Thomas K. Atkins

thomaskatkins.github.io

atkin423@umn.edu

612-413-9506

Education

University of Minnesota Twin Cities, Minneapolis MN **Fall 2019-Spring 2023**

Bachelor of Science in Computer Science
Bachelor of Science in Statistical Science
Computational Biology Minor
Thesis: FIST-nD: A tool for n-dimensional spatial transcriptomics data imputation via graph-regularized tensor completion.
4.0/4.0 GPA (165 credits)

Research Experience

Dr. Rui Kuang Computational Biology Lab **August 2021 -**
Department of Computer Science and Engineering, University of Minnesota
Does imputing 3D spatial transcriptomic data give us accurate and useful results?

- Extended a tensor decomposition and graph regularization based algorithm for spatial transcriptomic data imputation from two to three spatial dimensions, making it the first method of its kind
- Implemented this algorithm in an easy-to-use, documented command line tool for 2D and 3D ST data imputation
- Measured performance of our method as superior to existing scRNA-seq imputation methods
- Was awarded an NSF Research Experience for Undergraduates (REU) supplement

Dr. Julie Segre Skin Microbiome Lab **June 2022 - Aug. 2022**
National Human Genome Research Institute, National Institutes of Health
How do we diagnose errors in fungal genome variant calling pipelines?

- Developed an extensible all-in-one variant calling pipeline for population genomics by filtering different combinations of bcftools, freebayes, and GATK variant callers
- Created a suite of diagnostic plots that identified inconsistent results in popular workflows and assumptions from human genetics that did not hold in a fungal context

Dr. Rémi Mégret Computer Vision Lab **May 2021 - July 2021**
Department of Computer Science, University of Puerto Rico, Río Piedras
How do genetic factors contribute to colony-scale honeybee circadian rhythms?

- Following a literature review, implemented an attention time-based machine learning model to recognize honeybees based on abdominal striping patterns
- Developed an occlusion sensitivity metric that allowed for detection of data leakage

Dr. Matthew Johnson Neuromodulation Research and Technology Lab **Nov. 2019 - Dec. 2020**

Department of Biomedical Engineering, University of Minnesota

Can non-deep learning methods accurately classify non-human primate behavior in a controlled environment?

- Implemented a model based on histograms of oriented optical flow (HOOF) for classification of non-human primate behavior
- Demonstrated performance of HOOF was comparable to a simple pixel masking logistic classifier

Publications/Presentations

- **Atkins TK**, Song T, Kuang R. FIST-nD: A tool for n-dimensional spatial transcriptomics data imputation via graph-regularized tensor completion. (Forthcoming).
- Proctor DM, **Atkins TK**, Chen Q, Conlan S, Deming C, Samson SE, Hayden MK, Segre JA. Integrating data types to understand the genomic epidemiology of the emerging fungal pathogen Candida auris. Presented at: NHGRI Annual Retreat; October 14-15 2022; Natcher Conference Center, Bethesda, MD.
- **Atkins TK**, Proctor DM, Deming C, Chen Q, Conlan SP, Segre JA. Diagnostic Measures for Fungal Genome Variant Callers. Poster session presented at: NIH Summer Poster Day; Aug. 3 2022; Virtual.
- **Atkins TK**, Song T, Kuang R. FIST-GT: A tool for multidimensional spatial transcriptomics data imputation via graph-regularized tensor completion. Poster session presented at: University of Minnesota Bioinformatics and Computational Biology Research Symposium; Jan. 13. 2022; Virtual.
- **Atkins TK**, Chan-Santiago JA, Megret R. Re-Identification of Honeybees via Attention-Based Feature Aggregation along Trajectories. Presented at: IQ BIO REU, NEURO-ID, & IBD2K Research Presentations; Virtual.

Teaching Experience

CSCI 1933: Introduction to Data Structures and Algorithms **Aug 2020 - Dec 2020**

Teaching Assistant under Dr. Chris Dovolis

- Gave weekly lab presentations
- Designed and implemented a lab manual covering an introduction to Object-Oriented Programming
- Created a course feedback survey to better understand student needs and satisfaction
- Met with students three times over the semester to discuss course performance and feedback
- Assisted students at office hours

CSCI 2021: Machine Architecture and Organization **Jan. 2021 - May 2021**

Teaching Assistant under Dr. Christopher Kauffman

- Co-led lab sections on low-level programming concepts

- Offered feedback on course design and problem descriptions
- Assisted students at office hours

Coursework

- **Computational Biology:** Functional Genomics, Systems Biology, and Bioinformatics; Computational Techniques in Genomics; Bioinformatic Analysis; Personal Genome Analysis; Large Scale Omic Data in Plant Biology; Genetics; *Theoretical Neuroscience (in progress)*; *Immunology (in progress)*
- **Computer Science:** Algorithms and Data Structures; Data Visualization; Special Topics in Computer Science (Teaching in Computer Science); Honors Discrete Structures of Computer Science; Program Design and Development; *Natural Language Processing (in progress)*
- **Statistics and Mathematics:** Regression and Correlated Data; Introduction to Statistical Computing; Applied Statistics I/II; Theory of Statistics I/II; Applied Linear Algebra; *Bayesian Astrostatistics (in progress)*

Skills

- **Bioinformatics methods and tools:** NCBI databases; UCSC Genome browser; BLAST/BLAT; Bcftools; Freebayes; GATK; MSA creation and analysis (ClustalW); Phylogenetic tree creation and analysis (IQTREE); AlphaFold2; mFold; PyMOL
- **Programming Languages**: Python (matplotlib, numpy, pandas, Tensorflow); R (ggplot2, Shiny); Bash; LaTeX; Java; C/C++; MATLAB; HTML/CSS/JS