

Benjamin Kaminow

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EDUCATION

Memorial Sloan Kettering Cancer Center and Weill Cornell Medical College

Program: Tri-Institutional Program in Computational Biology and Medicine
Thesis Lab: John Chodera

New York, NY
July 2021-Present

The Johns Hopkins University

Major: Chemical and Biomolecular Engineering
Minor: Computer Science
GPA: 3.69
Major GPA: 3.88

Baltimore, MD
September 2015-May 2019

RESEARCH EXPERIENCE

The Chodera Lab, Memorial Sloan Kettering Cancer Center

Graduate Student

New York, NY
January 2022-Present

- Assessing the performance, data efficiency, and generalizability of structure-based graph neural networks in the task of predicting protein-ligand binding affinities
- Developing a framework for modularly adapting arbitrary neural network architectures for structure-based machine learning
- Supporting the drug discovery efforts of the AI-driven Structure-enabled Antiviral Platform through development of a computational chemistry software suite designed to assist at key stages of the drug discovery pipeline
- Conceptualizing and planning appropriately scoped projects for rotation graduate students and summer undergraduate interns, and mentoring these students during their time in the lab
- Implemented an alternative atom enumeration scheme in the Espaloma molecular machine learning model

The Dobin Lab, Cold Spring Harbor Laboratory

Computational Science Developer

Cold Spring Harbor, NY
June 2019-June 2021

- Evaluated functional effects of replacing the current reference genome with different consensus genomes using the 1000 Genomes Project
- Analyzed scRNA-seq data from Tabula Muris to find differential splicing usage
- Developed ConsDB, a Python package for facilitating the use of large databases of genome variation
- Analyzed ChIP-seq data from different maize tissues as a part of the MaizeCODE project, in order to better understand maize epigenetics

The Karchin Lab, Institute for Computational Medicine

Research Assistant

Baltimore, MD
June 2018-May 2019

- Developed an updated method of finding similar alleles to increase the accuracy of the MHCnuggets predictor on rare MHC alleles
- Explored and analyzed protein structure files to find new, biologically relevant features to add to the MHCnuggets machine learning model
- Generated predicted IC50 values using Python and Bash scripting to run the MHCnuggets pipeline
- Analyzed generated IC50 data using Python and R to perform Mann-Whitney U tests and generate Kaplan-Meier curves

The Betenbaugh Lab, Advanced Mammalian Biomanufacturing Innovation Center

Research Assistant

Baltimore, MD
January 2017-September 2018

- Developed an integrated platform to combine Flux Balance Analysis and glycosylation modeling technologies by writing a MATLAB script to convert FBA results into the appropriate format, and interface between MATLAB and Excel
- Performed *in silico* optimization experiments on Chinese hamster ovary cells using the COBRA Toolbox for MATLAB to improve cell culture growth medium
- Utilized the COBRApy toolbox and high-performance computing to perform sampling experiments on Genome Scale Models in order to increase understanding of cell amino acid needs

The Schulman Lab, Institute for NanoBioTechnology

Research Assistant

Baltimore, MD
March 2016-January 2017

- Quantitated and analyzed data from experiments pertaining to the degree of swelling of DNA-crosslinked hydrogels
- Designed experiments to measure and quantitate the extent of polymerization of DNA-crosslinked hydrogels in order to better understand the chemical properties of the system

PUBLICATIONS AND CONFERENCE PRESENTATIONS

Boby, M. L., Fearon, D., Ferla, M., Mihajlo, F., Koekemoer, L., Robinson, M. C., **The COVID Moonshot Consortium**, Chodera, J. D., Lee, A., London, N., von Delft, A., von Delft, F. (2023). Open science discovery of potent noncovalent SARS-CoV-2 main protease inhibitors. *Science*, 382(6671). <https://doi.org/10.1126/science.abo7201>

Wang, Y., Fass, J., **Kaminow, B.**, Herr, J. E., Rufa, D., Zhang, I., Pulido, I., Henry, M., Bruce Macdonald, H. E., Takaba, K., Chodera, J. D. (2022). End-to-end differentiable construction of Molecular Mechanics Force Fields. *Chemical Science*, 13(41), 12016–12033. <https://doi.org/10.1039/d2sc02739a>

Kaminow, B., Ballouz, S., Gillis, J., Dobin, A. (2022). Pan-human consensus genome significantly improves the accuracy of RNA-seq analyses. *Genome Research*, 32(4), 738-749. <https://doi.org/10.1101/gr.275613.121>

Shao, X. M., Bhattacharya, R., Huang, J., Sivakumar, I. A., Tokheim, C., Zheng, L., Hirsch, D., **Kaminow, B.**, Om-dahl, A., Bonsack, M., Riemer, A., Velculescu, V., Anagnostou, V., Pagel, K., Karchin, R. (2019). High-Throughput Prediction of MHC Class I and II Neopeptides with MHCnuggets. *Cancer Immunology Research*, 8(3), 396-408. <https://doi.org/10.1158/2326-6066.CIR-19-0464>

Kaminow, B., Yunusov, D., Blibaum, A., Dobin, A. (2020, November 4-6). *STARsolo—Ultra-fast comprehensive single-cell RNA-seq quantification beyond gene expression* [Poster Presentation]. Biological Data Science (Virtual), Cold Spring Harbor, NY.

Kaminow, B., Ballouz, S., Gillis, J., Dobin, A. (2019, November 6-9). *Creating pan-human and population-specific consensus representations of the reference genome and assessing their effect on functional genomic data analysis* [Oral Presentation]. Genome Informatics, Cold Spring Harbor, NY.

TEACHING EXPERIENCE

Foundations of Computational Biology and Bioinformatics

Baltimore, MD

Teaching Assistant

January 2019-May 2019

- Assisted in planning of lectures and practical assignments
- Led weekly two-hour practical programming sessions for around 40 undergraduate and graduate students
- Mentored students through an original final project
- Automated the process of grading homework assignments by creating Bash scripts

Peer Led Team-Learning Academic Support Group

Baltimore, MD

Physics I Head PILOT Leader

September 2017-January 2019

- Acted as a liaison between other Physics I PILOT Leaders and our supervisor
- Facilitated meetings with 5-10 other Physics I PILOT Leaders once a week for two hours
- Led problem-solving sessions for 10-15 undergraduate students in Physics I one-two times a week for two hours each

LEADERSHIP ROLES

Tri-I Program in Computational Biology and Medicine

New York, NY

Social Chair

January 2022-September 2023

- Acted as an ambassador for prospective students
- Organized social events within the program and with other PhD programs
- Interacted with program administration to manage a budget

JHU Rockhoppers Climbing Team

Baltimore, MD

Team President

September 2015-May 2019

- Created programming for and led team practices and training sessions
- Organized team climbing trips, including transportation to and registration for competitions

HONORS AND AWARDS

NSF Graduate Research Program

2023

Dean's List

Fall 2015-Spring 2016, Spring 2017-Spring 2019

Graduated from Johns Hopkins University with General Honors and Departmental Honors

2019

Joseph L. Katz award for excellence in the Chemical and Biomolecular Engineering Senior Lab course

2019

NOTABLE TECHNICAL SKILLS

Computational chemistry; Machine learning; Protein modeling; Molecular dynamics; Scientific computing; Data visualization; Linux; High-performance computing; Python; Git; R; Rust; C++; Java; MATLAB; C