Thomas Karl Atkins

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EDUCATION

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-nD: A tool for n-dimensional spatial transcriptomics data imputation via graph-regularized tensor completion. (`https://hdl.handle.net/11299/254602`)

RESEARCH EXPERIENCE

with Drs. Julien Ayroles and Lydia Lynch   **Jan 2024 -**
Lewis-Sigler Institute for Integrative Genomics, Princeton University
How do we understand variation in immunological systems?

- Working with data from communities in Northern Kenya who are undergoing transitions from pastoralist to market-integrated lifestyles
- Analyzing genomic, transcriptomic, and immunological data to determine the impact of genetic and environmental factors on immunological variation

with Dr. Marc Riedel   **May 2023 - Aug 2023**
Department of Electrical Engineering, University of Minnesota
Do HLA-peptide binding predictors perform better on alleles common in European populations?

- Found strong geographic biases in frequency of training data used to train popular HLA-peptide binding prediction model NetMHCpan and NetMHCIIpan
- Evaluated performance of these models on non-European alleles, finding no difference in prediction accuracy between populations
- Published results in *Frontiers in Immunology* as first and corresponding author

with Dr. Rui Kuang   **August 2021 - April 2023**
Department of Computer Science, 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

with Dr. Julie Segre   **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

with Dr. Rémi Mégret   **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

Publications & Presentations

- **Atkins TK**, Garske KM, Peng JZ, Chao M, Kahumbu J, Lea A, Ayroles JF. A multiomic atlas of a Northern Kenyan cohort. Presented at Chan-Zuckerburg Initiative Cell Science Meeting; 10 Sep 2024.

- **Atkins TK**, Solanki A, Vasmatzis G, Cornette J, Riedel M. Evaluating NetMHCpan performance on non-European HLA alleles not present in training data. *Frontiers in Immunology*, 15 Jan 2024. `https://doi.org/10.3389/fimmu.2023.1288105`

- **Atkins TK**, Song T, Kuang R. FIST-nD: A tool for n-dimensional spatial transcriptomics data imputation via graph-regularized tensor completion. Presented at University of Minnesota Undergraduate Research Symposium; 9 Dec 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; 25-29 Oct 2022.

- **Atkins TK**, Song T, Kuang R. FIST-nD: A tool for n-dimensional spatial transcriptomics data imputation via graph-regularized tensor completion. *bioRxiv*; 16 Oct 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. Presented at: NIH Summer Poster Day; 3 Aug 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; 29 Jul 2021; Virtual.

TEACHING EXPERIENCE

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

- **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