Yuhan Hao

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Yuhan.hao@nyu.edu	

EDUCATION		
New York Unive	rsity, New York, USA	
Ph.D. in Biology;	Spring 2023	
Honors:	Fleur Strand Graduate Fellowship from New York University (2022)	
	New York Genome Center Outstanding Contribution (2021)	
	JTech Scholarship from The James P. Taylor Foundation (2020)	
	The Eugene Bell Award from New York University (2020)	
	The Chair's Award from New York University (2019)	
Fordham Unive	rsity, New York, USA	
M.S. in Data Scie	Aug. 2017	
Honors:	Professional Development Grant of Fordham University	
Fordham Unive	rsity, New York, USA	
M.S. in Biologica	May 2016	
Honors:	Professional Development Grant of Fordham University	
Dalian Universit	t y of Technology , Dalian, China	
B.S. in Biotechno	ology; GPA: 87.9/100; Class Ranking: Top 3/60	June 2014
Honors:	Academic Scholarship (Equivalent to the Dean's List), 2010-13	
	National Scholarship (Highest Scholarship for Undergraduate), 2010	
Study Abroad:	Royal Institute of Technology, Sweden	Fall 2011

SELECTED PUBLICATIONS

FULCATION

Full profile: https://scholar.google.com/citations?user=UeuueiYAAAAJ&hl=en&oi=ao

- 1. <u>Hao Y</u>, Stuart T, Kowalski M, Choudhary S, Hoffman P, Hartman A, ... & Satija R. Dictionary learning for integrative, multimodal, and scalable single-cell analysis. *Nature Biotechnology* (In press). 2023.
- 2. <u>Hao Y</u>, Hao S*, Andersen-Nissen E, Mauck WM, Zheng S, Butler A, ... & Smibert P, Satija R. Integrated analysis of multimodal single-cell data. *Cell*. 2021 May.
- 3. <u>Hao Y</u>, Yang L, Neto A G, Amin M, Kelly D, Brown S, Branski R, Pei Z. HPViewer: Sensitive and specific genotyping of human papillomavirus in metagenomic DNA, *Bioinformatics*. 2018 Jun.
- Wessels H-H, Méndez-Mancilla A, <u>Hao Y</u>, ... & Sanjana N, Satija R. Efficient combinatorial targeting of RNA transcripts in single cells with Cas13 RNA Perturb-seq. *Nature Method*. 2022 Dec.
- 5. Kedmi R, Najar TA, Mesa KR, Grayson A, Kroehling L, <u>Hao Y</u>, ... & Littman D. A RORγt+ cell instructs gut microbiota-specific Treg cell differentiation. *Nature*. 2022 Sep.
- Wu L, Hollinshead KE, <u>Hao Y</u>, Au C, Kroehling L, Ng C, ... & Littman D. Niche-selective inhibition of pathogenic Th17 cells by targeting metabolic redundancy. *Cell*. 2020 Aug.
- Stuart T*, Butler A*, Hoffman P, Hafemeister C, Papalexi E, Mauck III WM, <u>Hao Y</u>, Stoeckius M, Smibert P, Satija R. Comprehensive integration of single-cell data. *Cell*. 2019 Jun.

SELECTED CONFERENCE PRESENTATIONS AND INVITED TALKS

- Dictionary Learning for Integrative, Multimodal, and Scalable Single-cell Analysis. <u>Centers of Excellence</u> in <u>Genomic Science (CEGS)</u> annual meeting, USA, Oct. 2022
- Integrated analysis of single-cell data across modalities and technologies. <u>Genentech Monthly</u> <u>Single-Cell seminar</u>, USA, May 2022
- Dictionary Learning for Integrative, Multimodal, and Scalable Single-cell Analysis. <u>NYGC's Scientific</u> <u>Advisory Board (SAB) meeting</u>, USA, Apr. 2022
- 4. Multi-modal cell profiling and data integration to atlas the immune system. <u>CZI Single-Cell Biology</u> <u>monthly webinar</u>, USA, Apr. 2022
- Integrated analysis and reference mapping of single-cell multimodal data. <u>MRC Weatherall Institute of</u> <u>Molecular Medicine Seminar, University of Oxford</u>, UK, Jan. 2022
- 6. Multimodal representation and mapping of single cell data. <u>Biological Data Science | Cold Spring Harbor</u> <u>Laboratory</u>, USA, Aug. 2020
- Joint representation of single cell multi-omics data. <u>The Biology of Genomes | Cold Spring Harbor</u> <u>Laboratory</u>, USA, May 2020

WORK EXPERIENCE

- 1. *Teaching Assistant* of Statistics and machine learning for genomics in NYU Fall 2020, Fall 2022
- 2. Bioinformatics programmer in Applied Bioinformatics Laboratories NYU Langone Health
- Analyzed metagenomic, ATAC-seq, RNA-seq, whole genome seq data
- 3. Bioinformatics Research Assistant in NYU Langone Health
- 4. *Teaching Assistant* of Discrete Mathematics in Fordham University Fall 2016, Spring 2017

June 2017 – May 2018

June 2016 - May 2017

5. Teaching Fellow of Intro Biology Lab in Fordham University Sept. 2014 – May 2016

COMPUTATIONAL SKILLS

PROGRAMMING LANGUAGES: R, Python, Bash, PyTorch, TensorFlow, Keras, Matlab, Spark, SQL

SOFTWARE DEVELOPMENTS:

- 1. Seurat v4 / Seurat v5 (https://github.com/satijalab/seurat) lead developer
- 2. Azimuth (https://github.com/satijalab/azimuth) lead developer
- 3. HPViewer (https://github.com/yuhanH/HPViewer) lead developer
- 4. MGS-Fast (https://github.com/BCIL/MGS-Fast) developer
- 5. uwot (https://github.com/jlmelville/uwot) contributor