Joseph C. Mays, Ph.D.

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EDUCATION

New York University Grossman School of Medicine, New York, NY — December 2023
Ph.D., Cell Biology

New York University Grossman School of Medicine, New York, NY — September 2021
Master of Philosophy, Cell Biology

Colgate University, Hamilton, NY — May 2016
Bachelor of Arts, Molecular Biology (honors) & Classical Studies

HONORS, AWARDS, & GRANTS

2021	Special MacCracken Award, NYU School of Medicine
2020	T32 Cell Biology Training Grant, NYU School of Medicine
2019	T32 Genome Integrity Training Grant, NYU School of Medicine
2017	NIDCD Director's Award, NIH
2016	Magna Cum Laude, Colgate University
2016	Beta Beta Beta Biology Honor Society, Colgate University
2016	Eta Sigma Phi Classics Honor Society, Colgate University
2016	N.L. Andrews Prize for Excellence in the Classics, Colgate University
2013–2016	Dean's Award for Academic Excellence, Colgate University
2016	James M. Maury M.D. Scholarship, Colgate University
2016	Marion A. Cincotta Scholarship, Colgate University
2012–2015	North Eastern Roofing Educational Foundation Scholarship, NERCA

RESEARCH EXPERIENCE

New York University Grossman School of Medicine, New York, NY

Postdoctoral Fellow, Laboratory of Teresa Davoli, PhD — *December 2023–Present*
Ph.D. Student, Laboratory of Teresa Davoli, PhD — *April 2019–December 2023*

- Implement and optimize pipelines for next-generation sequencing and single-cell genomic analyses.
- Designed **KaryoTap** assay for high-sensitivity high-throughput detection of DNA copy number variants in single cells by adapting the Tapestri targeted sequencing platform.
- Developed **karyotapR** software package for R to automate analysis of single-cell DNA-seq data from KaryoTap.
- Utilized simulated data and experimental sample data to improve KaryoTap assay design and performance.
- Troubleshooted plasmid design and read alignment to enable lentiviral barcoding for KaryoTap.
- Created **KaryoCreate** technology to engineer CRISPR-mediated chromosome-specific aneuploidy in cells with a small team.
- Implemented single-cell RNA-seq analysis pipeline on HPC cluster to evaluate the efficiency of the KaryoCreate system.
- Constructed 3 R Shiny web apps to automate genomics-related analysis tasks for non-technical staff.
- Consult on single-cell genomics and bioinformatics projects with computational and experimental staff within our lab and with collaborating labs.
- Explore role of aneuploidy in human placenta development using cell culture methods and publicly available genomic sequencing data.
- Mentored a PhD student and Masters student with an emphasis on computational skills and project management.

National Institute on Deafness and other Communication Disorders, NIH, Bethesda, MD
Post-baccalaureate Fellow, Laboratory of Cochlear Development *July 2016–August 2018*
Student Intern, Laboratory of Cochlear Development *June 2015–December 2015*
Mentors: Michael Kelly, PhD; Kathryn Ellis, PhD; Matthew Kelley, PhD

- Evaluated the role of histone acetylation in cell fate plasticity in the developing mammalian cochlea.
- Characterized heterogeneity within the mammalian cochlea using several single-cell RNA-seq platforms.
- Profiled single-cell transcriptomes of the mammalian pineal gland and their role in circadian rhythm regulation in collaboration with the Nat'l Institute of Child Health and Development.
- Mentored undergraduate students in project management and experimental techniques.
- Collaborated with several NIH labs to share single-cell omics experience and skills.

SKILLS

- **Coding Languages**: R (7+ years; package development, tidyverse modules [SQL equivalent]), Bash (working knowledge), Python (basic knowledge; NumPy)
- **Software**: Git, Nextflow, Snakemake and GNU Make, Docker, Linux command line tools (bwa, samtools, trimmomatic, fastqc, GATK HaplotypeCaller), high-performance computing clusters, Slurm, R Shiny, Snapgene
- **Bioinformatics Skills**: NGS DNA sequence analysis (QC, adaptor trimming, alignment), short-read whole genome sequencing and variant analysis, single-cell omics sequencing analysis (e.g. Seurat), data visualization, statistical analyses (data wrangling, hypothesis testing, supervised/unsupervised machine learning and clustering, linear and logistic statistical modeling)
- **Laboratory Skills and Equipment**: DNA extraction and purification, genomic library preparation, mammalian cell culture, 10X Genomics scRNA-seq, Tapestri scDNA-seq, FACS/flow cytometry, PCR

EMPLOYMENT EXPERIENCE

Colgate University, Hamilton, NY
Technology Assistant, Classics Department *February–May 2016*

- Prepared and maintained presentation equipment for Prof. Ammerman's weekly classes

MedLabs Diagnostics, Cedar Knolls, NJ
Intern, Department of Molecular Diagnostics *June–August 2014*

- Performed amplification-based diagnostic assays to test samples for bacteria and parasites
- Participated in diagnostic method comparison studies and method validations
- Compiled and edited standard operating procedures for new diagnostic instruments and methods

LEADERSHIP EXPERIENCE

New York University Grossman School of Medicine, New York, NY
Leadership Committee, Student Interview Initiative *November 2020–February 2021*

- Organized and executed a new program allowing PhD student interviews to be conducted by current students

Secretary, Student Council *July 2019–July 2020*

- Coordinated with administration to organize and execute PhD program recruitment
- Organized orientation events and onboarding for matriculating students
- Organized meetings and resources for student council members and collaborators

TEACHING EXPERIENCE

New York University Grossman School of Medicine, New York, NY
Teaching Assistant, Rigor and Reproducibility Course *Fall 2021, Fall 2022, Fall 2023*

National Institute on Deafness and other Communication Disorders, National Institutes of Health, Bethesda, MD
Instructor, EARssentials Mouse Cochlea Dissection Workshop *July 2016, July 2017*

- Co-taught laboratory workshop on neonatal mouse cochlea micro-dissection

ORAL PRESENTATIONS

- *Developing a toolkit to detect aneuploidy in single cells at scale.*
  Institute for Systems Genetics Nano Seminar, NYU School of Medicine, October 2023.
- *Exploration of a multicellular phenotype in cochlear tissue using single-cell RNA-sequencing methods.*
  NIDCD Trainee Talks, NIH, June 2017.
- *Drop-Seq as a low-cost, high-throughput method for single-cell gene expression profiling of cochlear cells.*
  NIDCD Division of Intramural Research Retreat, NIH, May 2017.
- *Using Seurat and Monocle for analysis of single-cell RNA-sequencing data.*
  NIAMS Bioinformatics Interest Group, NIH, April 2017.
- *Lineage tracing in the developing mammalian cochlea.*
  Colgate University Honors Talks, April 2016.
- *Doing science in college.* (Invited Speaker)
  West Milford High School Science Honor Society, March 2016.

POSTER PRESENTATIONS

- *Single-cell pineal gland neuro-transcriptomic analysis reveals cell type-specific day/night changes.*
  NICHD Division of Intramural Research Retreat, NIH, September 2017.
- *Drop-seq as a low-cost, high-throughput method for single-cell gene expression profiling of cochlear cells.*
  Post-baccalaureate Fellow Poster Day, NIH, May 2017.
- *Demonstration of analysis of high-throughput single cell RNA-Seq data using open-source R packages.*
  Pi Day, NIH, March 2017.
- *Drop-seq as a low-cost, high-throughput method for single-cell gene expression profiling of cochlear cells.*
  Association for Research in Otolaryngology Mid-Winter Meeting, February 2017.

OTHER CONFERENCES ATTENDED

- *Wellcome Connecting Science Single Cell Biology.* Hinxton, UK (Virtual), June 2022.
- *Next-Generation Genomics.* New York University, New York, NY (Virtual), August 2021.
- *New York Stem Cell Foundation.* The Rockefeller University, New York, NY, October 2019.
- *Next-Generation Genomics.* New York University, New York, NY, August 2019.
- *Eastern Auditory Retreat.* Georgetown University, Washington, DC, June 2017.
- *Single Cell Analysis Investigators Meeting.* National Institutes of Health, Bethesda, MD, June 2017.

PUBLICATIONS

Mays JC, Mei S, Bosco N, Zhao X, ... Davoli T. (2023). KaryoTap enables aneuploidy detection in thousands of single human cells. *bioRxiv*.
bioRxiv </> Github Codebook

Bosco N*, Goldberg A*, Zhao X*, **Mays JC***, Cheng P*, Johnson AD*, ... Davoli T. (2023). KaryoCreate: A CRISPR-based technology to study chromosome-specific aneuploidy by targeting human centromeres. *Cell*.
PubMed 37075754 </> Github Codebook *equal contribution

Kolla L, Kelly MC, Mann ZF, Ellis K, Lemons A, Palermo AT, So KS, **Mays JC**, Orvis J, Burns JC, Hertzano R, Driver EC, and Kelley MW. (2020). Characterization of cochlear hair cell development at the single cell level. *Nat Commun* 11:2389.
PubMed 32404924

Bianchi JJ*, Zhao X*, **Mays JC**, and Davoli T. (2020). Not all cancers are created equal: Tissue specificity in cancer genes and pathways. *Curr Opin Cell Biol* 63:135-143.
PubMed 32092639

Coon SL, Fu C, Hartley S, Holtzclaw L, **Mays JC**, Kelly MC, Kelley MW, Mullikin JC, Rath MF, Savastano LE and Klein DC. (2019). Single Cell Sequencing of the Pineal Gland: The Next Chapter. *Front Endocrinol* 10:590.
PubMed 31616371

Mays JC, Kelly MC, Coon SL, Holtzclaw L, Rath MF, Kelley MW, and Klein DC. (2018). Single-cell RNA sequencing of the mammalian pineal gland identifies two pinealocyte subtypes and cell type-specific daily patterns of gene expression. *PLOS ONE* 13(10): e0205883.
PubMed 30347410 </> Github Codebook