

MATTHEW N. BERNSTEIN

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EDUCATION

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

WORK EXPERIENCE

Stellaromics Staff Scientist, Machine Learning	Boston, MA July 2024 – Present
Immunitas Therapeutics Principal Scientist, Computational Biology Senior Scientist, Computational Biology Scientist, Computational Biology	Waltham, MA Oct. 2023 – July 2024 Sept. 2022 – Oct. 2023 March 2022 – Sept. 2022
Morgridge Institute for Research Postdoctoral Fellow	Madison, WI 2019 – 2022
University of Wisconsin – Madison Research Assistant	Madison, WI 2014 - 2019
Amazon Software Development Engineering Intern	Seattle, WA Summer 2014
Amazon Software Development Engineering Intern	New York, NY Summer 2013
Space and Naval Warfare Systems Command (SPAWAR) Research Intern	San Diego, CA 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., Kendzierski, 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

Workshop on Spatial Data Analysis at the Festival of Genomics <i>Software tools for the analysis of cellular niches in the tissue microenvironment</i>	June 13, 2024 Boston, MA
Spatial Biology US 2024 (Oxford Global) <i>Software tools for the analysis of cellular niches in the tissue microenvironment</i>	June 11, 2024 Boston, MA
Cohere for AI Community Talk <i>A primer on variational autoencoders and their applications in single-cell genomics</i>	April. 22, 2024 Virtual
Workshop on AI for Precision Health & Precision Medicine <i>Annotating cell types and cell states in single-cell omics data: A challenging problem</i>	Nov. 16, 2023 Cambridge, MA
Spatial Biology for Drug Development (Hanson Wade) <i>Software tools for the analysis of cellular niches in spatial transcriptomics data</i>	Oct. 12, 2023 Boston, MA
Spatial Biology US 2023 (Oxford Global) <i>Identifying gene sets with spatially varying correlation structure</i>	June 8, 2023 Boston, MA
Discovery Seminar Series (UW-Madison) <i>Unleashing the untapped potential of public genomics data</i>	Oct. 19, 2021 Madison, WI
Computation and Informatics in Biology and Medicine Seminar (UW-Madison) <i>Unleashing the untapped potential of public genomics data</i>	March 23, 2021 Virtual
Workshop on Computational Advances for Single-Cell Omics Data Analysis <i>CellO: Comprehensive and hierarchical cell type classification of human cells with the Cell Ontology</i>	Dec. 12, 2020 Virtual

International Conference on Intelligent Systems for Molecular Biology (ISMB) <i>MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive</i>	July 7, 2018 Chicago, IL
Center for Predictive Computational Phenotyping Annual Retreat <i>Cellular phenotyping with mass, heterogeneous transcriptomic data</i>	May 31, 2018 Madison, WI
Computation and Informatics in Biology and Medicine Seminar (UW-Madison) <i>Towards cell type prediction with public RNA-seq data</i>	Jan. 30, 2018 Madison, WI
Center for Predictive Computational Phenotyping Annual Retreat <i>MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive</i>	June 1, 2017 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 International Conference on Intelligent Systems for Molecular Biology	July 6-10, 2018 Chicago, IL
Best Plenary Talk National Library of Medicine Informatics Training Conference	June 6, 2017 San Diego, CA
CIBM Predoctoral Fellowship University of Wisconsin – Madison	2015-2018 Madison, WI
University Housing Honored Instructor Award University of Wisconsin – Madison	Fall 2013 Madison, WI

TEACHING

Guest lecture - Workshop on RNA-seq <i>Computational methods for the analysis of spatial transcriptomics data</i>	July 26, 2024 Montgomery College
Guest lecture, STAT 877 - Statistical Methods for Molecular Biology <i>Visualizing high dimensional data with dimensionality reduction</i>	Sept. 22, 2020 University of Wisconsin – Madison
Guest lecture, STAT 877 - Statistical Methods for Molecular Biology <i>Cellular phenotyping with public, heterogeneous RNA-seq data</i>	Feb. 7, 2019 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