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

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

Webinar hosted by Watershed Bio	March 26, 2025
From Data to Discovery: Computational Tools for the Analysis of Spatial Transcriptomics Data	Virtual
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 |
| | Virtual |

Unleashing the untapped potential of public genomics data

| **Workshop on Computational Advances for Single-Cell Omics Data Analysis** | Dec. 12, 2020 |
| | Virtual |

CellO: Comprehensive and hierarchical cell type classification of human cells with the Cell Ontology

| **International Conference on Intelligent Systems for Molecular Biology (ISMB)** | July 7, 2018 |
| | Chicago, IL |

MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive

| **Center for Predictive Computational Phenotyping Annual Retreat** | May 31, 2018 |
| | Madison, WI |

Cellular phenotyping with mass, heterogeneous transcriptomic data

| **Computation and Informatics in Biology and Medicine Seminar (UW-Madison)** | Jan. 30, 2018 |
| | Madison, WI |

Towards cell type prediction with public RNA-seq data

| **Center for Predictive Computational Phenotyping Annual Retreat** | June 1, 2017 |
| | Madison, WI |

MetaSRA: Normalized sample-specific metadata for the Sequence Read Archive

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 |
| | Chicago, IL |

International Conference on Intelligent Systems for Molecular Biology

| **Best Plenary Talk** | June 6, 2017 |
| | San Diego, CA |

National Library of Medicine Informatics Training Conference

| **CIBM Predoctoral Fellowship** | 2015-2018 |
| | Madison, WI |

University of Wisconsin – Madison

| **University Housing Honored Instructor Award** | Fall 2013 |
| | Madison, WI |

University of Wisconsin – Madison

TEACHING

| **Guest lecture - Workshop on RNA-seq** | July 26, 2024 |
| | Montgomery College |

Computational methods for the analysis of spatial transcriptomics data

| **Guest lecture, STAT 877 - Statistical Methods for Molecular Biology** | Sept. 22, 2020 |
| | University of Wisconsin – Madison |

Visualizing high dimensional data with dimensionality reduction

| **Guest lecture, STAT 877 - Statistical Methods for Molecular Biology** | Feb. 7, 2019 |
| | University of Wisconsin – Madison |

Cellular phenotyping with public, heterogeneous RNA-seq data

| **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