

AAKARSH ANAND

☎ 408.813.0119 | ✉ aanand2@g.ucla.edu | 🏠 aakarsh-anand.github.io

OBJECTIVE

Large-scale machine learning and statistical modeling for high-dimensional data. Currently, I am working on applications of AI/ML in biomedical data, particularly to understand the genetic architecture of complex human traits and diseases. I have recently published in Genome Research and RECOMB 2024.

EDUCATION

Ph.D. in Computer Science

UCLA | Los Angeles, CA

Major Field: Artificial Intelligence

Minor Fields: Data Science Computing, Computational Systems Biology

Sep 2024 – Present

B.S. in Computer Science

UCLA | Los Angeles, CA

Sep 2020 – Jun 2024

EXPERIENCE

Research Assistant

Advisor: Sriram Sankararaman | UCLA

Jan 2022 – Present

- Devising self-supervised approaches for learning useful representations in high-dimensional time-series data (in progress)
- Developed a scalable algorithm for detecting pairwise interaction effects between genetic variants on a trait in biobank datasets (Genome Research, RECOMB 2024)
- Leveraged a randomized method of moments statistical framework to build an algorithm for efficient variance component estimation in biobank datasets (preprint)

Software Engineering Intern

LabCorp | Burlington, NC

Jun 2023 – Sep 2023

- Designed and implemented reproducible/efficient Snakemake pipelines to analyze adenovirus and phage genetic sequencing data

Research Intern

Bruins in Genomics Summer Program | UCLA

Jun 2022 – Sep 2022

- Applied interpretable machine learning strategies to improve understanding of non-linear models of genetic data

Research Assistant

Advisor: Paul Boutros | UCLA

Jan 2021 – Apr 2022

- Implemented new alignment method (HISAT2) in cancer sequencing pipeline and redesigned configuration file for ease of use
- Benchmarked pipeline performance in downstream tasks, created new documentation and diagrams

PUBLICATIONS

- Fu, B.*, Anand, P.*, **Anand, A.***, Mefford, J., & Sankararaman, S. (2024a). A scalable adaptive quadratic kernel method for interpretable epistasis analysis in complex traits. *Genome Research*.
<https://doi.org/10.1101/2024.03.09.584250>
- Fu, B., Pazokitoroudi, A., Xue, A., **Anand, A.**, Anand, P., Zaitlen, N., & Sankararaman, S. (2023a). A Biobank-scale test of marginal epistasis reveals genome-wide signals of polygenic epistasis. *bioRxiv*.
<https://doi.org/10.1101/2023.09.10.557084> (Pending submission to *ASHG* and *Nature Genetics*)

AWARDS

- Warren Alpert AI and Computational Biology Fellow Jun 2024
- Dean's Honors List | UCLA All quarters 2020 – 2023
- NSF REU Scholarship | Bruins in Genomics Aug 2022
- Andy Grove Intel Scholarship | Intel Aug 2020

TEACHING AND MENTORSHIP

Machine Learning Reader

Winter 2023, Winter 2024

Samueli School of Engineering | UCLA

- Provided feedback and grading on students' homework, projects, and exams in machine learning class (CS 146)

SKILLS

Languages Python, C++

Frameworks PyTorch, Sci-kit Learn, NumPy/Pandas, Git

Other Machine Learning, Statistics, Probabilistic Models, Deep Learning, Pipelines