

Xide Xia

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OBJECTIVE

Summer internship in computer vision, machine learning, or related areas for 2018.

EDUCATION

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| Boston University <i>Ph.D.</i> candidate in Computer Science Advisor: Professor Brian Kulis | Sept 2016 - Present Boston, MA |
| Harvard University , Institute for Applied Computational Science <i>M.E.</i> in Computational Science and Engineering | Sept 2014 – May 2016 Cambridge, MA |
| Brown University , School of Engineering <i>M.S.</i> in Electrical Science | Sept 2012 – Dec 2013 Providence, RI |
| Beijing Institute of Technology , College of Information and Electronics <i>B.S.</i> in Electrical and Information Engineering | Sept 2008 – May 2012 Beijing, China |

RESEARCH INTERESTS

Machine Learning, Deep Learning, Video Learning, Image Segmentation, Representation Learning, Data Mining

PROFESSIONAL EXPERIENCE

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| Legendary Applied Analytics , Boston, MA Graduate Quantitative Research Intern advised by Dr. Jonathan Foster. <ul style="list-style-type: none">Develop and implement a 3D Convolutional Network for spatial-temporal representation learning. | Sept 2017 – Present |
| Information and Data Sciences (IDS) group , Boston University , Boston, MA Research advised by Professor Brian Kulis. <ul style="list-style-type: none">Designed and implemented an end-to-end Convolutional Neural Network Architecture for fully-unsupervised image segmentation and learning the underlying lower-dimensional representation for input image data on the hidden layer.Trained a deep generative model for unsupervised clustering task in the hidden space. | Sept 2016 – Present |
| Image and Video Computing (IVC) Lab , Boston University , Boston, MA Research advised by Professor Margrit Betke. <ul style="list-style-type: none">Designed and implemented a Convolutional Neural Network (CNN) model to make age/gender/ethnicity prediction on the data of Twitter users profile images. | Feb 2017 – June 2017 |
| Laboratory of Systems Pharmacology (LSP) , Harvard Medical School , Boston, MA Graduate Research Fellow at Department of Systems Biology advised by Dr. Mohammed AlQuraishi and Professor Peter Sorger. <ul style="list-style-type: none">Developed a new computational method for predicting protein-DNA interactions based on sequences information.Developed a Protein-DNA Structure-Affinity Database(PDSA) in which the experimental and quantitative DNA binding affinities of helix-turn-helix proteins were mapped onto the crystal structures of the corresponding protein-DNA complexes. | Aug 2013 – June 2016 |
| <i>M.E. Thesis: Batch Mode Active Learning and Its Application to Astronomy</i> , Harvard University Advisors: Professor Finale Doshi-Velez and Dr. Pavlos Protopoulos. <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 considered the annotation costs.Designed a selection criterion that combined uncertainty and representativeness by using a synthesized heuristic argument.Applied the approach to optimize astronomical observations for object classification. | Feb 2015 – May 2016 |
| IACS Capstone Project , Harvard University , Cambridge, MA Research advised by Professor Finale Doshi-Velez. <ul style="list-style-type: none">Designed and implemented a Recurrent Neural Network (RNN) model for intervention and outcome predictions in ICU.Simulated multidimensional physiological time series of patients during vasopressor administration. | Dec 2015 – May 2016 |

Agilent Technologies Co., Ltd, Beijing, China
Undergraduate intern at mobile broadband division.

Sept 2011- Jan 2012

- Quality assurance engineer for 3G mobile telecommunication (TD-SCDMA) RF.

PUBLICATION

[P.2] Xide Xia, Finale Doshi-Velez, Pavlos Protopapas. “Cost-Sensitive Batch Mode Active learning: Designing Astronomical Observation by Optimizing Telescope Time and Telescope Choice.” In Proceedings of SIAM Data Mining Conference (SDM). 2016.

[P.1] AlQuraishi, M., Tang, S., Xia, X. “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/>).

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

HONORS & AWARDS

2017

- Dean’s Fellow Scholarship (Boston University, Boston, MA)
- CRA-Women Graduate Cohort Workshop Student Award

2016

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

Before 2016

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

TECHNICAL STRENGTHS

Proficient in programming languages: Python, Matlab, C/C++

Familiar with deep learning packages: Tensorflow, PyTorch, Keras, Caffe