

CONTACT INFORMATION	Kuchroo Lab and Klarman Cell Observatory 5407G, 415 Main Street The Broad Institute of MIT and Harvard Cambridge, MA 02412 USA	twitter: @ayshwaryas website: ayshwaryas.github.io email: subraman@broadinstitute.org
AREAS OF EXPERTISE	Computational Biology (Kidney disease, Cancer, Inflammatory Bowel Disease, RNA Biology), Genomic Data Analysis (Single-cell and Bulk-RNA-seq, Bulk-ATAC-seq, Metagenomics, Exome and single-nucleus DNA sequencing), Machine Learning, Probabilistic modeling, Phylogenetics, Applied Statistics	
EDUCATION	<p>2021 <b>Kaufman Teaching Certificate Program</b> Massachusetts Institute of Technology, Cambridge, MA USA</p> <p>2013 <b>Ph.D., Biological Sciences</b> Carnegie Mellon University, Pittsburgh, PA USA <i>Doctoral Advisor:</i> Russell Schwartz, Ph.D. <i>Dissertation:</i> Inferring tumor evolution using computational phylogenetics</p> <p>2007 <b>M.Sc. (Hons), Biological Sciences (Undergraduate degree)</b> Birla Institute of Technology and Science (BITS-Pilani), Rajasthan, India <i>CGPA 9.21/10, Major GPA 10/10, with Distinction</i> <i>Undergraduate Honors Thesis:</i> A mathematical model for phototactic responses in <i>Halobacterium salinarum</i>, Max Planck Institute for Complex Technical Systems, Magdeburg, Germany.</p>	
CURRENT APPOINTMENT	<b>Senior Computational Scientist</b> Klarman Cell Observatory, The Broad Institute of MIT and Harvard, Cambridge, MA 02142 <i>Mentors:</i> Aviv Regev, Ph.D. & Vijay Kuchroo, Ph.D., D.V.M <i>Research Summary:</i> Single-cell portraits of disease and normal states using human data, mouse and organoid models	2017–Present
PUBLICATIONS	<b>Pre-prints/Under review</b>	

- [1] **Subramanian A<sup>†</sup>**, Alperovich M<sup>†</sup>, Yang Y and Li Bo. Biology-inspired data-driven quality control for scientific discovery in single-cell transcriptomics. bioRxiv 2021.10.27.466176; doi: <https://doi.org/10.1101/2021.10.27.466176>.
- [2] **Subramanian A<sup>†</sup>**, Vernon KA<sup>†</sup>, Zhou Y<sup>†</sup> et al. Obesity-instructed TREM2high macrophages identified by comparative analysis of diabetic mouse and human kidney at single cell resolution. bioRxiv 2021.05.30.446342; doi: <https://doi.org/10.1101/2021.05.30.446342>.
- [3] **Subramanian A<sup>†</sup>**, Vernon KA<sup>†</sup>, Slyper M, Waldman J, et al. RAAS blockade, kidney disease, and expression of ACE2, the entry receptor for SARS-CoV-2, in kidney epithelial and endothelial cells. 2020. bioRxiv doi: <https://doi.org/10.1101/2020.06.23.167098>
- [4] Kaur G, Porter C.B.M., Ashenberg O, Lee J, Riesenfeld S.J., Hofree M, Aggelakopoulou M, **Subramanian A**, et al. 2021. Parental-fetal interplay of immune genes leads to intrauterine growth restriction. bioRxiv 2021.03.26.437292; doi: <https://doi.org/10.1101/2021.03.26.437292>

#### Peer-reviewed Journal Articles

20. Zhang Y, Bhosle A, Bae S, McIver L, Accorsi E, Thompson K, Arze C, Wang Y, **Subramanian A**, et al. Identifying Novel Bioactive Microbial Gene Products in Inflammatory Bowel Disease. **Nature** 2022 (*in press*).
19. Eraslan G<sup>†</sup>, Drokhyansky E<sup>†</sup>, Anand S<sup>‡</sup>, Fiskin E<sup>‡</sup>, **Subramanian A<sup>‡</sup>**, et al. Single-nucleus cross-tissue molecular reference maps to decipher disease gene function. bioRxiv 2021.07.19.452954; doi: <https://doi.org/10.1101/2021.07.19.452954>. **Science** 2022 (*in press*).

18. Marshall JL<sup>†</sup>, Noel T<sup>†</sup>, Wang QS<sup>†</sup>, Bazua-Valenti S<sup>†</sup>, Chen H<sup>†</sup>, Murray E, **Subramanian A** et al. High Resolution Slide-seqV2 Spatial Transcriptomics Enables Discovery of Disease-Specific Cell Neighborhoods and Pathways. *bioRxiv* 2021.10.10.463829; doi: <https://doi.org/10.1101/2021.10.10.463829>; **iScience**. 2022 (*in press*).
17. Tang R, Acharya N, **Subramanian A**, et al. Tim-3 adapter protein Bat3 acts as an endogenous regulator of tolerogenic dendritic cell function. **Science Immunology**. 2022 Mar 11;7(69):eabm0631. doi: 10.1126/sciimmunol.abm0631. Epub 2022 Mar 11. PMID: 35275752.
16. Mallick H, Rahnavard A, McIver LJ, Ma S, Zhang Y, Nguyen LH, Tickle TL, Weingart G, Ren B, Schwager EH, Chatterjee S, Thompson KN, Wilkinson JE, **Subramanian A**, et al. Multivariable Association Discovery in Population-scale Meta-omics Studies. **PLoS Computational Biology**. 2021 Nov 16;17(11):e1009442. doi: 10.1371/journal.pcbi.1009442. PMID: 34784344.
15. Biancalani T, Scalia G, Buffoni L, Avasthi R, Lu Z, Sanger A, Tokcan N, Vanderburg CR, Segerstolpe A, Zhang M, Avraham-David I, Vickovic S, Nitzan M, Ma S, Subramanian A, et al. Deep learning and alignment of spatially-resolved whole transcriptomes of single cells in the mouse brain with Tangram. **Nature Methods**. 2021 Nov;18(11):1352-1362. doi: 10.1038/s41592-021-01264-7. Epub 2021 Oct 28. PMID: 34711971
14. Delorey TM<sup>†</sup>, Ziegler CGK<sup>†</sup>, Heimberg G<sup>†</sup>, Normand R<sup>†</sup>, Yang Y<sup>†</sup>, Segerstolpe A<sup>†</sup>, Abbondanza D<sup>†</sup>, Fleming SJ<sup>†</sup>, **Subramanian A**<sup>†</sup>, et al. COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. **Nature**. 2021 Apr 29. doi: 10.1038/s41586-021-03570-8. Epub ahead of print. PMID: 33915569.
13. Muus C<sup>†</sup>, Luecken MD<sup>†</sup>, Eraslan G<sup>†</sup>, Sikkema L<sup>†</sup>, Waghay A<sup>†</sup>, Heimberg G<sup>†</sup>, Kobayashi Y<sup>†</sup>, Vaishnav ED<sup>†</sup>, **Subramanian A**<sup>†</sup>, et al. Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. **Nature Medicine**. 2021 Mar;27(3):546-559. doi: 10.1038/s41591-020-01227-z. Epub 2021 Mar 2. PMID: 33654293.
12. Kost-Alimova M, Sidhom EH, Satyam A, Chamberlain BT, Dvela-Levitt M, Melanson M, Alper SL, Santos J, Gutierrez J, **Subramanian A** et al. A High-Content Screen for Mucin-1-Reducing Compounds Identifies Fostamatinib as a Candidate for Rapid Repurposing for Acute Lung Injury. **Cell Reports Medicine**. 2020 Oct 29;1(8):100137. doi: 10.1016/j.xcrm.2020.100137. PMID: 33294858; PMCID: PMC7691435.
11. Marjanovic ND, Hofree M, Chan JE, Canner D, Wu K, Trakala M, Hartmann GG, Smith OC, Kim JY, Evans KV, Hudson A, Ashenberg O, Porter CBM, Bejnood A, **Subramanian A**, et al. Emergence of a High-Plasticity Cell State during Lung Cancer Evolution. *Cancer Cell*. 2020 Aug 10;38(2):229-246.e13. doi: 10.1016/j.ccell.2020.06.012. Epub 2020 Jul 23. PMID: 32707077; PMCID: PMC7745838.
10. **Subramanian A**<sup>†</sup>, Sidhom EH<sup>†</sup>, Emani M<sup>†</sup>, Sahakian N, Vernon K, Zhou Y, Kost-Alimova Maria, Weins A, Slyper M, Waldman J, Dionne D, Nguyen L, Marshall JL, Rozenblatt-Rosen O, Regev A, Greka A. (2019). Single cell census of human kidney organoids shows reproducibility and diminished off-target cells after transplantation. **Nature Communications**. 2019 Nov 29 <https://www.nature.com/articles/s41467-019-13382-0>
9. Korthauer K<sup>†</sup>, Kimes PK<sup>†</sup>, Duvallet C<sup>‡</sup>, Reyes A<sup>‡</sup>, **Subramanian A**<sup>‡</sup>, Teng M, Shukla C, Alm EJ, Hicks SC. A Practical Guide to Methods Controlling False Discoveries in Computational Biology. **Genome Biology**. 2019 Jun 4. doi: <https://genomebiology.biomedcentral.com/articles/10.1186/s13059-019-1716-1>.
8. Kalluri AS, Vellarikkal SK, Edelman ER, Nguyen L, **Subramanian A**, Ellinor PT, Regev A, Kathiresan S, Gupta RM. Single cell analysis of the normal mouse aorta reveals functionally distinct endothelial cell populations. **Circulation**. 2019. <https://www.ahajournals.org/doi/abs/10.1161/CIRCULATIONAHA.118.038362>.

---

<sup>†</sup>co-first

<sup>‡</sup>co-second, CD, AR, AS contributed equally and are listed alphabetically

7. Baryawno N, Przybylski D, Kowalczyk MS, Kfoury Y, Severe N, Gustafsson K, Kokkaliaris KD, Mercier F, Tabaka M, Hofree M, Dionne D, Papazian A, Lee D, Ashenberg O, **Subramanian A**, Vaishnav ED, Rozenblatt-Rosen O, Regev A, Scadden DT. A cellular taxonomy of the bone marrow stroma in homeostasis and leukemia demonstrates cancer-crosstalk with stroma to impair normal tissue function. **Cell**. 2019 May 23. <https://doi.org/10.1016/j.cell.2019.04.040>
6. Mehta RS, Abu-Ali GS, Drew DA, Lloyd-Price J, **Subramanian A**, Lochhead P, Joshi AD, Ivey KL, Khalili H, Brown GT, DuLong C, Song M, Nguyen LH, Mallick H, Rimm E, Izard J, Huttenhower C, Chan AT. Stability of the human faecal microbiome in a cohort of adult men. **Nat Microbiol**. 2018 Mar;3(3):347-355.PMID: 29335554
5. **Subramanian A** and Schwartz R. Reference-free inference of tumor phylogenies from single-cell sequencing data. **BMC Genomics**. 2015;16 Suppl 11:S7. PMID: 26576947
4. **Subramanian A**, Shackney S, Schwartz R. Novel multi-sample scheme for inferring phylogenetic markers from whole genome tumor profiles. **IEEE/ACM Trans Comput Biol Bioinform**. 2013 Apr 23. PMID: 24407301
3. **Subramanian A**, Shackney S, Schwartz R. Inference of tumor phylogenies from genomic assays on heterogeneous samples. **J Biomed Biotechnol**. 2012; 2012:797812. PMID:22654484
2. Tolliver D, Tsourakakis C, **Subramanian A**, Shackney S, Schwartz R. Robust unmixing of tumor states in array comparative genomic hybridization data. *Bioinformatics*. 2010 Jun 15; 26(12): i106-14. PMID:20529894
1. Adithi M, Kandalam M, Ramkumar HL, **Subramanian A**, Venkatesan N, Krishnakumar S. Retinoblastoma: expression of HLA-G. **Ocul Immunol Inflamm**. 2006 Aug; 14(4): 207-13. PMID: 16911982

#### Peer-reviewed full-length Conference Papers

4. **Subramanian A** and Schwartz R, “Reference-free inference of tumor phylogenies from single-cell sequencing data,” 2014 IEEE 4th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), Miami, FL, 2014, pp. 1-1. *Oral Presentation*
3. **Subramanian A**, Shackney S, Schwartz R. Novel multi-sample scheme for inferring phylogenetic markers from whole genome tumor profiles. Proceedings of the 8th International Symposium on Bioinformatics Research and Applications (ISBRA) 2012, Dallas, TX, USA, May 21-23, 2012. Bioinformatics Research and Applications. Lecture Notes in Computer Science Volume 7292, 2012, pp 250-262. *Oral Presentation*.
2. **Subramanian A**, Shackney S, Schwartz R. Inference of tumor phylogenies from genomic assays on heterogeneous samples. ACM-BCB, Chicago, IL, August 01 - 03, 2011. BCB '11 Proceedings of the 2nd ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB). pp 172-181. *Oral Presentation*.
1. Tolliver D, Tsourakakis C, **Subramanian A**, Shackney S, Schwartz R. Robust unmixing of tumor states in array comparative genomic hybridization data. Intelligent Systems for Molecular biology (ISMB) 2010. *Oral Presentation*.

#### Book Chapters and Commentaries

2. Le Cao KA, Abadi A.J, Davis-Marcisak E.F, ...,**Subramanian A** et al. Community-wide hackathons to identify central themes in single-cell multi-omics. **Genome Biology** 22, 220 (2021). <https://doi.org/10.1186/s13059-021-02433-9>
1. **Subramanian A**, Shackney S, Schwartz R. Tumor phylogenetics in the Next Generation Sequencing era: Strategies and Challenges. **Applications of Next Generation Sequencing in Cancer Research**. 2013.

## Selected Poster Presentations

7. **Subramanian A**, Vernon KA, Slyper M, Waldman J, Zhou Y, Keller KH, Dionne D, Nguyen L, Weins A, Rozenblatt-Rosen O, Regev A, Greka A. [Comprehensive Transcriptomic Mapping of Baseline and Pathological Human Kidneys at Single-Cell Resolution](#). American Society for Nephrology (ASN) Kidney Week 2018.
6. Mallick H, Tickle TL, McIver LJ, Weingart G, Paulson JN, Ma S, Ren B, Schwager E, **Subramanian A**, Franzosa EA, Bravo HC, Huttenhower C. Multivariable Association in Population-scale Meta'omic Surveys (Oral Presentation at the Intelligent Systems for Molecular Biology (ISMB), Chicago, IL, July 2018).
5. **Subramanian A**, Francoza E, Vlamakis H, Xavier R and Huttenhower C. de novo functional genomic annotation of the gut microbiome in inflammatory bowel disease. 2015 Annual Broad Institute retreat.
4. **Subramanian A**, and Schwartz R. Reference-free inference of tumor phylogenies from single-cell sequencing data. 2015 Annual Program in Quantitative Genetics (PQG) symposium.
3. **Subramanian A**, Mehta RS, Dulong Casey et al. Diet-linked gut microbial risk factors in Colorectal Carcinogenesis. STARR Cancer Consortium Annual Retreat 2015.
2. **Subramanian A**, Shackney S, Schwartz R. Inference of robust tumor phylogenetic markers from multi-sample data. GLBIO (Great Lakes Bioinformatics Conference) 2012.
1. **Subramanian A**, Shackney S, Schwartz R. Phylogenetic Methods for inferring tumor progression pathways from aCGH profiles of mixed cell populations. Poster, Intelligent Systems in Molecular Biology (ISMB) 2010.

## Conference Proceedings

5. Chang Y-L, Harre N, Rossetti M, **Subramanian A**, Kostic A, Huttenhower C, Xavier R, Stappenbeck T, Simpson K W., Sartor R. B, Wu G D., Lewis J, Bushman F D., McGovern D, Salzman N, Borneman J, Braun J. Su1873 Identification of IBD-Related Microbial Metabolites Affecting Human Th17 Differentiation. [Gastroenterology Volume 150, Issue 4, Supplement 1, April 2016, Page S576](#).
4. Chowdhury SA, **Subramanian A**, Schaffer AA, Shackney SE, Wangsa D, Heselmeyer-Haddad K, Ried T, Schwartz RS. Inferring evolutionary models of tumor progression from single-cell heterogeneity data.[abstract]. In: Proceedings of the 105th Annual Meeting of the American Association for Cancer Research; 2014 Apr 5-9; San Diego, CA. Philadelphia (PA): AACR; Cancer Res 2014;74(19 Suppl):Abstract nr 5338. doi:10.1158/1538-7445.AM2014-533.
3. **Subramanian A**, Shackney S, Schwartz R. Inference of tumor phylogenetic markers from large copy number datasets.[abstract]. In: Proceedings of the 104th Annual Meeting of the American Association for Cancer Research; 2013 Apr 6-10; Washington, DC. Philadelphia (PA): AACR; Cancer Res 2013;73(8 Suppl):Abstract nr 5133. doi:10.1158/1538-7445.AM2013-5133
2. **Subramanian A**, Shackney S, Schwartz R. Inference of robust tumor phylogenetic markers from multi-sample data.[abstract]. In: Proceedings of the 103rd Annual Meeting of the American Association for Cancer Research; 2012 Mar 31-Apr 4; Chicago, IL. Philadelphia (PA): AACR; Cancer Res 2012;72(8 Suppl):Abstract nr 3964. doi:1538-7445.AM2012-3964
1. **Subramanian A**, Shackney S, Schwartz R. Towards novel marker discovery from phylogenetic analysis of heterogeneous tumor samples.[abstract]. In: Proceedings of the 102nd Annual Meeting of the American Association for Cancer Research; 2011 Apr 2-6; Orlando, FL. Philadelphia (PA): AACR; Cancer Res 2011;71(8 Suppl):Abstract nr 44. doi:10.1158/1538-7445.AM2011-44

## Ph.D. Dissertation

1. **Subramanian A**, "Inferring tumor evolution using computational phylogenetics" (2013). [Dissertations](#). 275.

GRANTS AND FELLOWSHIP	2019	<i>Co-Investigator</i> The Broad Institute Chemical Biology and Therapeutics Science (CBTS) Shark Tank Program, (\$200,000 direct costs)
	2016	<i>Principal Investigator</i> Broadnext10 Round 3 Catalytic Steps Trainee Award by the Broad Institute, (\$40,000 direct costs)
	2006	Undergraduate Summer Science Fellowship Award by the Indian Academy of Science (IAS)
	2006	Undergraduate Summer Science Fellowship Award by the Jawaharlal Nehru Center for Advanced Scientific Research (JNCASR) ( <i>declined</i> ).
	2001	Ford Environment and Conservation grant awarded to only 3 high-school science projects, Ford Motors, USA.
AWARDS AND HONORS	2015	Stellar Abstract Award at the Harvard Program in Quantitative Genetics (PQG) Annual Conference
	2015	Travel Award for oral presentation at the Human Microbiome Data (HMD) workshop by the Statistical and Applied Mathematical Sciences Institute (SAMSI)
	2011	Only Invited Student Panelist, ACM Women in Bioinformatics, ACM-BCB
	2010	Global Champion, Hult Global Case Challenge for social innovation and entrepreneurship
	2010	2nd Place, Carnegie Mellon Open Innovation Competition
	2003	National Certificate of Merit in Physics and Biology (Top 0.1% All India Senior Secondary Certificate Examination (AISSCE))
	2003	Score of 485/500 (Known highest score in STEM in 2003 = 487/500) in AISSCE Grade 12 examinations
OTHER AWARDS	2019	Broad Institute Staff Scientist Travel Award
	2017	American Statistical Association (ASA) Travel award to attend the Women in Statistics and Data Science (WSDS) conference, La Jolla, CA
	2017	RStudio Diversity Scholarship to attend the RStudio International Conference at Orlando, FL
	2016	UseR! Diversity Scholarship to attend UseR!, the largest conference for users of the statistical programming language R
	2014	NSF Travel Fellowship for the 4th IEEE International Conference on Computational Advances in Bio and Medical Sciences (IEEE/ICCABS)
	2012	Travel Fellowship for oral presentation at the International Symposium on Bioinformatics Research and Applications (ISBRA)
	2011	Travel Fellowship by the Department of Biological Sciences, Carnegie Mellon University
	2011	Travel Fellowship for oral presentation at the ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)
TALKS	<b>Invited Talks</b>	
	[1]	Comparative transcriptomics of mouse and human kidney reveals altered macrophage states in kidney disease. Basic Science Research Seminar, Brigham Women's Hospital Division of Renal Medicine, Harvard Medical School, Boston MA, 8 December 2021.
	[2]	Insights into kidney disease from single-cell genomics. KidneyNext6 international conference, The Broad Institute of MIT and Harvard, Cambridge MA, 30 September 2021
	[3]	Introduction to Perturb-seq analysis. Medical and Populations Genetics Program Primer series, The Broad Institute of MIT and Harvard. 2021 June 17. Cambridge, MA
	[4]	Data Science: An alternative path for biomedical scientists. Postdoctoral Association and Career Development, Boston Children's Hospital. 2019 October 15. Boston, MA.
	[5]	An introduction to single-cell transcriptomics. Broad Institute Data Sciences Program. 2018 November. Cambridge, MA.
	[6]	An introduction to single-cell transcriptomics. Broad Institute Cancer Program Bootcamp. 2018 May. Cambridge, MA.
	[7]	Inferring Insights from Omics Data with Applications in Tumor Evolution and Inflammatory Bowel Disease. Department of Bioinformatics and Computational Biology, Genentech. 2017 June 8. South San Francisco, USA



- [8] Computational methods for inferring insights from 'omics data with applications in Inflammatory Bowel Disease and Cancer. Inflammation and Immunology Research Unit, Pfizer. 2017 May 17. Cambridge, MA
- [9] Defining transcriptional activity states by leveraging massive, public RNAseq datasets. Bioinformatics Meeting, Division of Immunology, Harvard Medical School. 2017 May 11. Boston, MA.
- [10] *de novo* functional genomic annotation of the gut microbiome in inflammatory bowel disease. Bioinformatics Meeting, Division of Immunology, Harvard Medical School. 2016 May 12. Boston, MA.
- [11] Computational Screens for identifying bioactive microbial compounds in Inflammatory Bowel Disease. Novartis Institute for Biomedical Research (NIBR). 2015 July 13. Cambridge, MA.
- [12] Reference-free inference of tumor phylogenies from single-cell sequencing data. Workshop on Computational Advances for Next Generation Sequencing (CANGS). 2014 June 06. Miami Beach, FL
- [13] Inferring tumor progression using computational phylogenetics. MIT-Computer Science and Artificial Intelligence Laboratory (CSAIL). 2013 August 22. Boston, MA.

### Contributed Talks

- [1] Domain Knowledge as a Key Enabler of Impactful Data Analyses in Single-Cell Genomics. [Women in Statistics and Data Science Conference](#). 2018 October 18. Cincinnati, OH.
- [2] Defining transcriptional activity states by leveraging massive, public RNAseq datasets. [Women in Statistics and Data Science Conference](#). 2017 October 19. La Jolla, CA.
- [3] Computational screens for novel gut microbial bioactive compounds. [Discovering Patterns in Human Microbiome Data \(HMD\) Workshop](#). Statistical and Applied Mathematical Sciences Institute (SAMSI) 2015 March 17. Research Triangle Park, NC.

### TEACHING EXPERIENCE

- 2017 **Teaching Fellow**, [Introduction to 'Omics' Research](#)  
Prepared course assessment questions and answered online discussion forum. Harvard Catalyst, The Harvard Clinical and Translational Science Center, Harvard University, MA, USA
- 2016 **Teaching Fellow**, [BIO 261/ CS107-E Introduction to Data Science](#)  
Contributed to and graded HWs, advised final projects, assisted in-class, held office hours for online students. Course by Rafael Irizarry at Harvard T. H. Chan School of Public Health & Harvard Extension School
- 2010 **Teaching Assistant**, [03712 Computational Methods for Biological Modeling and Simulation](#).  
Graded exams and HWs, held office hours. Course by Russell Schwartz at Carnegie Mellon.
- 2009 **Teaching Assistant**, [03711 Computational Molecular Biology and Genomics](#).  
Graded exams and HWs, held office hours. Course by Dannie Durand at Carnegie Mellon.
- 2009 **Teaching Assistant**, [03710 Computational Biology](#).  
Created and graded quizzes, held recitations and office hours, graded HWs and exams. Course by Robert Murphy at Carnegie Mellon.
- 2006 **Professional Assistant**, [BIO C461 Recombinant DNA Technology](#)  
Course by Ashis K. Das at Birla Institute of Technology & Science (BITS-Pilani)

### TUTORIALS AND SHORT COURSES

- [1] Guest Lecture on single-cell RNAseq analysis. [NGS Data Analysis Course 2018](#), Harvard T.H. Chan Bioinformatics Core. 27 September 2018. Boston, USA
- [2] co-Instructor. [Single Cell Data Analysis Lab](#), Center for Excellence in Genomics (CEGS) Workshop. 12 September 2018. Cambridge, USA
- [3] co-Instructor. [Single cell RNA-seq toolkit](#), tutorial at the 25th Intelligent Systems in Molecular Biology (ISMB) Conference. 6 July 2018. Chicago, USA
- [4] Computational Lead. [CyTOF Analysis Workshop](#). 5 December 2017. Dana-Farber Cancer Institute cBio Center. Boston, USA.

PROFESSIONAL EXPERIENCE	05/14-10/17	<b>Postdoctoral Research Associate</b> Department of Biostatistics, Harvard T. H. Chan School of Public Health, Boston, MA, Department of Biostatistics and Computational Biology
	11/15-10/17	PI: Dr. Rafael Irizarry
	05/14-10/15	PI: Dr. Curtis Huttenhower
	01/14-05/14	<b>Bridge Postdoctoral Research Associate</b>
	08/07-12/13	<b>Graduate Research and Teaching Assistant.</b> Department of Biological Sciences, Carnegie Mellon University, Pittsburgh
	Summer 2011	<b>Summer Research Intern</b> (Mentor: Dr. Peter Haverty). Department of Bioinformatics and Computational Biology, Genentech, South San Francisco
	01/07-06/07	<b>Undergraduate Honors Thesis Advisee</b> (Mentor: Dr. Wolfgang Marwan) Molecular Network Analysis Group, Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany
	2005-2007	<b>Undergraduate Research Assistant</b> (Mentor: Dr. A.K. Das). Birla Institute of Technology & Science (BITS Pilani), India
	Summer 2006	<b>Indian Academy of Science Summer Research Fellow</b> (Mentor: Dr. M.S. Shaila). Indian Institute of Science (IISc), Bangalore, India
	Summer 2005	<b>Undergraduate Summer Research Intern</b> (Mentor: Dr. Krishnakumar Subramanian). Sankara Nethralaya Eye Hospitals, Chennai, India
	2002	<b>High School Term project.</b> Childs Trust Hospital, Human Genetics Department, Chennai, India
TECHNICAL SKILLS	<b>Programming:</b> Stan, R, Python, Git, Perl, LaTeX, Matlab, Shell scripting, Java (basic), C(basic)	
	<b>Operating Systems:</b> Mac OS X, Unix, Linux	
	<b>Relevant Graduate coursework:</b> 10701 Machine Learning, 10705 Intermediate Statistics, 10702 Statistical Machine Learning, 15211 Data Structures and Algorithms, 03712 Computational Methods for Biological Modeling and Simulation, 03210-A3 Information Noise and Entropy in the Brain	
SERVICE	<b>Program Committee</b>	
	2017, 2019	International Conference on Machine Learning (ICML) Workshop on Computational Biology
	<b>Grant reviewing</b>	
	2018	Florida Department of Health William G. "Bill" Bankhead, Jr., and David Coley Cancer Research Program.
	2016	Medical Research Council (MRC) UK
	2015	Florida Department of Health
	<b>Ad hoc Peer-Review</b>	
	Journals	Bioinformatics, PLOS Computational Biology, Nature, BMC Genomics
	Conferences	Annual International Conference on Research in Computational Molecular Biology (RECOMB), Intelligent Systems in Molecular Biology (ISMB), International Symposium on Bioinformatics Research and Applications (ISBRA), Workshop on Algorithms in Bioinformatics (WABI), IEEE International Conference on Bioinformatics and Biomedicine (BIBM)
	<b>Research Mentoring</b>	

2021–present	Anish Mudide, MIT PRIMES
2021–present	Yufan Wu, Associate Computational Biologist
2021	Brad Fortunato, Boston University Masters in Bioinformatics intern
2021	Neha Gupta, Boston University Masters in Bioinformatics intern
2019–present	Mikhail Alperovich, MIT Primes
2019	Sam Nitz, MIT UROP
2011–2012	Titas Banerjee, Carnegie Mellon University

### **STEM Outreach**

2020, 2021	Selection Committee, Broad Institute Summer Research Program (BSRP)
2019, 2021	Session Chair, MIT PRIMES Fall Conference for high-school students
2016, 2017, 2018	Career exploration day for high school students, Broad Institute & MassBioEd
2012	Mentor, “Creative Tech Nights” outreach program for Pittsburgh middle school girls, Carnegie Mellon Women@SCS (School of Computer Science)
2010–13	Co-president, Scientists and Engineers for America (SEA) student group for Science and Technology policy-making education for graduate students

### **Community**

06/14–present	Volunteer, Haley House Shelter for Homeless, Boston, MA
2017	Charles River Watershed Association Earth Day cleanup
2016	Started the “Rally for Jimmy Fund” employee personal electronics upcycling program at the Department of Biostatistics & Computational Biology, DFCI
2014, 2016	Volunteer, Perkins School for the Blind, Watertown, MA
03/08–12/12	Volunteer Teacher (Human Values Character Education Program), Allegheny County Shuman Juvenile Detention Center, Pittsburgh, PA
07/10–12/13	Volunteer, Bethlehem Haven, Pittsburgh, PA
07/10–02/14	Volunteer, Alice Davis Personal Care Home, Braddock, PA
2009	Founding member, CMU Panama Global Business Brigade, Pittsburgh PA