

MATTHEW N. BERNSTEIN

Sept. 15, 2023

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

WORK EXPERIENCE

Immunitas Therapeutics Senior Scientist, Computational Biology Scientist, Computational Biology	Waltham, MA Sept. 2022 – Present 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

† 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., Kendzioriski, 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., Kendzioriski, 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., Shishkova, 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 <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

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
<i>Visualizing high dimensional data with dimensionality reduction</i>	University of Wisconsin – Madison
Guest lecture, STAT 877 - Statistical Methods for Molecular Biology	Feb. 7, 2019
<i>Cellular phenotyping with public, heterogeneous RNA-seq data</i>	University of Wisconsin – Madison
Primary lecturer, CS 302 - Introduction to Programming	Aug. 2013 - May 2014
	University of Wisconsin – Madison
<ul style="list-style-type: none">• 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
<ul style="list-style-type: none">• 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 <i>Frontiers in Genetics</i>	2021-Present
Committee Member, Prospective Student Welcome Weekend	Spring 2016
Department of Computer Sciences, University of Wisconsin – Madison	
<ul style="list-style-type: none">• 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

- International Society for Computational Biology**
- Tau Beta Pi**
- Upsilon Pi Epsilon**