Avi Srivastava

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✇ *http://k3yavi.github.io/*
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 data

Education

2014–2019 **Ph.D.**, *Department of Computer Science*, Stony Brook University, New York, USA.
<u>Advisor:</u> Prof. Rob Patro, <u>Research Area:</u> Computational Biology, Machine Learning, (bio)Statistics.

2008–2012 **B.Tech.**, *Department of Computer Science*, College of Engineering Roorkee, Roorkee, India.
<u>Advisor:</u> Prof. Ankush Mittal, <u>Research Area:</u> Medical Imaging (CBIR), Parallel Computing.

Employment

New York Genome Center, *Manhattan, New York, USA.*
2020-Present *Postdoctoral Research Associate*.

10x Genomics, *Pleasanton, California, USA.*
2018(Summer) *Computaional Biology Research Intern*.

Roche Sequencing Solutions, *Pleasanton, California, USA.*
2016(Summer) *Research Intern*, *Infectious Diseases Unit*.

Stony Brook university, *Stony Brook, New York, USA.*
2015–2019 *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)

2020 <u>Avi Srivastava</u>, Laraib Malik, Hirak Sarkar and Robert Patro, *"A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification"*, ISMB-2020.

2020 Hirak Sarkar, <u>Avi Srivastava</u>, Hector Corrada Bravo, Michael I. Love and Rob Patro, *"Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data"*, ISMB-2020.

2020 Charlotte Soneson, <u>Avi Srivastava</u>, Rob Patro, Michael B Stadler, *"Preprocessing choices affect RNA velocity results for droplet-based scRNA-seq data"*, (Under Peer Review-2020).

2020 <u>Avi Srivastava</u>, 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 (Accepted with Revision-2020).

2019 Hirak Sarkar, <u>Avi Srivastava</u>, 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, <u>Avi Srivastava</u>, Joseph Ibrahim, Robert Patro, Michael Love, *"Nonparametric expression analysis using inferential replicate counts"*, NAR, 2019.

2019 <u>Avi Srivastava</u>, 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, <u>Avi Srivastava</u>, 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, <u>Avi Srivastava</u>, 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   <u>Avi Srivastava</u>, 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   <u>Avi Srivastava</u>, 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, <u>Avi Srivastava</u>, 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, <u>Avi Srivastava</u>, 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, <u>Avi Srivastava</u>, *"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   <u>Avi Srivastava</u>, 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   <u>Avi Srivastava</u>, 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

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

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

2019 **PeerJ**, Reviewer.

2018 **Bioinformatics**, Reviewer.

2018 **AMIA**, Reviewer.

2018 **RECOMB**, sub-reviewer.

2017 **ISMB**, sub-reviewer.

Skills

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

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

References

Post Doc Advisor **Prof. Rahul Satija**, *Assistant Professor*, NYU Center for Genomics and Systems Biology, New York University & New York Genome Center.
rsatija@nygenome.org

Ph.D. 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