

# MATTHEW N. BERNSTEIN

February 23, 2020

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## EDUCATION

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

## WORK EXPERIENCE

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

## AWARDS AND FELLOWSHIPS

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

## PROFESSIONAL MEMBERSHIPS

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**International Society for Computational Biology**  
**Tau Beta Pi**  
**Upsilon Pi Epsilon**

## PEER-REVIEWED PUBLICATIONS

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† corresponding author

1. **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).
2. **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.
3. 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., 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.
4. **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).
5. **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

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1. 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  $\beta$ -cell proliferation in human islets.

## TALKS AND SEMINARS

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

## POSTER PRESENTATIONS

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<b>Cold Spring Harbor Laboratory conference on Biological Data Science</b>	Virtual, Nov. 4-6, 2020
<b>International Conference on Intelligent Systems for Molecular Biology</b>	Virtual, July 13-16, 2020
<b>Great Lakes Bioinformatics Conference</b>	Madison, WI, May 19-22, 2019
<b>RNA-Seq Summit</b>	San Francisco, CA, April 25-27, 2017
<b>National Library of Medicine Informatics Training Conference</b>	Columbus, OH, June 27-28 2016

## UNDERGRADUATE MENTORSHIP

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

## TEACHING

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

## SERVICE

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<b>Journal Reviewer</b> <ul style="list-style-type: none"><li>Bioinformatics (1 review)</li><li>BMC Bioinformatics (3 reviews)</li><li>Journal of Computational Biology (1 review)</li><li>Nature Biotechnology (1 review)</li><li>Nature Communications (1 review)</li><li>Nucleic Acids Research (1 review)</li></ul>	Ongoing
<b>Review Editor for Frontiers in Genetics</b>	2021-Present
<b>Committee Member, Prospective Student Welcome Weekend</b> Department of Computer Sciences, University of Wisconsin – Madison <ul style="list-style-type: none"><li>Organized the department's graduate student recruitment weekend</li><li>Coordinated lodging, transportation, and social events</li></ul>	Spring 2016
<b>Committee Chair, Prospective Student Welcome Weekend</b> Department of Computer Sciences, University of Wisconsin – Madison <ul style="list-style-type: none"><li>Led the organization of the department's graduate student recruitment weekend</li></ul>	Spring 2015
<b>Club Leader, After-school Computer Programming Club</b> Stephen's Point Elementary School, Madison, WI <ul style="list-style-type: none"><li>Led an after-school computer programming club for 4th and 5th graders</li><li>Taught the Scratch computer programming language</li></ul>	Spring 2015
<b>Committee Member, Prospective Student Welcome Weekend</b> Department of Computer Sciences, University of Wisconsin – Madison	Spring 2014

## PROFESSIONAL ACTIVITIES

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<b>NCBI Single-cell in the Cloud Codeathon</b> Team Lead <ul style="list-style-type: none"><li>Led a team at a bioinformatics codeathon held at the New York Genome Center</li></ul>	January 15-17, 2020 New York, NY
<b>NCBI RNA-seq in the Cloud Codeathon</b> Team Lead <ul style="list-style-type: none"><li>Led a team at a bioinformatics codeathon held at the University of North Carolina, Chapel Hill</li></ul>	March 11-13, 2019 Chapel Hill, NC