

Yutong Wang

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Research interests

Domain adaptation and its application to deep learning on genomics datasets.

Clustering with side information about the centroids.

Education

- Sep'16–May'21 **University of Michigan, Ann Arbor** 3.9 GPA
Ph.D. candidate in electrical engineering & computer science (EECS)
Courses: Machine learning, statistical signal processing, approximation algorithms, random graphs, multi-armed bandits, mathematical biology.
- Sep'14–Jun'16 **University of California, Davis** 3.9 GPA
M.A. in mathematics
Courses: Integer and numerical optimization, algebraic geometry.
Teaching assistant: calculus, differential equations.
- Sep'10–Apr'14 **University of Michigan, Ann Arbor** 3.7 GPA
B.S.E. in EECS with minor in mathematics
Courses: Programming and data structure, computer organization, information theory, algebraic topology, differential and Riemannian geometry.

Professional Experience

- Sep'16–present **Graduate student research assistant** — Advisors: C. Scott and L. Balzano
Department of EECS, University of Michigan
- Jun'16–Sep'16 **Research assistant** — Advisors: D. Neuhoff and V. Subramanian.
Department of EECS, University of Michigan
- Jun'15–Sep'15 **Research in algebraic geometry** — Advisor: B. Osserman.
Department of Mathematics, UC Davis

Publications in preparation

Y. Wang and C. Scott. **"Generalized triangle inequality for domain adaptation learning bounds."** *In preparation for ICML 2020.*

Y. Wang, H. Raja, and L. Balzano. **"Low-rank matrix approximation under entrywise multiplicative noise."** *In preparation for ICML 2020.*

Y. Wang and J. Welch. **"Domain adaptation for spatial and dissociated gene expression data integration"** *In preparation for Genome Biology. Accepted for poster presentation at the Learning Meaningful Representations of Life Workshop at NeurIPS 2019*

Technical reports

Y. Wang, T. Thong, V. Saligrama, J. Colacino, L. Balzano, and C. Scott. **"A Gene Filter for Comparative Analysis of Single-Cell RNA-Sequencing Trajectory Datasets."** *BioRxiv*, <https://doi.org/10.1101/637488>.

We present a heuristic algorithm for unsupervised feature selection, also known as a gene filter in bioinformatics. The heuristic attempts to solve a difficult combinatorial optimization. Future work includes finding a more theoretically justified approach to the combinatorial optimization problem.

Y. Wang, M. Reyes, and D. Neuhoff. “**Correct Convergence of Min-Sum Loopy Belief Propagation in a Block Interpolation Problem**” arXiv, <https://arxiv.org/abs/1702.06391>.

Belief propagation is a powerful heuristic for solving problems in probabilistic graphical model. However, few theory results are available when the underlying graph is not a tree. We present a proof that a variant of belief propagation converges for the grid graph. For future work, we plan to generalize our result to a larger family of graphs with loops.

Y. Wang, L. Balzano, and C. Scott. “**Matrix completion for integrative analysis of bulk and single-cell RNA-sequencing data**”.

Single-cell RNA-seq data suffer from high amount of dropouts. We model these dropouts as missing data and apply matrix completion to infer them. Using our approach, we found that incorporating bulk RNA-seq as side-information empirically boosts the performance of matrix completion.

Course projects

- Fall 2017 **Community detection in multilayer graphs using spectral methods and core-finding** with D. Zhang
EECS 598: Random Graphs
Proposed a model for time-varying random graph model and a “core finding” algorithm for detecting communities in the proposed model. We demonstrate our algorithm is able to detect time-invariant communities in certain cases.
- Fall 2016 **Coordinating message-passing algorithms using contextual bandits**
STATS 710: Sequential Decision Making With MHealth Applications
Applied contextual bandits to improve the convergence property of message-passing algorithms. I find that applying contextual bandits slightly decreased the number of iterations needed for the message-passing algorithm to converge.

Poster presentations

- Dec’19 **Domain adaptation for spatial and dissociated gene expression data integration**
Learning Meaningful Representations of Life Workshop at NeurIPS 2019
- Jan’19 **Unsupervised feature selection for manifold alignment of scRNA-seq data**
Single Cell Biology - Keystone Symposia
- Jun’17 **Joint analysis of bulk and single-cell RNA-Seq data via matrix factorization**
Midwest Machine Learning Symposium
- Oct’17 **A convex clustering formulation using the similarity matrix**
3rd Annual MIDAS Symposium
Won the “Most Interesting Methodological Advancement” poster award.

Skills

Programming languages/libraries — Python/Pytorch, R, MATLAB, C.

Spoken languages — English & Mandarin Chinese.

Softwares — L^AT_EX, graphic design in Adobe Photoshop and Illustrator.