

# Matthew N. Bernstein

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Morgridge Institute for Research  
Regenerative Biology Group  
Madison, WI 53715

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Education	<b>University of Wisconsin - Madison</b> Ph.D., Computer Sciences Advisor: Colin Dewey, Ph.D.	Madison, WI Aug. 2019
	<b>University of Wisconsin - Madison</b> M.S., Computer Sciences	Madison, WI Dec. 2015
	<b>University of Notre Dame</b> B.S., Computer Science	South Bend, IN May 2013
Experience	<b>Morgridge Institute for Research</b> Postdoctoral Fellow Advisors: Christina Kendzierski, Ph.D. Ron Stewart, Ph.D.	Madison, WI 2019 - Present
	<b>University of Wisconsin - Madison</b> Research Assistant Advisor: Colin Dewey, Ph.D.	Madison, WI 2014 - 2019
	<b>Amazon</b> Software Development Engineering Intern	Seattle, WA Summer 2014
	<b>University of Wisconsin - Madison</b> Teaching Assistant (Lecturer) Course taught: CS302 - Introduction to Programming	Madison, WI Fall 2013, Spring 2014
	<b>Amazon</b> Software Development Engineering Intern	New York City, NY Summer 2013
	<b>Space and Naval Warfare Systems Command</b> Research Intern	San Diego, CA Summer 2012
	<b>NIH/BD2K Young Investigator Travel Scholarship</b> International Conference on Intelligent Systems for Molecular Biology Chicago, IL, July 6-10, 2018	
Awards and Fellowships		

**Best Plenary Talk**

National Library of Medicine Informatics Training Conference  
San Diego, CA, June 6, 2017

**CIBM Training Program**

University of Wisconsin - Madison  
Feb. 2015 - Feb. 2018

**University Housing Honored Instructor Award**

University of Wisconsin – Madison  
Fall 2013

**Professional Memberships**

International Society for Computational Biology  
Upsilon Pi Epsilon  
Tau Beta Pi

**Peer-reviewed Publications**

**Bernstein, M.N.**, Doan, A., Dewey, C.N. (2017). MetaSRA: normalized human sample-specific metadata for the Sequence Read Archive. *Bioinformatics*, 33(18), 2914–2923.

**Pre-prints**

**Bernstein, M.N. et al.** (2020). Jupyter notebook-based tools for building structured datasets from the Sequence Read Archive. *F1000Research*, 9:376

**Bernstein, M.N.** and Dewey, C.N. (2019). Hierarchical cell type classification using mass, heterogeneous RNA-seq data from human primary cells. *bioRxiv*.

**Talks and Seminars**

**Guest lecture for STAT 877 - Statistical Methods for Molecular Biology**  
*Cellular phenotyping with public, heterogeneous RNA-seq data*  
University of Wisconsin - Madison, Feb. 7, 2019

**International Conference on Intelligent Systems for Molecular Biology**  
*MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive*  
Chicago, IL, July 7, 2018

**Center for Predictive Computational Phenotyping Annual Retreat**  
*Cellular phenotyping with mass, heterogeneous transcriptomic data*  
Madison, WI, May 31, 2018

**Computation and Informatics in Biology and Medicine Seminar**  
*Towards cell type prediction with public RNA-seq data*  
University of Wisconsin - Madison, January 30, 2018

**National Library of Medicine Informatics Training Conference**  
*MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive*  
San Diego, CA, June 6, 2017

**Center for Predictive Computational Phenotyping Annual Retreat**  
*MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive*  
Madison, WI, June 1, 2017

Poster  
Presentations

**Great Lakes Bioinformatics Conference**  
Madison, WI, May 19-22, 2019

**RNA-Seq Summit**  
San Francisco, CA, April 25-27, 2017

**National Library of Medicine Informatics Training Conference**  
Columbus, OH, June 27-28m 2016

Undergraduate  
Mentorship

Aparna Maddala (Georgia Institute of Technology)  
Integrated Biological Sciences Summer Research Program, Summer 2019  
Project: *Hierarchical deconvolution of bulk RNA-seq data in the MetaSRA*

Brett VanTassel (Ramapo College of New Jersey)  
Integrated Biological Sciences Summer Research Program, Summer 2017  
Project: *Compression of RNA-seq alignments*

Kevin Liao (University of North Carolina at Chapel Hill)  
Integrated Biological Sciences Summer Research Program, Summer 2016  
Project: *Comparing similarity measures over RNA-seq derived gene expression profiles*

Teaching

**CS 302 - Introduction to Programming**  
University of Wisconsin - Madison, Fall 2013 & Spring 2014  
Teaching Assistant (primary lecturer to class of approximately 30 students)

Service

**Journal Reviewer:** Nature Biotechnology, Bioinformatics,  
BMC Bioinformatics

**Committee Member, Prospective Student Welcome Weekend**  
Department of Computer Sciences, University of Wisconsin - Madison,  
Spring 2016 & Spring 2014

**Committee Chair, Prospective Student Welcome Weekend**  
Department of Computer Sciences, University of Wisconsin - Madison,  
Spring 2015

**Club Leader, After School Computer Programming Club**  
Stephen's Point Elementary School, Madison, WI, Spring 2015

Professional  
Activities

**Team Lead, NCBI's Single-cell in the Cloud Codeathon**  
New York Genome Center, NY, January 15-17, 2020

**Team Lead, NCBI's RNA-Seq in the Cloud Codeathon**  
University of North Carolina at Chapel Hill, NC, March 11-13, 2019