

Thomas K. Atkins  
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## EDUCATION

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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

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**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    Nov. 2019 - Dec. 2020**  
**Lab**

*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**

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- **Atkins TK**, Song T, Kuang R. FIST-nD: A tool for  $n$ -dimensional spatial transcriptomics data imputation via graph-regularized tensor completion. In *bioRxiv*; October 16, 2022. Doi: <https://doi.org/10.1101/2022.10.12.511928>.
- 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; November 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; July 29, 2021; Virtual.

**TEACHING EXPERIENCE**

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**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

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- **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

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- **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; L<sup>A</sup>T<sub>E</sub>X; Java; C/C++; MATLAB; HTML/CSS/JS