

# Avi Srivastava

## Current Research Interests

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

## Education

2014–Present **Ph.D. Candidate (Graduation Expected December 2019)** , *Department of Computer Science*, Stony Brook University, New York, USA.

Advisor: Prof. 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: Prof. Ankush Mittal, Research Area: Medical Imaging (CBIR), Parallel Computing.

## Employment

**10x Genomics**, *Pleasanton, California, USA*.

2018(Summer) *Computational Biology Research Intern*.

**Roche Sequencing Solutions**, *Pleasanton, California, USA*.

2016(Summer) *Research Intern, Infectious Diseases Unit*.

**Stony Brook university**, *Stony Brook, New York, USA*.

2015–Present *Research Assistant, Department of Computer Science*.

2014–2015 *Teaching Assistant, Department of Computer Science*.

**Accenture Services Pvt Ltd.**, *Pune, India*.

2013–2014 *Software Engineer, Service-Oriented Architecture Development Group*.

## Publications

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

- 2019 Avi Srivastava, Laraib Malik, Hira Sarkar, Mohsen Zakeri, Charlotte Soneson, Michael I. Love, Carl Kingsford and Rob Patro, "Alignment and mapping methodology impact transcript abundance estimation", [BioRxiv](#) (preprint-2019).
- 2019 Hira 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, Hira 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

- 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, Orlando, Florida.

### Open Source Softwares

- Alevin (2018) **Alevin efficiently estimates accurate gene abundances from dscRNA-seq data.**  
[www.github.com/COMBINE-lab/salmon](http://www.github.com/COMBINE-lab/salmon)
- RapClust (2016) **Accurate, Fast and Lightweight Clustering of de novo Transcriptomes using Fragment Equivalence Classes.**  
[www.github.com/COMBINE-lab/RapClust](http://www.github.com/COMBINE-lab/RapClust)
- RapMap (2015) **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

- 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

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## Honors

- 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

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## Professional Activities

- 2019 **PeerJ**, Reviewer.
- 2018 **Bioinformatics**, 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, Rust  
Experience Git, Java, R, Snakemake, Spacemacs(Vim+Emacs)

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## Teaching Assistant

- 2015-Fall **CSE-537**, *Artificial Intelligence*, Department of Computer Science.  
Prof. I.V. Ramakrishnan
- 2015-Spring **CSE-320**, *System Fundamentals II*, Department of Computer Science.  
Prof. Jeniffer Wong
- 2014-Fall **CSE-220**, *System Fundamentals I*, Department of Computer Science.  
Prof. Jeniffer Wong

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## References

- Advisor **Prof. Rob Patro**, *Assistant 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