

# Samuel Sledzieski

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RESEARCH			
	<b>Flatiron Institute</b>		<b>New York, NY</b>
	Flatiron Research Fellow, Center for Computational Biology	Sep 2024 – Present	
	<b>Princeton University</b>	<b>Princeton, NJ</b>	
	Visiting Research Collaborator, Lewis-Sigler Institute for Integrative Genomics	Sep 2024 – Present	
	<b>Massachusetts Institute of Technology</b>	<b>Cambridge, MA</b>	
	Research Assistant, Computation and Biology Group	Feb 2020 – Aug 2024	
	<b>Centre Scientifique de Monaco</b>	<b>Monaco</b>	
	Visiting Researcher	Jan 2024 – Feb 2024	
	<b>Serinus Biosciences</b>	<b>Cambridge, MA</b>	
	Consultant	Feb 2023 – Dec 2023	
	<b>Microsoft Research</b>	<b>Redmond, WA</b>	
	Research Intern, AI For Good Lab	May 2023 – Oct 2023	
	<b>Cellarity</b>	<b>Cambridge, MA</b>	
	Machine Learning Intern, Perturbation Biology Group	May 2021 – Aug 2021	
	<b>MIT Lincoln Laboratory</b>	<b>Lexington, MA</b>	
	Summer Research Program, Advanced Lasercom Systems Group	May 2019 – Aug 2019	
	<b>University of Connecticut</b>	<b>Storrs, CT</b>	
	Undergraduate Research Assistant, Computational Biology Lab	Jan 2017 – May 2019	
	Software Developer, Jackson Laboratory for Genomic Medicine	Aug 2018 – May 2019	
	Undergraduate Research Assistant, Nelson Lab	Oct 2015 – Dec 2016	
EDUCATION			
	<b>Massachusetts Institute of Technology</b>	<b>Cambridge, MA</b>	
	PhD, Computer Science	2019 – 2024	
	• Minor in Biological Engineering		
	• Concentration: Protein language models, protein and drug interactions, protein structure		
	• Advisor: Dr. Bonnie Berger		
	SM, Electrical Engineering and Computer Science	2019 – 2021	
	<b>University of Connecticut</b>	<b>Storrs, CT</b>	
	BS, Computer Science	2015 – 2019	
	• Minor in Molecular and Cellular Biology		
	• Concentration: Bioinformatics, Data Science		
	• Advisor: Dr. Mukul Bansal		
	• Magna Cum Laude, Honors Scholar		
TEACHING			
	<b>Massachusetts Institute of Technology</b>	<b>Cambridge, MA</b>	
	Teaching Assistant, Intro to Deep Learning (6.S191)	Winter 2021, 2022, 2023	
	Teaching Assistant, Machine Learning in Genomics (6.878)	Fall 2021	
	<b>University of Connecticut</b>	<b>Storrs, CT</b>	
	Teaching Assistant, Theory of Computation	Spring 2018	
JOURNAL			
	[11] Ullanat, Jing, <b>Sledzieski</b> , Berger, “Learning the language of protein-protein interactions,” <i>Nature Communications</i> , In Press, 2025.		

- [10] Schäffer, **Sledzieski**, Cowen, Berger, “Memory-efficient, accelerated protein interaction inference with Blocked, Multi-GPU D-SCRIPT,” *Bioinformatics*, 41(10):btaf564, 2025.
- [9] Kshirsagar, Meller, Humphreys, **Sledzieski**, Xu, Dodhia, Horvitz, Berger, Bowman, Lavista Ferres, Baker, Baek, “Rapid and accurate prediction of protein homo-oligomer symmetry,” *Nature Communications*, 16(2017), 2025.
- [8] Singh, Im, Qiu, Macnke, Gupta, Sorenson, **Sledzieski**, Erlach, Wendt, Nanfack, Bryson, Berger, “Learning the language of antibody hypervariability,” *Proceedings of the National Academy of Sciences*, 122(1):e2418918121, 2024.
- [7] **Sledzieski**, Kshirsagar, Baek, Berger, Dodhia, Lavista Ferres, “Democratizing protein language models with parameter-efficient fine-tuning,” *Proceedings of the National Academy of Sciences*, 121(26):e2405840121, 2024.
- [6] **Sledzieski\***, Devkota\*, Singh, Cowen, Berger, “TT3D: Leveraging pre-computed protein sequence models to predict protein-protein interactions,” *Bioinformatics*, 39(11):btad663, 2023.
- [5] Singh\*, **Sledzieski\***, Bryson, Cowen, Berger, “Contrastive learning in protein language space predicts interactions between drugs and protein targets,” *Proceedings of the National Academy of Sciences*, 120(24):e2220778120, 2023.
- [4] Kumar, Brenner, **Sledzieski**, Olaosebikan, Lynn-Goin, Putnam, Yang, Lewinski, Singh, Daniels, Cowen, Klein-Seetharaman, “Transfer of knowledge from model organisms to evolutionarily distant non-model organisms: The coral Pocillopora damicornis membrane signaling receptome,” *Plos one*, 18(2):e0270965, 2023.
- [3] Zaman\*, **Sledzieski\***, Wu, Bansal, “virDTL: Viral recombination analysis through phylogenetic reconciliation and its application to sarbecoviruses and SARS-CoV-2,” *J Comput Biol*, 30(1):3–20, 2023.
- [2] Singh\*, Devkota\*, **Sledzieski**, Berger, Cowen, “Topsy-Turvy: integrating a global view into sequence-based PPI prediction,” *Bioinformatics*, 38(Supplement 1):i264-i272, 2022.
- [1] **Sledzieski\***, Singh\*, Cowen, Berger, “D-SCRIPT translates genome to phenotype with sequence-based, structure-aware, genome-scale predictions of protein-protein interactions,” *Cell Systems*, 12(10):969-982, 2021.

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**CONFERENCE AND WORKSHOPS**

- [7] Ocitti, Versavel, **Sledzieski**, Cowen, “RDS: A ReCIPE for overlapping community detection in biological networks,” *ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, 2025.
- [6] **Sledzieski**, Versavel, Singh, Ocitti, Devkota, Kumar, Shhpilker, Roger, Yang, Lewinski, Putnam, Berger, Klein-Seetharaman, Cowen, “Decoding the functional interactome of non-model organisms with PHILHARMONIC,” *Conference on Research in Computational Molecular Biology (RECOMB)*, 2025.
- [5] **Sledzieski**, Kshirsagar, Baek, Berger, Dodhia, Lavista Ferres, “Parameter-efficient fine-tuning of protein language models improves prediction of protein-protein interactions,” *Machine Learning for Structural Biology Workshop at NeurIPS*, 2023.
- [4] **Sledzieski\***, Singh\*, Cowen, Berger, “Contrasting drugs from decoys,” *Machine Learning for Structural Biology Workshop at NeurIPS*, 2022.
- [3] **Sledzieski\***, Singh\*, Cowen, Berger, “Adapting protein language models for rapid drug-target interaction prediction,” *Machine Learning for Structural Biology Workshop at NeurIPS*, 2021.
- [2] **Sledzieski\***, Singh\*, Cowen, Berger, “Sequence-based prediction of protein-protein interactions: a structure-aware interpretable deep learning model,” *Conference on Research in Computational Molecular Biology (RECOMB)*, 2021.
- [1] **Sledzieski\***, Zhang, Mandoiu, Bansal, “TreeFix-TP: Phylogenetic error correction for accurate reconstruction of viral transmission networks,” *Pacific Symposium on Biocomputing (PSB)*, 2021.

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**PREPRINTS**

- [3] **Sledzieski**, Hanson, “RocketSHP: Ultra-fast proteome-scale prediction of protein dynamics,” *bioRxiv*, 2025. 10.1101/2025.06.12.659353.

- [2] Vizgaudis, Kumar, Olaosebikan, Roger, Brenner, **Sledzieski**, Yang, Lewinski, Singh, Daniels, Cowen, Klein-Seetharaman, "Insulin Signaling and Pharmacology in Corals," *Authorea Preprints*, 2024. 10.22541/au.170666200.07483513/v1.
- [1] Kousi, Boix, Park, Mathys, **Sledzieski**, Peng, Bennett, Tsai, Kellis, "Single-cell mosaicism analysis reveals cell-type-specific somatic mutational burden in Alzheimers Dementia," *bioRxiv*, 2022. 10.1101/2022.04.21.489103.

<b>PRESENTATIONS</b>	Machine Learning in Computational Biology (MLCB) Cold Spring Harbor Laboratory Meeting on Network Biology Biophysical Society Annual Meeting (BPS) Intelligent Systems for Molecular Biology (ISMB) Machine Learning in Structural Biology (MLSB) Workshop at NeurIPS Research on Computational Molecular Biology (RECOMB) Pacific Symposium on Biocomputing (PSB) IEEE ICCABS Workshop on Computational Advances for Next Generation Sequencing UConn Fall Frontiers in Undergraduate Research University of Connecticut Bioinformatics Seminar	Sep 2025 Mar 2021, Mar 2023, Mar 2025 Jan 2025 Jul 2022, Jul 2023, Jul 2024 Dec 2021, Dec 2022, Dec 2023 Apr 2019, May 2022, Apr 2025 Jan 2021 Oct 2018 Oct 2018 Mar 2018, Oct 2018
<b>AWARDS &amp; FELLOWSHIPS</b>	Flatiron Postdoctoral Research Fellowship National Science Foundation (NSF) Graduate Research Fellowship First Place, MIT Intro to Deep Learning Final Project Competition New England Scholar, University of Connecticut Dean's List, College of Liberal Arts and Sciences, School of Engineering Academic Excellence Scholarship, University of Connecticut National Merit Scholarship Finalist	2024 - 2026 2021 - 2024 2020 2017 – 2019 2015 – 2019 2015 – 2019 2014
<b>SOFTWARE</b>	<b>D-SCRIPT</b> 65k+ PyPI downloads <b>ConPLex</b> 27k+ PyPI downloads <b>PHILHARMONIC</b> 5k+ PyPI downloads <b>virDTL</b> <b>TreeFix-TP</b>	<a href="https://github.com/samsledje/D-SCRIPT">https://github.com/samsledje/D-SCRIPT</a> <a href="https://github.com/samsledje/ConPLex">https://github.com/samsledje/ConPLex</a> <a href="https://github.com/samsledje/phiharmonic">https://github.com/samsledje/phiharmonic</a> <a href="https://github.com/suz11001/virDTL">https://github.com/suz11001/virDTL</a> <a href="https://github.com/samsledje/TreeFix-TP">https://github.com/samsledje/TreeFix-TP</a>
<b>MENTORING</b>	MIT Undergraduate Research Opportunities Program (UROP) Advisor MIT Research Summer Institute (RSI) Advisor HackMIT Mentor	2021 – 2024 2022 – 2023 2019 – 2022
<b>PEER REVIEW</b>	<i>Nature, Nature Methods, Nature Communications, Nature Biotechnology, Current Opinions in Structural Biology, Bioinformatics, Genome Biology, Journal of Computational Biology, PLOS Computational Biology, IEEE Transactions on Artificial Intelligence, NeurIPS, Machine Learning in Structural Biology (MLSB), RECOMB, ISMB</i>	

[CV compiled on 2025-12-15]