

# Thomas Karl Atkins

thomaskatkins.github.io

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## EDUCATION

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**Princeton University**

**Fall 2023 -**

*Ph.D in Quantitative and Computational Biology*

**University of Minnesota - Twin Cities**

**Fall 2019-Spring 2023**

*Bachelor of Science in Computer Science*

*Bachelor of Science in Statistical Science*

*Computational Biology Minor*

Thesis: FIST- $n$ D: A tool for  $n$ -dimensional spatial transcriptomics data imputation via graph-regularized tensor completion. (<https://hdl.handle.net/11299/254602>)

## RESEARCH EXPERIENCE

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**Dr. Marc Riedel Circuits and Biology Lab**

**May 2023 -**

*Department of Electrical Engineering, University of Minnesota*

**Dr. Rui Kuang Computational Biology Lab**

**August 2021 - April 2023**

*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?

- Participated in the 2021 IQ BIO REU program
- 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

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- **Atkins TK**, Song T, Kuang R. FIST- $n$ D: A tool for  $n$ -dimensional spatial transcriptomics data imputation via graph-regularized tensor completion. Presented at University of Minnesota Undergraduate Research Symposium; December 9, 2022; Virtual. Url: <https://ugresearch.umn.edu/presentation-opportunities/fall-symposium/presenters-2022/thomas-atkins>
- Proctor DM, **Atkins TK**, Samson SE, Hayden MK, Segre JA. Integrating Data Types to Understand the Genomic Epidemiology of the Emerging Fungal Pathogen *Candida auris*. Presented at: Cold Spring Harbor Laboratory Microbiome; October 25-29 2022.
- **Atkins TK**, Song T, Kuang R. FIST- $n$ D: 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>.
- **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, Mégret 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 2021: Machine Architecture and Organization**

**Spring 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

### **CSCI 1933: Introduction to Data Structures and Algorithms**

**Fall 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

## 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; Theoretical Neuroscience; Pharmacogenomics; Circuits, Computation, and Biology
- **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
- **Statistics and Mathematics:** Regression and Correlated Data; Introduction to Statistical Computing; Applied Statistics I/II; Theory of Statistics I/II; Applied Linear Algebra; Honors Calculus III/IV; Bayesian Astrostatistics; Consultation and Communication for Statisticians
- **Biology:** Honors Introduction to Biology, Genetics; Immunology

## 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