MATTHEW N. BERNSTEIN

Februrary 22, 2020

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EDUCATION

Ph.D., Computer Sciences — Dec. 2015 – Aug. 2019
University of Wisconsin – Madison — Madison, WI

M.S., Computer Sciences — Aug. 2013 – Dec. 2015
University of Wisconsin — Madison, WI

B.S. *Magna Cum Laude*, Computer Science — Aug. 2009 – May 2013
University of Notre Dame — South Bend, IN

WORK EXPERIENCE

Postdoctoral Fellow — 2019 – Present
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

PROFESSIONAL MEMBERSHIPS

International Society for Computational Biology

Tau Beta Pi

Upsilon Pi Epsilon

Peer-reviewed Publications

† 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*. In Press.

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

1. Simonett, S.P., Shin, S., Bacher, R., Dong, C., Smith, L., Rabaglia, M., Stapleton, D., Schueler, K., Choi, J., **Bernstein, M.N.**, Perez-Cerventes, 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 -cell proliferation in human islets.

Talks and Seminars

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	January 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

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, April 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 (3 reviews)
- Journal of Computational Biology (1 review)
- Nature Biotechnology (1 review)
- Nature Communications (1 review)
- Nucleic Acids Research (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   January 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   March 11-13, 2019
Team Lead   Chapel Hill, NC
- Led a team at a bioinformatics codeathon held at the University of North Carolina, Chapel Hill