MATTHEW N. BERNSTEIN

January. 21, 2025

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

Stellaromics	Boston, MA
Staff Scientist, Machine Learning	July 2024 – Present
Immunitas Therapeutics	Waltham, MA
Principal Scientist, Computational Biology	Oct. 2023 – July 2024
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 & PREPRINTS

† corresponding author, * co-first author, ♯ co-second 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*.

2. 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.

3. **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.

4. 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.

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

6. 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.

7. **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).

8. **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.

9. 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.

10. **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).

11. **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.

Talks and Seminars

Panoramics – A Vision, Seminar on dimensionality reduction in single-cell analysis	Jan. 20, 2025
Assessing the utility of data visualizations based on dimensionality reduction	Toronto, ON
Workshop on Spatial Data Analysis at the Festival of Genomics	June 13, 2024
Software tools for the analysis of cellular niches in the tissue microenvironment	Boston, MA
Spatial Biology US 2024 (Oxford Global)	June 11, 2024
Software tools for the analysis of cellular niches in the tissue microenvironment	Boston, MA
Cohere for AI Community Talk	April 22, 2024
A primer on variational autoencoders and their applications in single-cell genomics	Virtual
Workshop on AI for Precision Health & Precision Medicine	Nov. 16, 2023
Annotating cell types and cell states in single-cell omics data: A challenging problem	Cambridge, MA
Spatial Biology for Drug Development (Hanson Wade)	Oct. 12, 2023
Software tools for the analysis of cellular niches in spatial transcriptomics data	Boston, MA
Spatial Biology US 2023 (Oxford Global)	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

American Society for Hematology Annual Meeting (ASH) — San Diego, CA, Dec. 8-12, 2023

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 (ISMB) — Virtual, July 13-16, 2020

Great Lakes Bioinformatics Conference — Madison, WI, May 19-22, 2019

RNA-Seq Summit (Hanson Wade) — 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 - Workshop on RNA-seq — July 26, 2024
Computational methods for the analysis of spatial transcriptomics data — Montgomery College

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

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

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* — 2021-2022

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