

YOUJIA ZHOU

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EDUCATION

University of Utah, UT *August 2018 - Present*
School of Computing *Overall GPA: 4.0/4.0*
Ph.D. student in Computer Science
Advisor: Dr. Bei Wang Phillips

University of Wisconsin-Madison, WI *September 2015 - May 2017*
Department of Statistics *Overall GPA: 3.87/4.0*
M.S. in Statistics

Renmin University of China, China *September 2012 - June 2016*
School of Statistics *Overall GPA: 3.51/4.0*
B.S. in Statistics

EXPERIENCE

Graduate Research Assistant *May 2019 - Present*
Scientific Computing and Imaging Institute *Salt Lake City, UT*
Data analysis and data visualization, mainly using topological techniques

Data Analyst *January 2018 - July 2018*
Pohoo Credit *Chengdu, China*
Data modeling and risk management

HONORS & AWARDS

- Best Poster Award at China Visualization and Visual Analytics Conference (ChinaVis), 2019
- Visiting International Student Academic Excellence Award, University of Wisconsin-Madison, 2016
- Outstanding Volunteer Award, Renmin University of China, 2015
- Scholarship for Academic Excellence, Renmin University of China, 2014
- Scholarship for Outstanding Student Leaders, Renmin University of China, 2014

TECHNICAL SKILLS

- **Programming:** C++, Java
- **Data Analysis:** Python(with NumPy, SciPy, Scikit-learn, Pandas), R
- **Web and back-end:** HTML, JavaScript(with D3), Python(with Flask)
- **Other tools:** Version Control : Git

SELECTED ACADEMIC PROJECTS

Persistence-Driven Design and Visualization of Morse Vector Fields *University of Utah*
Research Project *January 2019 - Present*

- We consider the idea of vector field design with a newfound motivation in computational topology.

- The goal is to allow computational topologists to explore the complex configuration space of Morse functions constrained by persistence.
- I am currently working on developing a new vector field design and visualization system that provides fine-grained control over vector field geometry, enables the editing of vector field topology, and supports a design process in a simple and efficient way using elementary building blocks.

Topological Diagnostic of Generative Adversarial Networks

Research Project

*University of Utah
July 2019 - Present*

- GAN Lab is an in-browser GPU-accelerated deep learning library.
- I am currently working on extending the original interface with topological features, which can be used to validate if the training process converges as the number of epochs increases and can help users form a better understanding of GAN.

Uncertainty Visualization of Vortex Core Lines

Research Project

*University of Utah
March 2019 - Present*

- The goal is to visualize the uncertainty of vortex core lines extracted from 3D complex-valued superconductor simulation data.
- I am currently working on exploring representative curves of vortex core lines using kernel density estimation and ridge extraction, and developing a web-based system that provides interactive visualization of the representations.
- We hope to generalize our results to any ensemble of curves.

Randomized Sampling Methods For Clique Counting

Course Group Project

*University of Utah
Fall, 2018*

- Worked to understand theories and heuristics applied in the topic paper, namely Turan shadows and degeneracy ordering.
- Justified the conclusion by doing experiments, including comparison experiments.
- Explored performances of proposed method in the topic paper on synthesized graph data and tried to give some intuitive explanations, such as the relationship between sparsity and estimation accuracy.
- Tried to generalize k-clique to Quasi-Clique by changing the original algorithm configurations and to provide some provable explanations when getting good results.

Identifying Differential Distributions in Single-cell RNA-seq

Course Project

(The project is an extension of Korthauer et al., Genome Biology, 2016.)

*UW-Madison
Spring, 2017*

- Evaluated scDD, an approach to identify differential distributions in single-cell RNA-seq.
- Proposed and evaluated a nonparametric method for clustering genes into groups.

Exploring Genealogical Patterns Using Genome Sequences

Course Project

*UW-Madison
Fall, 2016*

- Built individual genomes by mapping the SNPs (single nucleotide polymorphism data) onto the reference.
- Ran RAxML on each chromosome block of 10,000 base pairs to get the estimated genealogy (tree), calculate pairwise distances between the trees and compare these distances between trees.