Abhinav K. Adduri, aadduri@andrew.cmu.edu

ABOUT ME
My research interest is in applied deep learning and building and using foundation models to accelerate natural product discovery and drug discovery. I am currently a 5th year Ph.D. student in the Computational Biology Department at CMU. I have been advised by Dr. Hosein Mohimani for the past two years.

EDUCATION

Carnegie Mellon University   **Expected January 2025**

Ph.D. Computer Science / Computational Biology, GPA: 4.0

Ph.D. Minor Machine Learning (formerly secondary masters), GPA: 3.94

Teaching Assistant: 10-701 Machine Learning, 02-613 Algorithms and Advanced Data Structures

University of California, Berkeley   **May 2019**

B.A. Computer Science, GPA 3.8

B.A. Biochemistry and Molecular Biology, GPA 3.7

PROGRAMMING
Rust, Python, C++, Typescript, HTML, CSS, C, Java

TECHNOLOGIES
Linux, PyTorch, Git, React, Docker

PUBLICATIONS
Yan, D.*, Zhou, M.*, **Adduri, A.**, Guler, M., Liu, S., Shin, H., Kovach, T., Oh, G., Liu, X., Deng, Y., Cao, L., Behsaz, B., Mohimani, H. (Expected 2024). Seq2PKS: Discovering modular type I cis-AT polyketide natural products by integrating computational mass spectrometry and genome mining. *Manuscript awaiting final decision in Nature Communications.*

Adduri, A., Kim, S. (Expected 2024). Ornaments for accurate and efficient allele-specific expression estimation with bias correction. *Manuscript awaiting final decision in The American Journal of Human Genetics.* [ArXiv]

Mongia, M., Baral, R., **Adduri, A.**, Yan, D., Liu, Y., Bian, Y., Kim, P., Behsaz, B., Mohimani, H. (2023). AdenPredictor: Accurate prediction of the adenylation domain specificity of nonribosomal peptide biosynthetic gene clusters in microbial genomes. Bioinformatics, 39(Supplement 1), i40-i46.

Adduri, A. (2019). IoT integration in manufacturing processes. In Simulation for Industry 4.0: Past, Present, and Future (pp. 129-139).

Adduri, A., Schruben, L. (2017). The Tao of simulation. In 2017 Winter Simulation Conference (WSC) (pp. 607-616). IEEE.

PENDING PUBLICATIONS
Behsaz, B.*, **Adduri, A.**, Guler, M.*, Mohamed, O. G., Caraballo-Rodríguez, A. M., Duggan, B., Chaudhary, N., Miller, C., Liu, S., Krummenacher, B., Broders, K., Zamith-Miranda, D., Schultz, P. J., Sherman, D. H., Clement, J., Nakayasu, E., Nosanchuk, J., Dorrestein, P. C., Tripathi, A., Mohimani, H. (Expected 2024). Pathogen-oriented platform for large-scale natural product discovery identifies novel antifungal targeting drug-resistant candidiasis. *Manuscript in preparation for submission to Nature.*

Adduri, A., Donghui Y., McNutt, A., Mustafa, G, Chaitanya, S., Nan, F., Koes, D., Ashootosh, T., Hosein, M. (Expected 2024). Using protein language models for interpretable adenylation domain specificity prediction to discover novel type I polyketide and non-ribosomal peptide hybrids. *Manuscript in preparation for submission to Nature Methods.*

*Equal contribution.

ONGOING RESEARCH

NPDiscover   **January 2022 – Present**

- Developed algorithms and used protein language models to predict natural product structures with drug-like properties from microbial genomes
- Discovered a novel antifungal which displays promising mice model results against the multi-drug-resistant fungal pathogen *Candida Auris* (deemed an urgent threat by the CDC)
- Developed molecular structure clustering schemes to reduce the number of predicted drug candidates by 100x while retaining prediction quality

PLMs for interpretable A-domain specificity prediction   **August 2023 – Present**

- Used protein language models to improve small molecule binding prediction for adenylation (A-) domains, which recruit monomers into mature natural products
- Achieved state of the art performance and over 20% improvement in out-of-distribution generalization benchmark

Seq2Hybrid   **March 2023 − Present**

- Generalized previous approaches to predict hybrid natural product structures (e.g. non-ribosomal peptide and polyketide hybrid structures)
- Linked a microbial genome to the production of the immunosuppressants SW-163A and B

Ornaments   **May 2021 − August 2023**

- Developed *Ornaments*, a graph-based alignment tool for unbiased allele-specific read mapping. Improved runtime and accuracy over state of the art by 11.6x / 2x respectively

COURSEWORK

Relevant Graduate Coursework

10-701 Machine Learning, A	*10-707 Advanced Deep Learning, A*
10-708 Probabilistic Graphical Models, A	*36-705 Intermediate Statistics, A-*
02-730 Cellular & Systems Modeling, A	*02-710 Computational Genomics, A+*
10-725 Convex Optimization, A	*PT-2030 Intro to Computational Structural Biology, A+*

Relevant Undergraduate Coursework

CS 170 Efficient Algorithms, A-	*CS 162 Operating Systems, A-*
CS 186 Database Systems, A	*Math 110 Linear Algebra, A*
EE 120 Signals and Systems, A	*EE 123 Digital Signal Processing, A*
CS 189 Machine Learning, A	*EE 126 Probability and Random Processes, A*
CS 294 Machine Learning in Biology, A-	*CS 176 Algorithms in Computational Biology, A*

PREVIOUS
EXPERIENCE

Square / Caviar, San Francisco, CA

Data Science Engineer Intern   **May 2019 − August 2019**

- Improved recall / precision of chargeback fraud-detection models by 3.5x / 2.5x respectively
- Improved pre-checkout food delivery ETA predictions for restaurants

Rubrik, Palo Alto, CA

Software Developer Intern   **May 2018 − August 2018**

- Designed and implemented distributed cache system for filesystems team
- Designed RPCs to expose node cache space to other nodes in the same cluster

Mozilla, Portland, OR

Software Developer Intern   **May 2017 − August 2017**

- Designed and implemented Firefox Send, a tool for private, end-to-end encrypted file transfer
- Firefox Send was used globally and was covered by news outlets such as Forbes and TechRepublic

PATENTS

Automated Review of Source Code for Style Issues, Rubrik 2018

HONORS AND
AWARDS

CMU-Pitt Ph.D. in Computational Biology: Diversity, Equity and Inclusion Award
CMU SCS Graduate Student Service Award Winner

PAST
PROJECTS

Seqtools with Nir Yosef - A pipeline for processing ATAC-Seq and RNA-Seq data, 2018

Homolog Identification with Jennifer Doudna - Test and discern evolutionary origin for specific CRISPR mutations, 2017