

AVI SRIVASTAVA

SINGLE-CELL (EPI)GENOMICS · COMPUTATIONAL BIOLOGY

New York Genome Center, 101 6th Ave, New York, NY 10013, USA

☎ (+1) 631-974-8087 | ✉ avi.srivastava@nyu.edu | 🏠 k3yavi.github.io | 📱 k3yavi | 🎓 Avi Srivastava

“Multimodal cellular profiling is going to drive new discoveries.”

SUMMARY

Currently I am pursuing the mentored phase (**K99**) of the Pathway to Independence Award as a postdoctoral researcher under the mentorship of Rahul Satija. My research focus is to study the regulatory mechanism of the epigenome in a complex biological system, with a particular focus on studying developmental biological processes.

EDUCATION

Stony Brook University

New York, USA

DOCTOR OF PHILOSOPHY — COMPUTER SCIENCE

2014 - 2019

College of Engineering Roorkee

Roorkee, India

BACHELOR OF TECHNOLOGY — COMPUTER SCIENCE

2008 - 2012

RESEARCH EXPERIENCE

Postdoctoral research associate

New York Genome Center & NYU

MENTOR: RAHUL SATIJA

February 2020 - Present

- Design scalable computational models for the integration of single-cell epigenomic data.
- Develop methods to annotate chromatin states across genome at single-cell resolution — scChromHMM, *Nature Biotechnology*.
- Develop & support R packages for analyzing single-cell transcriptomic and epigenomic data — Seurat (Cell) & Signac (*Nature Methods*).

Ph.D. student

Stony Brook University

ADVISOR: ROBERT PATRO

August 2014 - December 2019

- Design probabilistic models for efficient quantification of bulk & single-cell RNA-seq quantification.
- Develop & maintain methods to perform fast pseudo-alignment of (single-cell)RNA-seq reads — RapMap, *ISMB* - 2016.
- Develop & maintain methods to perform end-to-end (FASTQ to count matrix) processing of RNA-seq data — Salmon (*Nature Biotechnology*) & alevin (*Genome Biology and Nature Methods*).

Computational biology research intern

10x Genomics

MANAGER: PATRICK MARKS

February 2018 - July 2018

- Develop memory-efficient software written in Rust language to perform pseudo-alignment of reads.
- Optimize the performance of the *cellranger* software for the quantification of the data generated by 10x Genomic's sequencing platform.

HONORS & AWARDS

2020	President's Award to Distinguished Doctoral Students
2019	ISCB Travel Fellowship
2019	BioC Travel Fellowship
2016	ISMB Student Travel Fellowship
2016	Distinguished Travel Award
2015	Best Teaching Assistant Award
2014	CS Department Chair Fellowship
2012	Best undergraduate thesis award

Stony Brook, USA
Basel, Switzerland
New York, USA
Florida, USA
Stony Brook, USA
Stony Brook, USA
Stony Brook, USA
Roorkee, India

RESEARCH GRANTS

(K99/R00) Pathway to Independence Award for Early Stage Postdoctoral Researchers

National Cancer Institute, NIH

PRINCIPAL INVESTIGATOR

December 2021 - December 2026

TITLE: Integrated analyses of the epigenome to understand the molecular basis of hematopoietic malignancies.

Essential Open Source Software for Science

Chan Zuckerberg Initiative

ROLE: LEAD STUDENT RESEARCHER; PI: ROB PATRO

December 2018 - December 2019

TITLE: Efficient tools for quantifying and simulating transcript-level abundance in single-cell RNA-seq.

Early CAREER award

National Science Foundation

ROLE: STUDENT RESEARCHER; PI: ROB PATRO

December 2018 - December 2023

TITLE: A Comprehensive and Lightweight Framework for Transcriptome Analysis.

OPEN SOURCE SOFTWARE

Characterizing cellular heterogeneity in chromatin state

A SOFTWARE METHOD TO PERFORM CHROMATIN STATE SEGMENTATION OF SINGLE-CELL DATA

[satijalab/scChromHMM](#)

Single-cell chromatin state analysis with Signac

A TOOLKIT WRITTEN IN R FOR ANALYZING SINGLE-CELL CHROMATIN DATA

[timoast/signac](#)

Integrated analysis of multimodal single-cell data

A R TOOLKIT TO PERFORM INTEGRATED SINGLE-CELL ANALYSIS

[satijalab/seurat](#)

Alevin efficiently estimates accurate gene abundances from dscRNA-seq data

A SUITE OF SOFTWARE METHODS TO PERFORM BULK AND SINGLE-CELL RNA-SEQ QUANTIFICATION

[COMBINE-lab/salmon](#)

A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes

A SUITE OF SOFTWARE METHODS TO PERFORM PSEUDO-ALIGNMENT OF RNA-SEQ READS

[COMBINE-lab/RapMap](#)

TEACHING EXPERIENCE

Swiss Institute of Bioinformatics

ADVANCED TOPICS IN SINGLE-CELL TRANSCRIPTOMICS

Virtual Workshop

[Basel, Switzerland](#)

May 2020

Bioconductor Conference

IMPORTING ALEVIN SCRNA-SEQ COUNTS INTO R/BIOCONDUCTOR

Virtual Workshop

[Boston, USA](#)

July 2020

Cold Spring Harbor Laboratory

STATISTICAL METHODS FOR FUNCTIONAL GENOMICS

Invited Lecturer

[Cold Spring Harbor, USA](#)

July 2018

Stony Brook University

ARTIFICIAL INTELLIGENCE – (CSE 537)

Lecturer & Teaching Assistant

[Stony Brook, USA](#)

Fall 2015

Stony Brook University

SYSTEM FUNDAMENTALS – (CSE 220, 320)

Teaching Assistant

[Stony Brook, USA](#)

Fall 2014 & Spring 2015

PUBLICATION

* DENOTES EQUAL CONTRIBUTIONS; † SUPERVISOR ROLE

Bingjie Zhang*, [Avi Srivastava](#)*, Eleni Mimitou, Tim Stuart, Ivan Raimondi, Yuhan Hao, Peter Smibert, Rahul Satija

Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro

[Nature Biotechnology](#)

March 2022

Wancen Mu, HIRAK SARKAR, [Avi Srivastava](#), KB Choi, Rob Patro, Michael Love

Airpart: Interpretable statistical models for analyzing allelic imbalance in single-cell datasets

[Oxford Bioinformatics](#)

April 2022

Dongze He, Mohsen Zakeri, HIRAK SARKAR, Charlotte Soneson, [Avi Srivastava](#)†, Rob Patro

Alevin-fry unlocks rapid, accurate, and memory-frugal quantification of single-cell RNA-seq data

[Nature Methods](#)

March 2022

Tim Stuart, [Avi Srivastava](#), Shaista Madad, Caleb Lareau, Rahul Satija

Single-cell chromatin state analysis with Signac

[Nature Methods](#)

November 2021

Scott Van Buren, HIRAK SARKAR, [Avi Srivastava](#), Naim U. Rashid, Rob Patro, Michael I. Love

Compression of quantification uncertainty for scRNA-seq counts

[Oxford Bioinformatics](#)

January 2021

Charlotte Soneson, [Avi Srivastava](#), Rob Patro, Michael B Stadler

Preprocessing choices affect RNA velocity results for droplet-based scRNA-seq data

[PLOS Computational Biology](#)

January 2021

[Avi Srivastava](#)*, Laraib Malik*, HIRAK SARKAR, Mohsen Zakeri, Charlotte Soneson, Michael I. Love, Carl Kingsford and Rob Patro

Alignment and mapping methodology impact transcript abundance estimation

[Genome Biology](#)

September 2020

[Avi Srivastava](#), Laraib Malik, HIRAK SARKAR and Robert Patro

A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification

[ISMB-Oxford Bioinformatics](#)

July 2020

HIRAK SARKAR, [Avi Srivastava](#), Hector Corrada Bravo, Michael I. Love and Rob Patro

Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data

[ISMB-Oxford Bioinformatics](#)

July 2020

Anqi Zhu, [Avi Srivastava](#), Joseph Ibrahim, Robert Patro, Michael Love
Nonparametric expression analysis using inferential replicate counts

Nucleic Acid research
August 2019

Hirak Sarkar, [Avi Srivastava](#), Rob Patro
Minnow: A principled framework for rapid simulation of dscRNA-seq data at the read level

ISMB-Oxford Bioinformatics
July 2019

[Avi Srivastava](#), Laraib Malik, Tom Sean Smith, Ian Sudbery, Rob Patro
Alevin efficiently estimates accurate gene abundances from dscRNA-seq data

Genome Biology
March 2019

B Gruning et. al. (listed as part of “The Bioconda Team”)
Alevin efficiently estimates accurate gene abundances from dscRNA-seq data

Nature Methods
July 2018

Fatemeh Almodaresi, Hirak Sarkar, [Avi Srivastava](#), Rob Patro
A space and time-efficient index for the compacted colored de Bruijn graph

ISMB-Oxford Bioinformatics
July 2018

Mohsen Zakeri, [Avi Srivastava](#), Fatemehalsadat Almodarresi TS, and Rob Patro
Improved data-driven likelihood factorizations for transcript abundance estimation

ISMB-Oxford Bioinformatics
July 2017

[Avi Srivastava](#), Hirak Sarkar, Nitish Gupta, and Rob Patro
RapMap: A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes

ISMB-Oxford Bioinformatics
July 2016

[Avi Srivastava](#), Hirak Sarkar, Laraib Malik, Rob Patro
Accurate, Fast and Lightweight Clustering of de novo Transcriptomes using Fragment Equivalence Classes

RECOMB-seq
April 2016

K Yadav, [Avi Srivastava](#), A Mittal, MA Ansari
Texture-based medical image retrieval in compressed domain using compressive sensing

IJBRA
March 2014

K Yadav, [Avi Srivastava](#), A Mittal, MA Ansari
GPU parallel implementation of B-spline non-rigid grid registration using free-form deformations

IJBET
July 2013

POSTER

Bingjie Zhang*, [Avi Srivastava](#)*, Eleni Mimitou, Tim Stuart, Ivan Raimondi, Yuhao Hao, Peter Smibert, Rahul Satija
Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro & scChromHMM

EpiCypher Conference
2021

[Avi Srivastava](#), Laraib Malik, Tom Sean Smith, Ian Sudbery, Rob Patro
Alevin efficiently estimates accurate gene abundances from dscRNA-seq data

BioC, ISMB & RECOMB-2019
2019

ACADEMIC SERVICE

PROGRAM COMMITTEE

ISMB, Genome Sequence Analysis - 2022

AD HOC PEER REVIEW

Regular peer review activity for Journals: Nature Communication, Genome Biology, Oxford Bioinformatics, Scientific report, BMC Bioinformatics, BMC Genomics, JOSS, PeerJ and Conferences: ISMB & RECOMB

PROFESSIONAL MEMBERSHIP

Rust-Bio Project
Bioconda Project
Bioconductor Project
International Society of Computational Biology

MENTORSHIP

Mian Hua Zheng & Ebube Michael, Summer Interns at the New York Genome Center

INVITED TALK

Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro
SEMINAR SERIES, DANA FARBER CANCER INSTITUTE

CFCE & CICA Virtual Series
December 2021 & February 2022

A Bayesian framework for inter-cellular information sharing for dscRNA-seq data
VIRTUAL CONFERENCE

ISMB
July 2020

Alevin efficiently estimates accurate gene abundances from dscRNA-seq data
CONFERENCE

ISCB-student council meeting, Basel
July 2019

Algorithmic Advancement in Transcriptome Analyses
CONFERENCE

The Laufer Center, Stony Brook
July 2017

RapMap: A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes
CONFERENCE

ISMB, Florida
July 2016

REFERENCE

Rahul Satija, Ph.D.

ASSOCIATE PROFESSOR OF BIOLOGY
rsatija@nygenome.org

New York Genome Center & NYU

Postdoctoral Mentor

Rob Patro, Ph.D.

ASSOCIATE PROFESSOR OF COMPUTER SCIENCE
rob@cs.umd.edu

University of Maryland

Ph.D. Advisor

Ross Levine, MD

PHYSICIAN-SCIENTIST, LEUKEMIAS
leviner@mskcc.org

Memorial Sloan Kettering

K99 co-mentor

James Fagin, MD

PHYSICIAN-SCIENTIST, THYROID CANCER
fagin@mskcc.org

Memorial Sloan Kettering

Collaborator