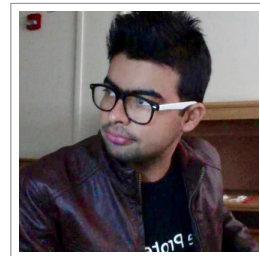


Avi Srivastava

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

Conference, ISMB every year – 2016 to present

- 2019 HIRAK SARKAR, **Avi Srivastava**, Rob Patro, "Minnow: A principled framework for rapid simulation of dscRNA-seq data at the read level", *ISMB-19*, under press for Oxford Bioinformatics.
- 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**, FATEMEH ALSADAT 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, 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.
- 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.

Scientific Journal

- 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 GrÄijning et. al., *Bioconda: sustainable and comprehensive software distribution for the life sciences*, Nature methods, **15**, pages 475 - 476 (2018).
- 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.

Under Peer Review

- 2019 **Avi Srivastava**, Laraib Malik, Hira Sarkar, Charlotte Soneson, Michael I. Love, Carl Kingsford and Rob Patro, "Alignment and mapping methodology impact transcript abundance estimation", BioRxiv(2019).
- 2019 Anqi Zhu, **Avi Srivastava**, Joseph Ibrahim, Robert Patro, Michael Love, "Nonparametric expression analysis using inferential replicate counts", BioRxiv(2019).

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**, Hira Sarkar, Nitish Gupta, and Rob Patro, "RapMap: A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes", ISMB, Orlando, Florida.

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 & 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.

Open Source Softwares

- Alevin (2018) **Alevin efficiently estimates accurate gene abundances from dscRNA-seq data.**
www.github.com/COMBINE-lab/salmon
- Shoal (2016) **Improved multi-sample transcript abundance estimates using adaptive priors.**
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
- RapMap (2015) **A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes.**
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

- 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

- 2018 **Bioinformatics**, Reviewer.
- 2018 **AMIA**, Reviewer.
- 2018 **RECOMB**, sub-reviewer.
- 2017 **ISMB**, sub-reviewer.

Skills

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

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

Hobbies

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

References

- Advisor **Prof. Rob Patro**, *Assistant Professor*, Department of Computer Science, Stony Brook University.
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