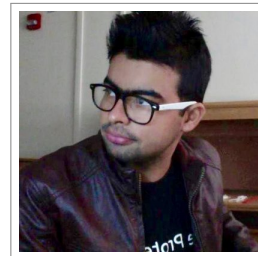


# Avi Srivastava

277 Sheep Pasture Road  
East Setauket, New York 11733  
☎ (631) - 974 - 8087  
✉ [asrivastava@cs.stonybrook.edu](mailto:asrivastava@cs.stonybrook.edu)  
📄 <http://k3yavi.github.io/>  
[www.github.com/k3yavi](http://www.github.com/k3yavi)



## Current Research Interests

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

## Education

- 2014–Present **Ph.D. Candidate**, *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

### Published

- 2019 Anqi Zhu, **Avi Srivastava**, Joseph Ibrahim, Robert Patro, Michael Love, "Nonparametric expression analysis using inferential replicate counts", **BioRxiv**(2019).
- 2019 **Avi Srivastava**, Laraib Malik, Tom Sean Smith, Ian Sudbery, Rob Patro, "Alevin efficiently estimates accurate gene abundances from dscRNA-seq data", to appear in Genome Biology, **BioRxiv**(2019).
- 2018 B GrÄijning 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", 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", ISMB-17, Oxford Bioinformatics, **Volume 33**, Issue 14, 15 July 2017.
- 2016 **Avi Srivastava**, HIRAK SARKAR, Laraib Malik, Rob Patro, "Accurate, Fast and Lightweight Clustering of de novo Transcriptomes using Fragment Equivalence Classes", Accepted in Recomb-seq, **arXiv**, 2016.

- 2015 **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, Oxford Bioinformatics, **Volume 32**, Issue 12, 15 June 2016.
- 2014 K Yadav, **A Srivastava**, A Mittal, MA Ansari, "*Texture-based medical image retrieval in compressed domain using compressive sensing*", International journal of bioinformatics research and applications, **Vol.10, No.2**, 2014.
- 2013 K Yadav, **A 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, **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, **Vol. 9 No. 3**, 2011.

#### Invited Talks

- 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.

#### Poster

- 2016 **Avi Srivastava**, Darya Filippova, Owen Solberg, Khai Luong, "*Understanding PacBio SMRT Sequencing consensus algorithm and possible improvements*", Roche Sequencing Solutions, Pleasanton, California.

### 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)
- Shoal (2016) **Improved multi-sample transcript abundance estimates using adaptive priors.**  
[www.github.com/COMBINE-lab/shoal](http://www.github.com/COMBINE-lab/shoal)
- 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

### Honors

- 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

- 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,  $\text{\LaTeX}$ , MATLAB, Python, Rust  
Experience GATB, Git, Java, R, Snakemake, Spacemacs(Vim+Emacs)

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## Teaching

### 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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## Hobbies

Hiking, Kayaking, Learning to never miss a game of Liverpool

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## References

Advisor **Prof. Rob Patro**, *Assistant Professor*, Department of Computer Science, Stony Brook Univeristy.  
rob.patro@cs.stonybrook.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