

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

EDUCATION	Carnegie Mellon University , Advised by Dr. Hosein Mohimani August 2024 <i>Thesis: Algorithms for Natural Drug Discovery via Machine Learning and Microbial Genome Mining</i> <i>Ph.D. Computer Science / Computational Biology, GPA: 4.0</i> <i>Ph.D. Minor Machine Learning, GPA: 4.0</i> <i>Teaching Assistant: 10-701 Machine Learning, 02-613 Algorithms and Advanced Data Structures</i> Relevant Graduate Coursework <div>10-701 Machine Learning, A 10-708 Probabilistic Graphical Models, A 02-730 Cellular & Systems Modeling, A 10-725 Convex Optimization, A</div> <div>10-707 Advanced Deep Learning, A 36-705 Intermediate Statistics, A- 02-710 Computational Genomics, A+ PT-2030 Intro to Computational Structural Biology, A+</div>
	University of California, Berkeley May 2019 <i>B.A. Computer Science, GPA 3.8</i> <i>B.A. Biochemistry and Molecular Biology, GPA 3.7</i> Relevant Undergraduate Coursework <div>CS 170 Efficient Algorithms, A- CS 186 Database Systems, A EE 120 Signals and Systems, A CS 189 Machine Learning, A CS 294 Machine Learning in Biology, A-</div> <div>CS 162 Operating Systems, A- Math 110 Linear Algebra, A EE 123 Digital Signal Processing, A EE 126 Probability and Random Processes, A CS 176 Algorithms in Computational Biology, A</div>
PROGRAMMING	Rust, Python, C++, Typescript / Javascript, HTML, CSS, C, Java
TECHNOLOGIES	Linux, Git, PyTorch, React, Docker
WORK EXPERIENCE	Carnegie Mellon University , Pittsburgh, PA <i>Ph.D. Candidate</i> August 2019 – Present <ul style="list-style-type: none">Developed machine learning methods and graph algorithms to predict novel peptide and polyketide drug structures from microbial genomesDiscovered a novel antifungal drug which kills the multidrug-resistant pathogen <i>Candida auris</i>, which the CDC has labeled as an urgent threatUsed 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 <i>Ornaments</i>, a graph-based alignment tool for unbiased allele-specific read mapping. Improved runtime and accuracy over state of the art by 11.6x / 2x respectivelyManaged over 10 undergrad and Master's students and served on a Master's thesis committeePublications and more project details listed below Square / Caviar , San Francisco, CA <i>Data Science Engineer Intern</i> May 2019 – August 2019 <ul style="list-style-type: none">Improved recall / precision of chargeback fraud-detection models by 3.5x / 2.5x respectivelyImproved pre-checkout food delivery ETA predictions for restaurants Rubrik , Palo Alto, CA <i>Software Developer Intern</i> May 2018 – August 2018 <ul style="list-style-type: none">Designed and implemented distributed cache system for filesystems teamDesigned RPCs to expose node cache space to other nodes in the same cluster Mozilla , Portland, OR <i>Software Developer Intern</i> May 2017 – August 2017 <ul style="list-style-type: none">Designed and implemented Firefox Send, a tool for private, end-to-end encrypted file transferFirefox 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. <i>Manuscript under review for publication in Nature Communications</i> .
	Adduri, Abhinav , and Seyoung Kim. Ornaments for Accurate and Efficient Allele-Specific Expression Estimation with Bias Correction. <i>bioRxiv</i> (2023): 2023-10. <i>Manuscript under review for publication in The American Journal of Human Genetics</i> .
	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. <i>Bioinformatics</i> 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.
PENDING PUBLICATIONS	Adduri, Abhinav . IoT integration in manufacturing Processes. <i>Simulation for Industry 4.0: Past, Present, and Future</i> (2019): 129-139.
	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. <i>Manuscript in preparation for submission to Nature</i> .
	*Equal contribution.
ONGOING RESEARCH	NPDDiscover January 2022 – Present
	<ul style="list-style-type: none"> • 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 <i>Candida Auris</i> • Publication pending preclinical mice model results
	Deep AdenPredictor March 2023 – Present
	<ul style="list-style-type: none"> • 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
PAST PROJECTS	Seq2Hybrid August 2023 – Present
	<ul style="list-style-type: none"> • Expanded previous approaches, which 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