MATTHEW N. BERNSTEIN

Aprils 19, 2022

Email: matthew.nathan.bernstein@gmail.com

Website: https://mbernste.github.io

EDUCATION

Ph.D., Computer Sciences Aug. 2019
University of Wisconsin – Madison Madison, WI

M.S., Computer Sciences Dec. 2015
University of Wisconsin – Madison Madison, WI

B.S. *Magna Cum Laude*, Computer Science May 2013
University of Notre Dame South Bend, IN

WORK EXPERIENCE

Scientist, Computational Biology 2022 – Present
Immunitas Therapeutics Waltham, MA

Postdoctoral Fellow 2019 – 2022
Morgridge Institute for Research Madison, WI
- Advised by Christina Kendziorski, Ph.D. and Ron Stewart, Ph.D.

Research Assistant 2014 - 2019
University of Wisconsin – Madison Madison, WI
- Advised by Colin Dewey, Ph.D.

Software Development Engineering Intern Summer 2014
Amazon Seattle, WA

Teaching Assistant (Lecturer) 2013 - 2014
University of Wisconsin – Madison Madison, WI

Software Development Engineering Intern Summer 2013
Amazon New York, NY

Research Intern Summer 2012
Space and Naval Warfare Systems Command (SPAWAR) San Diego, CA

AWARDS AND FELLOWSHIPS

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

Best Plenary Talk June 6, 2017
National Library of Medicine Informatics Training Conference San Diego, CA

CIBM Predoctoral Fellowship 2015-2018
University of Wisconsin – Madison Madison, WI

University Housing Honored Instructor Award Fall 2013
University of Wisconsin – Madison Madison, WI

Peer-reviewed Publications

† corresponding author, ♯ co-second author

1. Simonett, S.P., Shin, S., Herrinng, J.A., Bacher, R., Smith, L.A., Dong, C., Rabaglia, M., Stapleton, D., Schueler, K., Choi, J., **Bernstein, M.N.**, Turkewitz, D.R., Perez-Cerventes, C., Spaeth, J., Stein, R., Tessem, J.S., Kendziorski, C., Keles, S., Moskowitz, I.P., Keller, M.P., Attie, A.D. (2021). Identification of direct transcriptional targets of Nfatc2 that promote β-cell proliferation in human islets. *The Journal of Clinical Investigation*, 131(21), e144833.

2. **Bernstein, M.N.**, Dewey, C.N. (2021). Annotating cell types in human single-cell RNA-seq data with CellO. *STAR Protocols*, 2(3), 100705.

3. 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*, 70(9), 2058-2066.

4. **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).

5. **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.

6. 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.

7. **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).

8. **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.

Preprints

1. **Bernstein, M.N.**, Prasad, M., Ni, Z., Brown, J., Mohanty, C., Stewart, R., Newton, M.A., Kendziorski, C. (2022). SpatialCorr: Identifying gene sets with spatially varying correlation structure. *bioRxiv*.

Talks and Seminars

Discovery Seminar Series (UW-Madison)	Oct. 19, 2021
Unleashing the untapped potential of public genomics data	Madison, WI
Computation and Informatics in Biology and Medicine Seminar (UW-Madison)	March 23, 2021
Unleashing the untapped potential of public genomics data	Virtual
Workshop on Computational Advances for Single-Cell Omics Data Analysis	Dec. 12, 2020
CellO: Comprehensive and hierarchical cell type classification of human cells with the Cell Ontology	Virtual
International Conference on Intelligent Systems for Molecular Biology (ISMB)	July 7, 2018
MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive	Chicago, IL
Center for Predictive Computational Phenotyping Annual Retreat	May 31, 2018
Cellular phenotyping with mass, heterogeneous transcriptomic data	Madison, WI
Computation and Informatics in Biology and Medicine Seminar (UW-Madison)	Jan. 30, 2018
Towards cell type prediction with public RNA-seq data	Madison, WI

Center for Predictive Computational Phenotyping Annual Retreat   June 1, 2017
MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive   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
- Integrated Biological Sciences Summer Research Program
- Project: *Hierarchical deconvolution of bulk RNA-seq data in the MetaSRA*

Brett VanTassel (Ramapo College of New Jersey)   Summer 2017
- Integrated Biological Sciences Summer Research Program
- Project: *Compression of RNA-seq alignments*

Kevin Liao (University of North Carolina at Chapel Hill)   Summer 2016
- Integrated Biological Sciences Summer Research Program
- Project: *Comparing similarity measures over RNA-seq derived gene expression profiles*

TEACHING

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

Guest lecture, STAT 877 - Statistical Methods for Molecular Biology   Feb. 7, 2019
Cellular phenotyping with public, heterogeneous RNA-seq data   University of Wisconsin – Madison

Primary lecturer, CS 302 - Introduction to Programming   Aug. 2013 - May 2014
    University of Wisconsin – Madison

- Primary lecturer to approx. 30 out 700 students enrolled in CS 302
- Designed programming assignments for all approx. 700 students enrolled in CS 302

SERVICE

Journal Reviewer   Ongoing

- 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 (2 reviews)
- Nucleic Acids Research (1 review)
- STAR Protocols (1 review)

Review Editor for *Frontiers in Genetics*   2021-Present

Committee Member, Prospective Student Welcome Weekend   Spring 2016
Department of Computer Sciences, University of Wisconsin – Madison
- Organized the department's graduate student recruitment weekend

- Coordinated lodging, transportation, and social events

Committee Chair, Prospective Student Welcome Weekend　　　　Spring 2015

Department of Computer Sciences, University of Wisconsin – Madison
- 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