Matthew N. Bernstein

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Regenerative Biology Group
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Education		
	University of Wisconsin - Madison	Madison, WI
	Ph.D., Computer Sciences	Aug. 2019
	Advisor: Colin Dewey, Ph.D.	
	University of Wisconsin - Madison	Madison, WI
	M.S., Computer Sciences	Dec. 2015
	University of Notre Dame	South Bend, IN
	B.S., Computer Science	May 2013

Experience		
	Morgridge Institue for Research	Madison, WI
	Postdoctoral Fellow	2019 - Present
	Advisors: Christina Kendziorski, Ph.D.	
	Ron Stewart, Ph.D.	
	University of Wisconsin - Madison	Madison, WI
	Research Assistant	2014 - 2019
	Advisor: Colin Dewey, Ph.D.	
	Amazon	Seattle, WA
	Software Development Engineering Intern	Summer 2014
	University of Wisconsin - Madison	Madison, WI
	Teaching Assistant (Lecturer)	Fall 2013, Spring 2014
	Course taught: CS302 - Introduction to Programming	
	Amazon	New York City, NY
	Software Development Engineering Intern	Summer 2013
	Space and Naval Warfare Systems Command	San Diego, CA
	Research Intern	Summer 2012

Awards and Fellowships	
	NIH/BD2K Young Investigator Travel Scholarship
	International Conference on Intelligent Systems for Molecular Biology
	Chicago, IL, July 6-10, 2018

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

Publications
† corresponding
author

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.

Pre-prints

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

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. (2020). Large-scale Multi-omic Analysis of COVID-19 Severity. *medRxiv*.

Bernstein, M.N., Ma, J., Gleicher, M., Dewey, C.N. (2020).
CellO: Comprehensive and hierarchical cell type classification of human cells with the Cell Ontology. *bioRxiv*.

Talks and
Seminars

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

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, Nature Biotechnology
	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