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

EDUCATION

Carnegie Mellon University, Advised by Dr. Hosein Mohimani **August 2024**

Thesis: Algorithms for Natural Drug Discovery via Machine Learning and Microbial Genome Mining

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

Ph.D. Minor Machine Learning, GPA: 4.0

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

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+*

University of California, Berkeley **May 2019**

B.A. Computer Science, GPA 3.8

B.A. Biochemistry and Molecular Biology, GPA 3.7

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*

PROGRAMMING — Rust, Python, C++, Typescript / Javascript, HTML, CSS, C, Java

TECHNOLOGIES — Linux, Git, PyTorch, React, Docker

WORK EXPERIENCE

Carnegie Mellon University, Pittsburgh, PA

Ph.D. Candidate **August 2019 – Present**

- Developed machine learning methods and graph algorithms to predict novel peptide and polyketide drug structures from microbial genomes
- Discovered a novel antifungal drug which kills the multidrug-resistant pathogen *Candida auris*, which the CDC has labeled as an urgent threat
- Used protein language models and deep learning to improve small molecule binding prediction for a specific class of proteins. Improved accuracy in generalization benchmark by 20%
- 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
- Managed over 10 undergrad and Master's students and served on a Master's thesis committee
- Publications and more project details listed below

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

PUBLICATIONS   Yan, Donghui*, Muqing Zhou*, **Abhinav Adduri***, Mustafa Guler, Sitong Liu, Hyonyoung Shin, Torin Kovach, Gloria Oh, Xiao Liu, Yuting Deng, Liu Cao, Bahar Behsaz, and Hosein Mohimani. Seq2PKS: Discovering Modular Type I Cis-AT Polyketide Natural Products by Integrating Computational Mass Spectrometry and Genome Mining. *Manuscript under review for publication in Nature Communications.*

Adduri, Abhinav, and Seyoung Kim. Ornaments for Accurate and Efficient Allele-Specific Expression Estimation with Bias Correction. bioRxiv (2023): 2023-10. *Manuscript under review for publication in The American Journal of Human Genetics.*

Mongia, Mihir, Romel Baral, **Abhinav Adduri**, Donghui Yan, Yudong Liu, Yuying Bian, Paul Kim, Bahar Behsaz, and Hosein Mohimani. AdenPredictor: accurate prediction of the adenylation domain specificity of nonribosomal peptide biosynthetic gene clusters in microbial genomes. Bioinformatics 39, no. Supplement_1 (2023): i40-i46.

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

Adduri, Abhinav. IoT integration in manufacturing Processes. Simulation for Industry 4.0: Past, Present, and Future (2019): 129-139.

PENDING PUBLICATIONS   Behsaz, Bahar*, **Abhinav Adduri***, Mustafa Guler*, Osama G. Mohamed, Andrés Mauricio Caraballo-Rodríguez, Brendan Duggan, Nirmal Chaudhary, Cameron Miller, Sitong Liu, Benjamin Krummenacher, Kirk Broders, Daniel Zamith-Miranda, Pamela J. Schultz, David H. Sherman, Jason Clement, Ernesto Nakayasu, Joshua Nosanchuk, Peter C. Dorrestein, Ashootosh Tripathi, and Hosein Mohimani. Pathogen-Oriented Platform for Large-Scale Natural Product Discovery Identifies Novel Antifungal Targeting Drug-Resistant Candidiasis. *Manuscript in preparation for submission to Nature.*

Adduri, Abhinav, Donghui Yan, Mustafa Guler, Chaitanya Suraparaju, Nan Fang, Ashootosh Tripathi, and Hosein Mohimani. (Expected 2024). Seq2Hybrid: Discovering type I polyketide and non-ribosomal peptide hybrid natural products. *Manuscript in preparation for submission to Nature Communications.*

Adduri, Abhinav*, Andrew McNutt*, Chaitanya Suraparaju, Nan Fang, David Koes, and Hosein Mohimani. (Expected 2024). Protein foundation models for accurate and generalizable adenylation domain specificity prediction. *Manuscript in preparation for submission to NeurIPS.*

*Equal contribution.

ONGOING RESEARCH   **NPDiscover**   **January 2022 – Present**
- Developed machine learning methods and graph algorithms to predict non-ribosomal peptides (NRPs), a type of drug candidate naturally produced by bacteria and fungi
- Developed novel clustering and filtering techniques to reduce the number of predicted drug candidates by 100x while retaining prediction quality
- Used method to discover a novel antifungal drug which kills the multi-drug resistant *Candida Auris*
- Publication pending preclinical mice model results

Deep AdenPredictor   **March 2023 – Present**
- Used protein language models as foundation models to improve small molecule binding prediction for adenylation domains, which assemble natural drugs in microbes
- Achieved state of the art performance in normal benchmarks and over 20% improvement over state of the art in generalization benchmarks

Seq2Hybrid   **August 2023 – Present**
- Expanded previous approaches, which are are restricted to predicting a specific drug class (e.g. peptide drugs), to predict hybrid natural drugs (e.g. peptide + polyketide hybrid drugs)
- Used method to discover a natural producer for immunosuppressants SW-163A and B

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