MATTHEW N. BERNSTEIN

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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

Immunitas Therapeutics — Waltham, MA
Principal Scientist, Computational Biology — Oct. 2023 – Present
Senior Scientist, Computational Biology — Sept. 2022 – Oct. 2023
Scientist, Computational Biology — March 2022 – Sept. 2022

Morgridge Institute for Research — Madison, WI
Postdoctoral Fellow — 2019 – 2022

University of Wisconsin – Madison — Madison, WI
Research Assistant — 2014 - 2019

Amazon — Seattle, WA
Software Development Engineering Intern — Summer 2014

Amazon — New York, NY
Software Development Engineering Intern — Summer 2013

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

PEER-REVIEWED PUBLICATIONS

† corresponding author, ♯ co-second author

1. Zhang, J., Webster, S., Duffin, B., **Bernstein, M.N.**, Steill, J., Swanson, S., Forsberg, M.H., Bolin, J., Brown, M.E., Majumder, A., Capitini, C.M., Stewart, R., Thomson, J.A., Slukvin, I.I. (2023). Generation of anti-GD2 CAR macrophages from human pluripotent stem cells for cancer immunotherapies. *Stem Cell Reports*, 2(14), 585-596.

2. **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. *Cell Reports Methods*, 2(12), 100369.

3. 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.

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

5. 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.

6. **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).

7. **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.

8. 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.

9. **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).

10. **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

* co-first author

1. **Bernstein, M.N.***, Scott, D.*, Hession, C.C., Nieuwenhuis, T., Gerritsen, J., Tabrizi, S., Nandivada, V., Huggins, M.A., Duan, M., Malu, S., Tang, M. (2023). Monkeybread: A Python toolkit for the analysis of cellular niches in single-cell resolution spatial transcriptomics data. *bioRxiv*.

TALKS AND SEMINARS

Oxford Global's Spatial Biology US 2023	June 8, 2023
Identifying gene sets with spatially varying correlation structure	Boston, MA
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

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

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)
- Cell Reports Methods (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

Spatial Biology US 2023 (Oxford Global)
June 8-9, 2023

Panel participant | Boston, MA
- Invited panel member to discuss "Overcoming The Challenges Of Data Processing In Spatial Omics"

Immuno-Oncology Xchange (hubXchange), East Coast 2023
May 23, 2023

Led Round Table Discussion | Woburn, MA
- Led a round table discussion on the applications of machine learning for drug target discovery

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

Tau Beta Pi

Upsilon Pi Epsilon