Benjamin T. James

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Education

- **Massachusetts Institute of Technology** *September 2019 – August 2026*
  Ph.D in Electrical Engineering and Computer Science, minor in Econometrics Cambridge, Massachusetts
  - GPA: 4.80/5.00
- **University of Tulsa** *Aug 2015 – May 2019*
  BSc in Mathematics, BSc in Computer Science Tulsa, Oklahoma
  - GPA: 3.747/4.000

Selected Research Includes two (co-) first author **Cell** papers, one second-author **Nature** paper

- **Single-cell dissection of the human brain** *2021 - 2026*
  Tools: R, Python, Bash, C++ [GitHub]
  - Integrated high-dimensional, multimodal (scRNA-seq/scATAC-seq) data from **hundreds of postmortem human brains** and mouse brains from corresponding model systems
  - Analyzed these data across several **human disease contexts** and brain regions using **functional genomics**, careful integration/atlasing, and case-control causal inference to infer disease pathology.
  - Created new methods to make inferences on new technologies (e.g. spatial transcriptomics) and gene module discovery, mostly using random matrix theory and high-dimensional statistics
  - Connected millions of DNA elements active across human tissues to their target genes
  - Linville*, R. M., **James*, B. T.**, Galani, K., Ho, L., Shin, J., Oliver, E., Bock, R., Murray, E. M., Louca, M., Oke, O., Wang, C., Engelberg-Cook, E., DeTure, M., Farrell, V., Fitzwalter, B., Pineda, S., Sathitloetsakun, S., Liang, X., Madras, B., and Dickson, D. W., Mash, D. C., Turecki, G., Wheeler, V. C., Alvarez, V. A., Gabuzda, D., Kellis, M., Heiman, M. (2025). Cross-species single cell atlas of the striatum defines cell type and subregion disease vulnerabilities. **Cell**.
  - Xiong*, X., **James*, B. T.**, Boix*, C. A., Park, Y. P., Galani, K., Victor, M. B., Sun, N., Hou, L., Ho, L.-L., Mantero, J., Scannail, A. N., Dileep, V., Dong, W., Mathys, H., Bennett, D. A., Tsai, L.-H., & Kellis, M. (2023). Epigenomic dissection of Alzheimer's disease pinpoints causal variants and reveals epigenome erosion. *Cell*, *186*(20), 4422–4437.e21. https://doi.org/10.1016/j.cell.2023.08.040
  - Boix, C. A., **James, B. T.**, Park, Y. P., Meuleman, W., & Kellis, M. (2021). Regulatory genomic circuitry of human disease loci by integrative epigenomics. *Nature*, *590*(7845), 300–307. https://doi.org/10.1038/s41586-020-03145-z
- **Intelligent clustering of DNA sequences** *2016-2019*
  Tools: C++/OpenMP; gdb/valgrind [GitHub]
  - Developed a fast, concurrent method as an undergraduate student to approximate an expensive method for DNA similarity (alignment) and used for clustering. Led to **5** journal publications as an undergrad.
  - **James, B. T.**, Luczak, B. B., & Girgis, H. Z. (2018). MeShClust: an intelligent tool for clustering DNA sequences. *Nucleic Acids Research*, *46*(14), e83. https://doi.org/10.1093/nar/gky315

Skills

- **Programming Languages:** R and Python (Daily use), C++ (+pybind11/Rcpp), Golang, Bash/POSIX sh, C, AWK & Perl, Julia, Common Lisp
- **Research-specific Packages and Tools:** Bioconductor, scverse, samtools/bedtools, Eigen, NumPy/SciPy/SK-Learn, Snakemake & Nextflow, brms
- **DevOps/MLOps:** De-facto manager of two lab-wide compute clusters, managing software (Lmod, conda, Docker, singularity environments, CUDA/NV admin, Terraform, Ansible, etc). Experienced Linux user (Debian/Gentoo user since 2014), see `my dotfiles`, formerly an ArchLinux `maintainer`
- **Side projects:** Wrote an **agentic** harness tool to specify disposable agent virtual machines and deploy them, Contributed the dot-product distance into the `RcppAnnoy` package required by R genomics libraries, Wrote the sparse-matrix math for the `pychromVAR` package for transcription factor enrichment in snATAC-seq, wrote a complete BF compiler and a Pascal compiler frontend both in C, wrote and deployed a multi-user webapp on a VPS (Apache/Flask/PostgresQL)

Honors and Awards

- **NSF GRFP** *May 2019*
  National Science Foundation
- **Cronin Fellowship** *April 2019*
  MIT EECS department