

Benjamin T. James

Graduate research assistant

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Education

University of Tulsa

BSc in Computer Science, Mathematics

Tulsa, Oklahoma

2015 - 2019

- GPA: 3.747

Massachusetts Institute of Technology

SM in EECS

Cambridge, MA

2019-

- GPA: 3.5

Massachusetts Institute of Technology

Ph.D in EECS

Cambridge, MA

2019-

Research Experience

Massachusetts Institute of Technology

Graduate researcher, Kellis Lab

Cambridge, MA

September 2019-

- Single-cell epigenomic and transcriptomic analysis of human disease
- Single-cell methods development

University of Tulsa

Undergraduate researcher, Girgis Lab

Tulsa, Oklahoma

February 2016 - May 2019

- Performed research and development of intelligent methods to compare nucleotide sequences in the University of Tulsa's Bioinformatics Toolsmith Laboratory under the supervision of Hani Girgis

Awards, Grants & Honors

National Science Foundation Graduate Research Fellowship 2019
MIT Cronin Fellowship 2019
Tulsa Undergraduate Research Challenge 2017,2018

Journal Publications

- C. A. Boix, B. T. James, Y. P. Park, W. Meuleman, and M. Kellis. [Regulatory genomic circuitry of human disease loci by integrative epigenomics](#). *Nature*, 590(7845):300–307, 2021
- B. T. James, B. B. Luczak, and H. Z. Girgis. [MeShClust: an intelligent tool for clustering DNA sequences](#). *Nucleic Acids Research*, 46(14):e83, 2018
- B. B. Luczak, B. T. James, and H. Z. Girgis. [A survey and evaluations of histogram-based statistics in alignment-free sequence comparison](#). *Briefings in Bioinformatics*, page bbx161, 2017

- H. Z. Girgis, B. T. James, and B. B. Luczak. [Identity: rapid alignment-free prediction of sequence alignment identity scores using self-supervised general linear models](#). *NAR genomics and bioinformatics*, 3(1):lqab001, 2021
- A. Zielezinski, H. Z. Girgis, G. Bernard, C.-A. Leimeister, K. Tang, T. Dencker, A. K. Lau, S. Röhling, J. J. Choi, M. S. Waterman, M. Comin, S.-H. Kim, S. Vinga, J. S. Almeida, C. X. Chan, B. T. James, F. Sun, B. Morgenstern, and W. M. Karlowski. [Benchmarking of alignment-free sequence comparison methods](#). *Genome Biology*, 20(1):144, 2019
- A. Velasco, B. T. James, V. D. Wells, and H. Z. Girgis. [Look4TRs: a de novo tool for detecting simple tandem repeats using self-supervised hidden Markov models](#). *Bioinformatics*, 07 2019. btz551

Article preprints

- B. T. James and H. Z. Girgis. [MeShClust2: Application of alignment-free identity scores in clustering long DNA sequences](#). 2019

Talks and Posters

- X. Xiong, B. T. James, C. A. Boix, Y. Park, N. Sun, L. Hou, K. Galani, L.-L. Ho, H. Mathys, D. Bennett, L.-H. Tsai, and M. K. Kellis. Single-cell transcriptomic and epigenomic dissection of Alzheimer’s disease pinpoints causal GWAS variants and reveals epigenome erosion. Talk presented to American Society of Human Genetics, October 26, 2022
- B. T. James, N. Sun, R. Linville, K. Galani, L.-L. Ho, A. Renfro, S. Pineda, X. Xiong, C. Boix, B. Madras, D. Gabuzda, M. Heiman, and M. Kellis. Single-cell multi-omic transcriptomic and epigenomic dissection of opioid use disorder reveals regulatory circuitry changes across multiple brain regions. Talk presented to SCORCH consortium, February 23, 2022
- B. T. James, I. Jungreis, and M. Kellis. Completing gene annotations with regulatory information. Talk presented to GENCODE consortium, June 7, 2022
- B. T. James and M. Kellis. Single-cell multiomic snRNA and snATAC integration: approaches and challenges. Talk presented to SCORCH consortium, February 23, 2022
- B. T. James, C. A. Boix, and M. Kellis. Enhancer-gene benchmarking from regulatory networks. Talk presented to the ENCODE NAWG Distal Regulation group, June 25, 2021
- C. A. Boix, B. T. James, Y. P. Park, W. Meuleman, and M. Kellis. Regulatory genomic circuitry of human disease loci by integrative epigenomics. Talk presented to the ENCODE NAWG Distal Regulation group, December 9, 2020
- B. T. James, B. B. Luczak, and H. Z. Girgis. MeShClust: An intelligent tool for clustering DNA sequences. Poster presented at Intelligent Systems for Molecular Biology, Chicago, IL, July 6-10, 2018
- B. T. James, B. B. Luczak, and H. Z. Girgis. MeShClust: An intelligent tool for clustering DNA sequences. Talk presented at University of Tulsa Research Colloquium, Tulsa, OK, April 2-6, 2018

Mentoring

Research mentor for Masters students

Alex Berg

2022-

Service

Reviewer

- Nature Biotechnology
- ISMB 2022

SCORCH Consortium

<https://scorch.igs.umaryland.edu/>

Co-chair

2022

- Primary Analysis working group co-chair

Tulsa Hurricane Mathfest

Tulsa, Oklahoma

Organizer

2017, 2018, 2019

- Helped organize a math competition for high school students in the Tulsa area
- <http://mathfest.utulsa.edu>

Last updated

August 31, 2022