

Xide Xia
Curriculum Vitae

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EDUCATION

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|---|----------------|
| Boston University
Ph.D. candidate in Computer Science | 2016 - Present |
| Harvard University , Institute for Applied Computational Science
M.E. in Computational Science and Engineering | 2014 - 2016 |
| Brown University , School of Engineering
M.S. in Electrical Science | 2012 - 2013 |
| Beijing Institute of Technology , College of Information and Electronics
B.S. in Electrical and Information Engineering | 2008 - 2012 |

PUBLICATION

- 2016**
- Xide Xia, Mohammed AlQuraishi. “Computational prediction of protein-DNA interactions based on protein sequences information.” Forthcoming.
 - Xide Xia, Finale Doshi-Velez, Pavlos Protopapas. “Cost-Sensitive Batch Mode Active learning: Designing Astronomical Observation by Optimizing Telescope Time and Telescope Choice.” In In Proceedings of SIAM Data Mining Conference (SDM). 2016.
- 2015**
- AlQuraishi, M., Tang, S., & Xia, X. (2015). *An affinity-structure database of helix-turn-helix: DNA complexes with a universal coordinate system*. BMC bioinformatics, 16(1), 390. PMID:26586237. (Database: <http://staging.proteindna.hms.harvard.edu/>).

RESEARCH EXPERIENCE

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| Boston University , Boston, MA September
Research Assistant in Image and Video Computing (IVC) Lab. <ul style="list-style-type: none">• Efficient Deep Generative Models for Unsupervised Learning. | 2016 – Present |
| Harvard Medical School , Boston, MA
Graduate Research Fellow advised by Dr. Mohammed AlQuraishi and Professor Peter Sorger. <ul style="list-style-type: none">• Develop a new computational method for predicting protein-DNA interactions by implementing a whole machine learning pipeline for prediction protein-DNA interactions.• Build a model to simulate protein-DNA interactions, for which we formulate the problem as a convex optimization problem. In the model, we measure energies of binding between protein and DNA molecules to derive the energies of interactions between atoms.• Impose all the constraints and implement a regression problem that is specific to the formulation.• Predict protein-DNA interactions based on protein sequence even if the structure information is missing (i.e. CIS-BP database).• Implement large scale scientific computing in parallel and distributed environments.• Assist Dr. AlQuraishi to construct an affinity-structure database in which structural and biochemical data of protein-DNA interactions are integrated: http://staging.proteindna.hms.harvard.edu/. | June 2013 – May 2016 |
| Harvard University , Cambridge, MA
Intervention and Outcome Predictions: Understanding Vasopressor Administration and Weaning in the ICU
Research advised by Professor Finale Doshi-Velez. <ul style="list-style-type: none">• Analyze the MIMIC II 2.6 database gathered from four ICUs at the Beth Israel Deaconess Medical Center.• Design a recurrent neural network model to simulate multidimensional physiological time series of patients before, during, and after vasopressor administration.• Implement recurrent Neural Networks (RNNs) with Long Short-Term Memory (LSTM) units in Torch-Autograd.• Predict whether a patient will be administered a vasopressor. | Oct 2015 – Present |
| Batch Mode Active Learning and Its Application to Astronomy
Thesis project advised by Professor Finale Doshi-Velez and Dr. Pavlos Protopapas. <ul style="list-style-type: none">• Developed a batch-mode cost-sensitive active learning approach that not only exploited uncertainty and representativeness of the whole unlabeled dataset, but also took annotation cost into consideration.• Designed a selection criterion that combined uncertainty and representativeness by using a synthesized heuristic argument. Queried instances were selected from different clusters to have a good representativeness of the whole unlabeled dataset. The selection criterion also considers the overall cost of the experiment while keeping uncertainty and representativeness high.• Applied the approach to optimize astronomical observations for object classification, including an extension that incorporates the possibility that nearby objects is observed at the same time.• Used two large astronomical datasets (MACHO and EROS) to demonstrate how the approach balanced the trade-off among FOV, aperture, and time cost. | Feb 2015 – Nov 2015 |

TEACHING EXPERIENCE

Boston University, Boston, MA

- CS131 Combinatoric Structures 2016 Fall

Harvard University, Cambridge, MA

- AM207 Stochastic Methods for Data Analysis, Inference and Optimization 2016 Spring

WORK EXPERIENCE

Boston University, Boston, MA

Research fellow at IVC Lab

Sept 2016 – Present

Harvard Medical School, Boston, MA

Research fellow at Department of Systems Biology

June 2013 – May 2016

Huawei Technologies Co., Ltd, Shenzhen, China

Software development engineer intern

June 2012- Aug 2012

Agilent Technologies Co., Ltd, Beijing, China

Undergraduate intern at mobile broadband division

Sept 2011- Jan 2012

HONORS & AWARDS

2017

- Dean's Fellow Scholarship (Boston University, Boston, MA)

2016

- Harvard IACS Student Scholarship (Harvard University, Cambridge, MA)
- SDM Student Travel Award 2016

Before 2016

- Research Fellowship (2013-2016, Harvard Medical School, Cambridge, MA)
- Ren-Min Scholarship (2008-2012, Beijing Institute of Technology, Beijing, China)