

Matthew N. Bernstein

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

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

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

	<p>National Library of Medicine Informatics Training Conference <i>MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive</i> San Diego, CA, June 6, 2017</p> <p>Center for Predictive Computational Phenotyping Annual Retreat <i>MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive</i> Madison, WI, June 1, 2017</p>
Poster Presentations	<p>International Conference on Intelligent Systems for Molecular Biology Virtual, July 13-16, 2020</p> <p>Great Lakes Bioinformatics Conference Madison, WI, May 19-22, 2019</p> <p>RNA-Seq Summit San Francisco, CA, April 25-27, 2017</p> <p>National Library of Medicine Informatics Training Conference Columbus, OH, June 27-28m 2016</p>
Undergraduate Mentorship	<p>Aparna Maddala (Georgia Institute of Technology) Integrated Biological Sciences Summer Research Program, Summer 2019 Project: <i>Hierarchical deconvolution of bulk RNA-seq data in the MetaSRA</i></p> <p>Brett VanTassel (Ramapo College of New Jersey) Integrated Biological Sciences Summer Research Program, Summer 2017 Project: <i>Compression of RNA-seq alignments</i></p> <p>Kevin Liao (University of North Carolina at Chapel Hill) Integrated Biological Sciences Summer Research Program, Summer 2016 Project: <i>Comparing similarity measures over RNA-seq derived gene expression profiles</i></p>
Teaching	<p>Guest lecture for STAT 877 - Statistical Methods for Molecular Biology <i>Visualizing high dimensional data with dimensionality reduction</i> University of Wisconsin - Madison, Sept. 22, 2020</p> <p>Guest lecture for STAT 877 - Statistical Methods for Molecular Biology <i>Cellular phenotyping with public, heterogeneous RNA-seq data</i> University of Wisconsin - Madison, Feb. 7, 2019</p> <p>CS 302 - Introduction to Programming University of Wisconsin - Madison, Fall 2013 & Spring 2014 Teaching Assistant (primary lecturer to class of approximately 30 students)</p>
Service	<p>Journal Reviewer: Bioinformatics, BMC Bioinformatics, Nature Biotechnology</p>

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