

MATTHEW N. BERNSTEIN

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EDUCATION

Ph.D., Computer Sciences University of Wisconsin – Madison	Aug. 2019 Madison, WI
M.S., Computer Sciences University of Wisconsin – Madison	Dec. 2015 Madison, WI
B.S. <i>Magna Cum Laude</i>, Computer Science University of Notre Dame	May 2013 South Bend, IN

WORK EXPERIENCE

Postdoctoral Fellow Morgridge Institute for Research • Advised by Christina Kendziorski, Ph.D. and Ron Stewart, Ph.D.	2019 – Present Madison, WI
Research Assistant University of Wisconsin – Madison • Advised by Colin Dewey, Ph.D.	2014 - 2019 Madison, WI
Software Development Engineering Intern Amazon	Summer 2014 Seattle, WA
Teaching Assistant (Lecturer) University of Wisconsin – Madison	2013 - 2014 Madison, WI
Software Development Engineering Intern Amazon	Summer 2013 New York, NY
Research Intern Space and Naval Warfare Systems Command (SPAWAR)	Summer 2012 San Diego, CA

AWARDS AND FELLOWSHIPS

NIH/BD2K Young Investigator Travel Scholarship International Conference on Intelligent Systems for Molecular Biology	July 6-10, 2018 Chicago, IL
Best Plenary Talk National Library of Medicine Informatics Training Conference	June 6, 2017 San Diego, CA
CIBM Predoctoral Fellowship University of Wisconsin – Madison	2015-2018 Madison, WI
University Housing Honored Instructor Award University of Wisconsin – Madison	Fall 2013 Madison, WI

PEER-REVIEWED PUBLICATIONS

† corresponding author, ‡ co-second author

1. Nimkulrat, S.D., **Bernstein, M.N.**, Ni, Z., Brown, J., Kendziorski, C., Blum, B. (2021). The Anna Karenina model of β -cell maturation in development and their dedifferentiation in type 1 and type 2 diabetes. *Diabetes* (In Press).

2. **Bernstein, M.N.**, Ni, Z., Collins, M., Burkard, M.E., Kendziorski, C., Stewart, R. (2021). CHARTS: A web application for characterizing and comparing tumor subpopulations in publicly available single-cell RNA-seq datasets. *BMC Bioinformatics*. 22(83).
3. **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.
4. Overmyer, K.A., Shishkova, E., Miller, I.J., Balnisa, J., **Bernstein, M.N.** ‡, Peters-Clarke, T.M. ‡, Meyer, J.G. ‡, Quan, Q., Muehlbauer, L.K., Trujillo, E.A., Hei, 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.
5. **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).
6. **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

1. **Bernstein, M.N.** †, Dewey, C.N. (2021). Annotating cell types in human single-cell RNA-seq data with CellO. Manuscript under revision at *STAR Protocols*.
2. 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., Kendziorski, C., Keles, S., Moskowitz, I., Attie, A., Keller, M. (2020). Identification of direct transcriptional targets of Nfatc2 that promote β -cell proliferation in human islets. Manuscript under revision at *The Journal of Clinical Investigation*.

IN PREPARATION

1. **Bernstein, M.N.**, Ni, Z., Mohanty, C., Stewart, R., Newton, M., Kendziorski, C. SpatialCorr: Identifying gene sets with spatially varying correlation structure.

TALKS AND SEMINARS

Computation and Informatics in Biology and Medicine Seminar (UW-Madison) <i>Unleashing the untapped potential of public genomics data</i>	March 23, 2021 Virtual
Workshop on Computational Advances for Single-Cell Omics Data Analysis <i>CellO: Comprehensive and hierarchical cell type classification of human cells with the Cell Ontology</i>	Dec. 12, 2020 Virtual
International Conference on Intelligent Systems for Molecular Biology (ISMB) <i>MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive</i>	July 7, 2018 Chicago, IL
Center for Predictive Computational Phenotyping Annual Retreat <i>Cellular phenotyping with mass, heterogeneous transcriptomic data</i>	May 31, 2018 Madison, WI
Computation and Informatics in Biology and Medicine Seminar (UW-Madison) <i>Towards cell type prediction with public RNA-seq data</i>	Jan. 30, 2018 Madison, WI
Center for Predictive Computational Phenotyping Annual Retreat <i>MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive</i>	June 1, 2017 Madison, WI

POSTER PRESENTATIONS

Great Lakes Bioinformatics Conference	Virtual, May 11-13, 2021
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, Apr. 25-27, 2017
National Library of Medicine Informatics Training Conference	Columbus, OH, June 27-28 2016

UNDERGRADUATE MENTORSHIP

Aparna Maddala (Georgia Institute of Technology)	Summer 2019
<ul style="list-style-type: none">• Integrated Biological Sciences Summer Research Program• Project: <i>Hierarchical deconvolution of bulk RNA-seq data in the MetaSRA</i>	
Brett VanTassel (Ramapo College of New Jersey)	Summer 2017
<ul style="list-style-type: none">• Integrated Biological Sciences Summer Research Program• Project: <i>Compression of RNA-seq alignments</i>	
Kevin Liao (University of North Carolina at Chapel Hill)	Summer 2016
<ul style="list-style-type: none">• Integrated Biological Sciences Summer Research Program• Project: <i>Comparing similarity measures over RNA-seq derived gene expression profiles</i>	

TEACHING

Guest lecture, STAT 877 - Statistical Methods for Molecular Biology <i>Visualizing high dimensional data with dimensionality reduction</i>	Sept. 22, 2020 University of Wisconsin – Madison
Guest lecture, STAT 877 - Statistical Methods for Molecular Biology <i>Cellular phenotyping with public, heterogeneous RNA-seq data</i>	Feb. 7, 2019 University of Wisconsin – Madison
Primary lecturer, CS 302 - Introduction to Programming	Aug. 2013 - May 2014 University of Wisconsin – Madison
<ul style="list-style-type: none">• Primary lecturer to approx. 30 out of 700 students enrolled in CS 302• Designed programming assignments for all approx. 700 students enrolled in CS 302	

SERVICE

Journal Reviewer	Ongoing
<ul style="list-style-type: none">• Bioinformatics (1 review)• BMC Bioinformatics (4 reviews)• Breast Cancer Research and Treatment (1 review)• Genes (1 review)• Journal of Computational Biology (1 review)• Nature Biotechnology (1 review)• Nature Communications (1 review)• Nucleic Acids Research (1 review)	
Review Editor for <i>Frontiers in Genetics</i>	2021-Present
Committee Member, Prospective Student Welcome Weekend Department of Computer Sciences, University of Wisconsin – Madison	Spring 2016
<ul style="list-style-type: none">• Organized the department's graduate student recruitment weekend• Coordinated lodging, transportation, and social events	
Committee Chair, Prospective Student Welcome Weekend Department of Computer Sciences, University of Wisconsin – Madison	Spring 2015

- Led the organization of the department's graduate student recruitment weekend

Club Leader, After-school Computer Programming Club

Spring 2015

Stephen's Point Elementary School, Madison, WI

- Led an after-school computer programming club for 4th and 5th graders
- Taught the Scratch computer programming language

Committee Member, Prospective Student Welcome Weekend

Spring 2014

Department of Computer Sciences, University of Wisconsin – Madison

PROFESSIONAL ACTIVITIES

NCBI Single-cell in the Cloud Codeathon

Jan. 15-17, 2020

Team Lead

New York, NY

- Led a team at a bioinformatics codeathon held at the New York Genome Center

NCBI RNA-seq in the Cloud Codeathon

Mar. 11-13, 2019

Team Lead

Chapel Hill, NC

- Led a team at a bioinformatics codeathon held at the University of North Carolina, Chapel Hill

PROFESSIONAL MEMBERSHIPS

International Society for Computational Biology

Tau Beta Pi

Upsilon Pi Epsilon