

# Matthew N. Bernstein

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Morgridge Institute for Research  
Regenerative Biology Group  
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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. <i>Magna Cum Laude</i> , 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 Predoctoral Fellowship**

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**

† corresponding  
author

**Bernstein, M.N.**, Ma, J., Gleicher, M., Dewey, C.N. (2021).

Cello: Comprehensive and hierarchical cell type classification of human cells with the Cell Ontology. *iScience*, 24(1), 101913.

Overmyer, K.A., Shishkovaa, E., Miller, I.J., Balnisa, J., **Bernstein, M.N.**, Peters-Clarke, T.M., Meyer, J.G., Quan, Q., Muehlbauer, L.K., Trujillo1, E.A., He1, Y., Chopra, A., Chieng, H.C., Anupama Tiwari, A., Judson, M.A., Paulson, B., Brademan, D.R., Zhu, Y., Serrano, L.R., Linke, V., Drake, L.A., Adam, A.P., Schwartz, B.S., Singer, H.A., Swanson, S., Mosher, D.F., Stewart, R., Coon, J.J., Jaitovich, A. (2021). Large-scale Multi-omic Analysis of COVID-19 Severity. *Cell Systems*, 12(1), 23-40.

**Bernstein, M.N.**†, Gladstein, A., Latt, K.Z., Clough, E., Busby, B., Dillman, A. (2020). Jupyter notebook-based tools for building structured datasets from the Sequence Read Archive. *F1000Research*, 9(376).

**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.

**Submitted  
Manuscripts**

**Bernstein, M.N.**, Ni, Z., Collins, M., Burkard, M.E., Kendzierski, C., Stewart, R. (2020). CHARTS: A web application for characterizing and comparing tumor subpopulations in publicly available single-cell RNA-seq datasets. *bioRxiv*.

Simonett, S.P., Shin, S., Bacher, R., Dong, C., Smith, L., Rabaglia, M., Stapleton, D., Schueler, K., Choi, J., **Bernstein, M.N.**, Perez-Cervantes, C., Herring, J., Spaeth, J., Stein, R., Tessem, J., Kendzierski, C., Keles, S., Moskowitz, I., Attie, A., Keller, M. (2020). Identification of direct transcriptional targets of Nfatc2 that promote  $\beta$ -cell proliferation in human islets.

Talks and  
Seminars

**Workshop on Computational Advances for Single-Cell Omics  
Data Analysis (CASCODA)**

*CellO: Comprehensive and hierarchical cell type classification of human cells  
with the Cell Ontology*

Virtual, Dec. 12, 2020

**International Conference on Intelligent Systems for Molecular  
Biology (ISMB)**

*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

**Cold Spring Harbor Laboratory conference on Biological Data Science**

Virtual, Nov. 4-6, 2020

**International Conference on Intelligent Systems for Molecular Biology**

Virtual, July 13-16, 2020

**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

**Guest lecture for STAT 877 - Statistical Methods for Molecular Biology**  
*Visualizing high dimensional data with dimensionality reduction*  
University of Wisconsin - Madison, Sept. 22, 2020

**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

**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:** Bioinformatics, BMC Bioinformatics,  
Journal of Computational Biology, Nature Biotechnology,  
Nature Communications

**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