has working knowledge of HPC systems.
- Work on various gene-mapping techniques for software dev of statistical implementation.
- Worked with large genomic datasets (vcf, fasta, fastq, maf, etc). for the past 5years both academically and for research.
- Very used to data formatting, cleaning, and exploration using R and python.
- Is an advanced GitHub and git user.

## Literature

- Asad, S., Damicis, A., Heng, Y., Kananen, K., Collier, K., & Adams, E. et al. (2022). Association of Body Mass Index and Inflammatory Dietary Pattern with Breast Cancer Pathologic and Genomic Immunophenotype in the Nurses' Health Study. <https://doi.org/10.21203/rs.3.rs-1598621/v1>
- Asad, S., Kananen, K., Mueller, K., Symmans, W., Wen, Y., & Perou, C. et al. (2022). Challenges and Gaps in Clinical Trial Genomic Data Management. *JCO Clinical Cancer Informatics*, (6). <https://doi.org/10.1200/cci.21.00193>
- Hufnagel, D., Kananen, K., Glaubitz, J., de Jesús Sánchez-González, J., Doebley, J., & Hufford, M. (2021). Evidence for Multiple Teosinte Hybrid Zones in Central Mexico. <https://doi.org/10.1101/2021.02.11.430632>