Matthew N. Bernstein

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http://mbernste.github.io

EDUCATION

University of Wisconsin – Madison	Madison, WI
Ph.D. in Computer Sciences	*Aug. 2019*

- **Thesis**: Computational methods for transcriptome-based cellular phenotyping
- **Advisor**: Colin Dewey

University of Wisconsin – Madison	Madison, WI
M.S. in Computer Sciences	*Dec. 2015*
University of Notre Dame	South Bend, IN
B.S. in Computer Science; Magna Cum Laude	*May 2013*

EXPERIENCE

Morgridge Institute for Research	Madison, WI
Postdoctoral Fellow	*Sept. 2019 - Present*
University of Wisconsin - Madison	Madison, WI
Research Assistant under Prof. Colin Dewey	*Aug. 2014 - Aug. 2019*
Amazon	Seattle, WA
Software Development Engineering Intern	*Summer 2014*
University of Wisconsin - Madison	Madison, WI
Teaching Assistant (Lecturer)	*Aug. 2013 - May 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*

AWARDS AND FELLOWSHIPS

- **NIH/BD2K Young Investigator Travel Scholarship**, International Conference on Intelligent Systems for Molecular Biology (ISMB), Chicago, IL, July 6-10, 2018

- **Best Plenary Talk**, National Library of Medicine Informatics Training Conference, San Diego, CA, June 6, 2017

- Awarded three year, National Library of Medicine funded traineeship through the **Computation and Informatics in Biology and Medicine** training program between Feb. 2015 - Feb. 2018

- **University Housing Honored Instructor Award**. University of Wisconsin–Madison, Fall 2013

SOCIETY MEMBERSHIPS

- **International Society for Computational Biology**	*2019-present*
- **Tau Beta Pi** engineering honor society	*2011-present*
- **Upsilon Pi Epsilon** computing honor society	*2011-present*

PEER-REVIEWED PUBLICATIONS

- **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

- **Bernstein, M.N.** and Dewey, C.N. (2019). Hierarchical cell type classification using mass, heterogeneous RNA-seq data from human primary cells. *bioRxiv*.

Talks

- International Conference on Intelligent Systems for Molecular Biology   Chicago, IL, *July 2018*
- Center for Predictive Computational Phenotyping Annual Retreat   Madison, WI, *May 2018*
- National Library of Medicine Informatics Training Conference   San Diego, CA, *June 2017*
- Center for Predictive Computational Phenotyping Annual Retreat   Madison, WI, *June 2017*

Poster presentations

- Great Lakes Bioinformatics Conference   Madison, WI, *May 2019*
- RNA-Seq Summit   San Francisco, CA, *April 2017*
- National Library of Medicine Informatics Training Conference   Columbus, OH, *June 2016*

Teaching and Mentorship

Integrated Biological Sciences Summer Research Program   Madison, WI
Mentor   *Summer 2016, 2017, 2019*

- Co-mentored undergraduate students' summer research projects with Prof. Colin Dewey

STAT 877 - Statistical Methods for Molecular Biology   Madison, WI
Guest Lecturer   *Spring 2019*

- Gave a guest lecture on analyzing large, heterogeneous RNA-seq datasets

CS 302 - Introduction to Programming   Madison, WI
Lecturer   *Fall 2013, Spring 2014*

- Primary lecturer to 30 students in CS 302 - Introduction to Programming

- Designed two programming projects that all 700 students enrolled in CS 302 were required to complete

Service

- **Journal referee**: Bioinformatics

- **Computer Sciences Graduate Student Welcome Weekend**   Madison, WI
  Committee member, Committee chair   *Spring 2014, 2015, 2016*
  - Planned the department's prospective student visit weekend
  - Chaired the committee in Spring 2015

- **Scratch Computer Programming Club at Stephen's Point Elementary School**   Madison, WI
  Club Leader   *Spring 2015*
  - Led an after school computer science club for 4th and 5th grade students

Technical skills

- **Software Development**: Python (strong), Java (strong), C/C++ (familiar), JavaScript (familiar), HTML, CSS, SQL, MongoDB, Git, Numpy, Matplotlib, Scikit Learn

- **Computer Science & Machine Learning**: classification, probabilistic modeling, dimensionality reduction, named entity recognition, knowledge representation

- **Bioinformatics & Computational Biology**: RNA-seq, transcriptome quantification, gene expression analysis, biomedical text mining