

# Avi Srivastava

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📄 <http://k3yavi.github.io/>  
🌐 [www.github.com/k3yavi](http://www.github.com/k3yavi)

## Current Research Interests

Efficient and Scalable Algorithms for analysing bulk/single-cell RNA-seq data  
Uncertainty Aware Graphical Models for Transcriptomic/Epigenomic data

## Education

- 2014–2019 **Ph.D.**, *Department of Computer Science*, Stony Brook University, New York, USA.  
Advisor: Rob Patro, Research Area: Computational Biology, Machine Learning, (bio)Statistics.
- 2008–2012 **B.Tech.**, *Department of Computer Science*, College of Engineering Roorkee, Roorkee, India.  
Advisor: Ankush Mittal, Research Area: Medical Imaging (CBIR), Parallel Computing.

## Employment

- 2020–Present **New York Genome Center**, *Manhattan, New York, USA*.  
*Postdoctoral Research Associate*.  
Mentor: Rahul Satija
- 2018(Summer) **10x Genomics**, *Pleasanton, California, USA*.  
*Computational Biology Research Intern*.  
Mentor: Patrick Marks
- 2016(Summer) **Roche Sequencing Solutions**, *Pleasanton, California, USA*.  
*Research Intern, Infectious Diseases Unit*.  
Mentor: Darya Filippova
- 2014–2019 **Stony Brook university**, *Stony Brook, New York, USA*.  
2015–2019 *Research Assistant, Department of Computer Science*.  
2014–2015 *Teaching Assistant, Department of Computer Science*.  
2013–2014 **Accenture Services Pvt Ltd.**, *Pune, India*.  
*Software Engineer, Service-Oriented Architecture Development Group*.

## Publications

### Papers ([Google Scholar](#))

\* denotes equal contribution.

- 2021 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", *bioRxiv*, 2021.
- 2021 Avi Srivastava\*, Bingjie Zhang\*, Eleni Mimitou, Tim Stuart, Ivan Raimondi, Yuhao Hao, Peter Smibert, Rahul Satija, "Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro", *bioRxiv*, 2021.
- 2021 Wancen Mu, HIRAK SARKAR, Avi Srivastava, KB Choi, Rob Patro, Michael Love, "Airpart: Interpretable statistical models for analyzing allelic imbalance in single-cell datasets", *bioRxiv*, 2021.
- 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*, 2021.
- 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*, 2021.

- 2021 Y Hao et. al., "Integrated analysis of multimodal single-cell data", *Cell*, 2021.
- 2021 Tim Stuart, [Avi Srivastava](#), Shaista Madad, Caleb Lareau, Rahul Satija, "Single-cell chromatin state analysis with Signac.", *Nature methods*, 2021.
- 2020 [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*, 2020.
- 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", *Proceedings of ISMB-20*, Oxford Bioinformatics, 2020.
- 2020 [Avi Srivastava](#), Laraib Malik, Hirak Sarkar and Robert Patro, "A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification", *Proceedings of ISMB-20*, Oxford Bioinformatics, 2020.
- 2019 Hirak Sarkar, [Avi Srivastava](#), Rob Patro, "Minnow: A principled framework for rapid simulation of dscRNA-seq data at the read level", *Proceedings of ISMB-19*, Oxford Bioinformatics, 2019.
- 2019 Anqi Zhu, [Avi Srivastava](#), Joseph Ibrahim, Robert Patro, Michael Love, "Nonparametric expression analysis using inferential replicate counts", *NAR*, 2019.
- 2019 [Avi Srivastava](#), Laraib Malik, Tom Sean Smith, Ian Sudbery, Rob Patro, "Alevin efficiently estimates accurate gene abundances from dscRNA-seq data", *Genome Biology*, 20:65, 2019.
- 2018 B Gruning et. al., *Bioconda: sustainable and comprehensive software distribution for the life sciences*, *Nature methods*, 15, pages 475 - 476 (2018).
- 2018 Fatemeh Almodaresi, Hirak Sarkar, [Avi Srivastava](#), Rob Patro, "A space and time-efficient index for the compacted colored de Bruijn graph", *Proceedings of ISMB-18*, Oxford Bioinformatics, Volume 34, Issue 13, 1 July 2018.
- 2017 Mohsen Zakeri, [Avi Srivastava](#), Fatemehalsadat Almodarresi TS, and Rob Patro, "Improved data-driven likelihood factorizations for transcript abundance estimation", *Proceedings of ISMB-17*, Oxford Bioinformatics, Volume 33, Issue 14, 15 July 2017.
- 2016 [Avi Srivastava](#), Hirak Sarkar, Nitish Gupta, and Rob Patro, "RapMap: A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes", *Proceedings of ISMB-16*, Oxford Bioinformatics, Volume 32, Issue 12, 15 June 2016.
- 2016 [Avi Srivastava](#), Hirak Sarkar, Laraib Malik, Rob Patro, "Accurate, Fast and Lightweight Clustering of de novo Transcriptomes using Fragment Equivalence Classes", *Proceedings of Recomb-seq-16*, arXiv, 2016.
- 2014 K Yadav, [Avi Srivastava](#), A Mittal, MA Ansari, "Texture-based medical image retrieval in compressed domain using compressive sensing", *International journal of bioinformatics research and applications IJBRA*, Vol.10, No.2, 2014.
- 2013 K Yadav, [Avi Srivastava](#), A Mittal, MA Ansari, "GPU parallel implementation of B-spline non-rigid grid registration using free-form deformations", *International Journal of Biomedical Engineering and Technology IJBET*, Vol.11, No.2, 2013.
- 2011 K Yadav, A Mittal, MA Ansari, [Avi Srivastava](#), "Parallel Implementation of Compressed Sensing Algorithm on CUDA- GPU", *International Journal of Computer Science and Information Security IJCSIS*, Vol. 9 No. 3, 2011.

### Poster

- 2019 [Avi Srivastava](#), Laraib Malik, Tom Sean Smith, Ian Sudbery, Rob Patro, "Alevin efficiently estimates accurate gene abundances from dscRNA-seq data", *BioC-2019, ISCB-2019 & RECOMB-2019*, New York.
- 2016 [Avi Srivastava](#), Darya Filippova, Owen Solberg, Khai Luong, "Understanding PacBio SMRT Sequencing consensus algorithm and possible improvements", *Roche Sequencing Solutions*, Pleasanton, California.

### Invited Talks

- 2020 [Avi Srivastava](#) , "A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification", *ISMB-20*, Virtual Conference.

- 2019 Avi Srivastava , *"Statistical Methods for Functional Genomics"*, Cold Spring Harbor Labs, New York, USA.
- 2019 Avi Srivastava , *"Alevin efficiently estimates accurate gene abundances from dscRNA-seq data"*, Basel, Switzerland, ISCB-student council meeting-2019.
- 2017 Avi Srivastava and Rob Patro, *"Algorithmic Advancement in Transcriptome Analyses"*, Laufer Center for Physical and Quantitative Biology-Retreat, Stony Brook, New York.
- 2016 Avi Srivastava, Hirak Sarkar, Nitish Gupta, and Rob Patro, *"RapMap: A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes"*, ISMB-16, Orlando, Florida.

## Open Source Softwares

- scChromHMM (2021) **A fast and efficient tool to perform a genome wide Single cell Chromatin State Analysis using multimodal histone modification data..**  
<https://github.com/satijalab/scChromHMM>
- Alignment (2020) **Alignment and mapping methodology influence transcript abundance estimation.**  
[www.github.com/COMBINE-lab/salmon](http://www.github.com/COMBINE-lab/salmon)
- Alevin (2019) **Alevin efficiently estimates accurate gene abundances from dscRNA-seq data.**  
[www.github.com/COMBINE-lab/salmon](http://www.github.com/COMBINE-lab/salmon)
- RapMap (2016) **A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes.**  
[www.github.com/COMBINE-lab/RapMap](http://www.github.com/COMBINE-lab/RapMap)

## Grant Support

- 2021 **Integrated analyses of the epigenome to understand the molecular basis of hematopoietic malignancies,**  
*PI: Avi Srivastava*, Agency: NIH: 1K99CA267677-01.  
 Role: Principal Investigator
- 2018 **Efficient tools for quantifying and simulating transcript-level abundance in single-cell RNA-seq,**  
*PI: Robert Patro*, Agency: SVCF Award Number: 182752.  
 Role: Lead Student Researcher
- 2018 **A Comprehensive and Lightweight Framework for Transcriptome Analysis,**  
*PI: Robert Patro*, Agency: NSF Award Number: 1750472.  
 Role: Student Researcher

## Honors

- 2021 The NCI Pathway to Independence Award for Outstanding Early Stage Postdoctoral Researchers (K99/R00)
- 2020 Stony Brook 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 project award

## Professional Activities

- 2022 **ISMB**, Program Committee.
- 2021 **Genome Biology**, Reviewer.
- 2021 **BMC Bioinformatics**, Reviewer.
- 2021 **BMC Genomics**, Reviewer.

2021 **JOSS**, Reviewer.  
2018-2021 **Bioinformatics**, Reviewer.  
2019 **PeerJ**, Reviewer.  
2018 **AMIA**, Reviewer.  
2018 **RECOMB**, sub-reviewer.  
2017 **ISMB**, sub-reviewer.

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## Skills

Expert Bash, C/C++(including C++11), CUDA,  $\LaTeX$ , Python, R, Rust  
Experience Git, Java, Snakemake, Spacemacs(Vim+Emacs)

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## Teaching (\* Assistant)

2020 **Single-cell quantification**, *Advanced topics in single-cell transcriptomics*, Virtual workshop streamed from Basel, Swiss Institute of Bioinformatics.  
2020 **alevin2bioc**, *Importing alevin scRNA-seq counts into R/Bioconductor*, Virtual workshop streamed from Boston, BioC 2020.  
2015-Fall \* **CSE-537**, *Artificial Intelligence*, Department of Computer Science, Stony Brook University.  
Prof. I.V. Ramakrishnan  
2015-Spring \* **CSE-320**, *System Fundamentals II*, Department of Computer Science, Stony Brook University.  
Prof. Jeniffer Wong  
2014-Fall \* **CSE-220**, *System Fundamentals I*, Department of Computer Science, Stony Brook University.  
Prof. Jeniffer Wong

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## References

Post Doc Advisor **Prof. Rahul Satija**, *Associate Professor*, New York Genome Center & NYU Center for Genomics and Systems Biology, New York University .  
rsatija@nygenome.org  
Ph.D. Advisor **Prof. Rob Patro**, *Associate Professor*, Department of Computer Science, University of Maryland.  
rob@cs.umd.edu  
**Prof. Michael Love**, *Assistant Professor*, Department of Biostatistics, Department of Genetics, University of North Carolina-Chapel Hill.  
michaelisaiahlove@gmail.com  
**Mr. Patrick Marks**, *Director*, Computational Biology, 10x Genomics.  
patrick@10xgenomics.com