Matthew N. Bernstein

http://mbernste.github.io

EDUCATION

University of Wisconsin – Madison

Madison, WI Expected 2019

Email: matthewb@cs.wisc.edu

Ph.D. in Computer Sciences

o Advisor: Colin Dewey

• Thesis: Computational methods for transcriptome-based cellular phenotyping

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

University of Wisconsin - Madison

Madison, WI

Research Assistant under Prof. Colin Dewey

Aug. 2014 - Present

- Developing novel computational and statistical approaches for mining large, heterogeneous repositories of gene expression data
- $\circ\,$ Mentor undergraduate students working in the lab

Amazon

Software Development Engineering Intern

Seattle, WA Summer 2014

• Designed, implemented, and launched auto-complete search-suggestions for the Amazon Local website's search bar. Search suggestions are served as the user is typing a query

University of Wisconsin - Madison

Madison, WI

Teaching Assistant (Lecturer)

Aug. 2013 - May 2014

- Lecturer to ~30 students in CS 302 Introduction to Programming
- o Created assignments, quizzes, and lesson plans for my class
- \circ Designed two programming projects that all \sim 700 students enrolled in CS 302 were required to complete

Amazon New York, NY

Software Development Engineering Intern

Summer 2013

• Improved Amazon Posts - a tool that allows brands to create short, social messages that appear on various feeds across Amazon websites

Space and Naval Warfare Systems Command (SPAWAR)

San Diego, CA

Research Intern

 $Summer\ 2012$

• Developed a machine learning based solution for the task of determining political and group affiliation of anonymous internet authors

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, NLM 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

Professional memberships

Phi Kappa Phi (Honor Society), Tau Beta Pi (Engineering honor society), Upsilon Pi Epsilon (Computing honor society)

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.

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

RNA-Seq Summit
 National Library of Medicine Informatics Training Conference
 San Francisco, CA, April 2017
 Columbus, OH, June 2016

SERVICE

• Journal referee: Bioinformatics

Integrated Biological Sciences Summer Research Program Mentor

Madison, WI Summer 2015, 2016

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

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 Club Leader

Madison, WI Spring 2015

o 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