

Rika Chan

rc3517@barnard.edu | +1 (646) 255-9183 | [LinkedIn](#) | [rikaaaac.github.io](#)

EDUCATION

Barnard College, Columbia University | New York, NY

May 2026

B.A. in Computational Biology

Relevant Courses: Computational Genomics, Natural Language Processing, ML for Functional Genomics, DL for Biomedical Signal Processing, Molecular Genetics, Microbial Genomics, ML for Statistical Genomics

TECHNICAL SKILLS

Programming languages: Python (advanced), R (advanced), R Shiny (Proficient), Bash (Proficient), HTML/CSS (Proficient), Rust (Proficient), React (Proficient), Typescript (Proficient), Swift (Proficient), Snakemake (Proficient), Docker (Proficient), High-Performance Computing (Proficient)

RESEARCH & ANALYTICAL EXPERIENCES

Mansfield Lab, Barnard College | Researcher | New York, NY

Sep 2024 - Present

- Analyzed large-scale biological data (20,000+ cells, 18,000+ genes) across early development stages, uncovering 20+ new signals linked to brown fat cell formation, contributing to adipogenesis research.
- Designed a custom workflow to track how cells develop over time, mapping their journey from early stem-like states to mature brown fat cells.
- Evaluated and integrated cutting-edge spatial biology technologies with AI methods to improve detection of where brown fat cells emerge in tissue.
- Synthesized key findings from single cell datasets, leading to potential target genes for perturbation experiment presented at the Barnard College Summer Research Institute.

Rabadan Lab, Columbia Irving Medical Center | Researcher | New York, NY

Sep 2024 - Present

- Developed a machine learning framework leveraging protein language models and contrastive learning to predict how influenza viruses adapt to different hosts, enabling insights into cross-species transmission.
- Applied advanced AI techniques to identify host-specific mutations and key amino acid variants in the PB2 protein, highlighting evolutionary signatures that distinguish viral strains.
- Achieved high predictive performance, demonstrating the potential of AI-driven protein modeling to advance understanding of influenza subtype evolution and zoonotic risk assessment.

Empirical Reasoning Center | Student Fellow | New York, NY

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, Excel, 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 | Researcher | New York, NY

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 custom 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.

SELECTED PROJECTS

scViewer | Developer | New York, NY

Summer 2025

- Engineered support for .h5ad uploads up to 10GB with efficient memory management, enabling scalable single-cell data analysis for datasets over 20,000 cells.
- Built an interactive interface with integrated quality control, clustering, differential expression, and customizable visualizations to broaden accessibility of single-cell transcriptomics.

ArcCell | Developer | New York, NY

Spring 2025

- Developed an AI model to improve cell type identification, surpassing a leading benchmark tool and highlighting key genetic markers.
- Optimized data processing pipelines for large-scale single-cell datasets, ensuring faster and more reliable analysis across samples.