

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. <i>Magna Cum Laude</i>, Computer Science	May 2013
University of Notre Dame	South Bend, IN

WORK EXPERIENCE

Cellular Intelligence	Boston, MA
Principal Computational Scientist	June 2025 - Present
Stellaromics	Boston, MA
Staff Scientist, Machine Learning	July 2024 – June 2025
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., 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

Webinar hosted by Watershed Bio	March 26, 2025
<i>From Data to Discovery: Computational Tools for the Analysis of Spatial Transcriptomics Data</i>	Virtual
Panoramics – A Vision, Seminar on dimensionality reduction in single-cell analysis	Jan. 20, 2025
<i>Assessing the utility of data visualizations based on dimensionality reduction</i>	Toronto, ON
Workshop on Spatial Data Analysis at the Festival of Genomics	June 13, 2024
<i>Software tools for the analysis of cellular niches in the tissue microenvironment</i>	Boston, MA
Spatial Biology US 2024 (Oxford Global)	June 11, 2024
<i>Software tools for the analysis of cellular niches in the tissue microenvironment</i>	Boston, MA
Cohere for AI Community Talk	April 22, 2024
<i>A primer on variational autoencoders and their applications in single-cell genomics</i>	Virtual
Workshop on AI for Precision Health & Precision Medicine	Nov. 16, 2023
<i>Annotating cell types and cell states in single-cell omics data: A challenging problem</i>	Cambridge, MA
Spatial Biology for Drug Development (Hanson Wade)	Oct. 12, 2023
<i>Software tools for the analysis of cellular niches in spatial transcriptomics data</i>	Boston, MA
Spatial Biology US 2023 (Oxford Global)	June 8, 2023
<i>Identifying gene sets with spatially varying correlation structure</i>	Boston, MA
Discovery Seminar Series (UW-Madison)	Oct. 19, 2021
<i>Unleashing the untapped potential of public genomics data</i>	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

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
- 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