

# Rika Chan

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## RELEVANT WORK EXPERIENCES

### Mansfield Lab, Barnard College

New York, NY

Researcher

Sep 2024 - Present

- Processed and integrated 20,000+ cells and 18,000+ genes across 3 embryonic stages, **identifying 20+ novel markers** of brown adipocyte differentiation.
- Developed a **computational pipeline** combining RNA velocity, CellRank, and **composite kernels to reconstruct lineage trajectories** and identify terminal brown adipocyte states with upstream progenitors.
- Compared CosMx and Visium spatial transcriptomics platforms, assessing efficiency and resolution; **integrated data using Tangram deep learning**, enhancing detection of spatially localized progenitors.
- Co-authored a manuscript **published on bioRxiv** and **submitted to Developmental Biology**, contributing experimental and computational analyses.

### Empirical Reasoning Center, Barnard College

New York, NY

Student Fellow

Mar 2023 - Present

- Mentored **50+ students across 10+ disciplines** in advanced data analytics, quantitative reasoning, and statistical methodologies, enhancing their ability to design experiments, analyze data, and interpret results.
- Instructed students in **R, Python, Stata, ArcGIS, and QGIS**, creating tailored learning paths, interactive tutorials, and fostering peer-to-peer collaboration to strengthen technical proficiency and applied computational skills.
- Partnered with faculty and staff to **develop campus-wide data support strategies**, expanding access to statistical resources and promoting integration of data-driven analysis across the curriculum.

### Uhlemann Lab, Columbia Irving Medical Center

New York, NY

Researcher

Jan 2024 - Aug 2024

- Analyzed **whole-genome sequencing (WGS) data from 10+ liver transplant patients** to investigate bacterial adaptation and evolution in immunocompromised hosts.
- Developed and executed **5+ custom Bash scripts** for quality control, species classification, and detection of mobile genetic elements, improving workflow efficiency and reproducibility.
- Synthesized genomic datasets into **actionable insights with potential clinical relevance** and **presented findings** at the Barnard College Summer Research Institute through data visualizations and oral presentation.

## RELEVANT PROJECT EXPERIENCE

### scViewer: Single-cell analysis made easy

New York, NY

Developer

- Designed support for .h5ad uploads** up to 10GB, incorporating efficient memory management to **handle high-dimensional data** at scale.
- Implemented core single-cell analysis tools** within the interface, including a quality control pipeline, multiplet detection, dimensionality reduction (UMAP/PCA), clustering, differential gene expression, and customizable visualizations. These features allow users to conduct end-to-end analyses directly within the app.
- Created an **intuitive graphical interface** to enhance accessibility, lowering technical barriers and fostering broader adoption of single-cell transcriptomics analysis across disciplines.

## EDUCATION

### Barnard College, Columbia University

New York, NY

B.A. Computational Biology

Graduation Date: May 2026

## SKILLS

**Computer:** R, Python, Bash, HTML/CSS, Swift, bioinformatics (scRNA-seq, bulk RNA-seq, ATAC-seq, ChIP-seq, trajectory inference, gene regulatory networks), machine learning (ESM, CNNs), and data visualization/analysis tools (ArcGIS, QGIS, Tableau, Stata, Microsoft 365).