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| CONTACT INFORMATION                               | Kuchroo Lab and Klarman Cell Observatory<br>5407G, 415 Main Street<br>The Broad Institute of MIT and Harvard<br>Cambridge, MA 02412 USA  |   | twitter: @ayshwaryas<br>website: <a href="https://ayshwaryas.github.io">ayshwaryas.github.io</a><br>email: <a href="mailto:subraman@broadinstitute.org">subraman@broadinstitute.org</a> |
| CURRENT APPOINTMENT                               | <b>Senior Computational Scientist</b>  | 2017–Present  |   |
|   | Klarman Cell Observatory, The Broad Institute of MIT and Harvard, Cambridge, MA 02142<br><i>Mentors:</i> Vijay Kuchroo, Ph.D., D.V.M & Aviv Regev, Ph.D. & Anna Greka, M.D., Ph.D<br><i>Research Summary:</i> Dissecting principles governing context-specificity of cell states |   |   |
| EDUCATION AND TRAINING (STEM)                     | 2017   | <b>Postdoctoral research</b><br>Department of Biostatistics, Harvard T.H. Chan School of Public Health, Boston, MA USA<br><i>Advisors:</i> Curtis Huttenhower, Ph.D. and Rafael Irizarry, Ph.D.                             |   |
|   | 2014   | <b>Ph.D., Biological Sciences</b><br>Carnegie Mellon University, Pittsburgh, PA USA<br><i>Doctoral Advisor:</i> Russell Schwartz, Ph.D.<br><i>Dissertation:</i> Inferring tumor evolution using computational phylogenetics |   |
|   | 2007   | <b>M.Sc. (Hons), Biological Sciences</b> ( <i>Undergraduate degree</i> )<br>Birla Institute of Technology and Science (BITS–Pilani), Rajasthan, India<br><i>CGPA 9.21/10, Major GPA 10/10, with Distinction</i>             |   |
|   | 2007   | <i>Undergraduate Honors Thesis:</i> A mathematical model for phototactic responses in <i>Halobacterium salinarium</i> , Max Planck Institute for Complex Technical Systems, Magdeburg, Germany.                             |   |
| EDUCATION AND TRAINING (Professional Development) | 2022   | Center for the Improvement of Mentored Experiences in Research ( <b>CIMER</b> ) Research Mentor Training<br>Broad Institute,Cambridge, MA USA   |   |
|   | 2022   | <b>Manager-to-Leader (M2L) Program</b><br>A program in management in academia and science for early career scientists<br>Broad Institute, Cambridge, MA USA   |   |
|   | 2021   | <b>Kaufman Teaching Certificate Program</b><br>Massachussetts Institute of Technology, Cambridge, MA USA  |   |
| GRANTS AND FELLOWSHIP                             | 2022   | <i>Principal Investigator</i> BroadIgnite high-risk high-reward award for early-career investigators, (\$40,000 direct costs)   |   |
|   | 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> <a href="#">Broadnext10 Round 3 Catalytic Steps Trainee Award</a> 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, <a href="#">Hult Global Case Challenge for social innovation and entrepreneurship</a>  |   |
|   | 2010   | 2nd Place, <a href="#">Carnegie Mellon Open Innovation Competition</a>  |   |
|   | 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  |   |
| PUBLICATIONS                                      | <b>Pre-prints/Under review</b>   |   |   |
|   | [1] Kimura K <sup>†</sup> , <b>Subramanian A<sup>†</sup></b> et al. Cooperation of the immune checkpoint molecule Tim3 and TGF- $\beta$ pathway in microglial homeostasis and activation. <i>in review</i> .   |   |   |

- [2] Kuchroo V, Hou Y, LaFleur M, ..., **Subramanian A** et al. CRISPR screens reveal neuropeptide signaling orchestrates T helper cell differentiation. *Research Square*; 2022. doi: 10.21203/rs.3.rs-1953978/v1. *in review*.
- [3] **Subramanian A**<sup>†</sup>, Vernon KA<sup>†</sup>, Zhou Y<sup>†</sup> et al. Obesity-instructed TREM2<sup>high</sup> macrophages identified by comparative analysis of diabetic mouse and human kidney at single cell resolution. *bioRxiv*. doi: <https://doi.org/10.1101/2021.05.30.446342>. *in revisions*.
- [4] Mangani D, **Subramanian A**<sup>‡</sup>, Huang L<sup>‡</sup> et al. A TCF1-driven regulatory network determines homeostatic versus pathogenic Th17 cell state. *in revisions*.
- [5] Wilder A <sup>†</sup>, Supple M<sup>†</sup>, **Subramanian A** et al. Historical processes shape contemporary extinction risk in placental mammals. *in revisions*.
- [6] **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. *bioRxiv* doi: <https://doi.org/10.1101/2020.06.23.167098>

#### Peer-reviewed Journal Articles (First-author)

22. **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. **Genome Biology** 23, 267 (2022). <https://doi.org/10.1186/s13059-022-02820-w>.
21. 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. PMID: 33915569.
20. Muus C<sup>†</sup>, Luecken MD<sup>†</sup>, Eraslan G<sup>†</sup>, Sikkema L<sup>†</sup>, Waghray 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. doi: 10.1038/s41591-020-01227-z. PMID: 33654293.
19. **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. Single cell census of human kidney organoids shows reproducibility and diminished off-target cells after transplantation. **Nature Communications**. 2019 Nov 29. doi: 10.1038/s41467-019-13382-0. PMID: 31784515.
18. **Subramanian A** and Schwartz R. Reference-free inference of tumor phylogenies from single-cell sequencing data. **BMC Genomics**. 2015;16 Suppl 11:S7. doi: 10.1186/1471-2164-16-S11-S7. PMID: 26576947
17. **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. doi: 10.1109/TCBB.2013.33. PMID: 24407301.
16. **Subramanian A**, Shackney S, Schwartz R. Inference of tumor phylogenies from genomic assays on heterogeneous samples. **J Biomed Biotechnol**. 2012. doi: 10.1155/2012/797812. PMID:22654484.

#### Peer-reviewed Journal Articles (Major contribution)

15. Eraslan G<sup>†</sup>, Drokhlyansky 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. **Science** 2022 May 13. doi: 10.1126/science.abl4290. PMID: 35549429.
14. 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 11doi: 10.1126/sciimmunol.abm0631. PMID: 35275752.
13. 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: 10.1186/s13059-019-1716-1. PMID: 31164141.
12. 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. doi: 10.1093/bioinformatics/btq213. PMID: 20529894.

#### Peer-reviewed Journal Articles (Other)

11. Kaur G, Porter C.B.M., Ashenberg O, Lee J, Riesenfeld S.J., Hofree M, Aggelakopoulou M, **Subramanian A**, et al. Mouse fetal growth restriction through parental and fetal immune gene variation and intercellular communications cascade. **Nature Communications**. 2022 Jul. doi: 10.1038/s41467-022-32171-w. PMID: 35906236.

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<sup>†</sup>co-first

<sup>‡</sup>co-second

10. Zhang Y, Bhosle A, Bae S, McIver L, Accorsi E, Thompson K, Arze C, Wang Y, **Subramanian A**, et al. Discovery of bioactive microbial gene products in inflammatory bowel disease. **Nature**. 2022 Jun. doi: 10.1038/s41586-022-04648-7. PMID: 35614211.
9. 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. **iScience**. 2022 Mar 16. doi: 10.1016/j.isci.2022.104097. PMID: 35372810.
8. Mallick H, Rahnavard A, McIver LJ, Ma S, Zhang Y, Nguyen LH, Tickle TL, Weingart G, Ren B, Schwaiger 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. doi: 10.1371/journal.pcbi.1009442. PMID: 34784344.
7. Biancalani T, Scalia G, Buffoni L, Avasthi R, Lu Z, Sanger A, Tokcan N, Vanderburg CR, Segerstolpe A, Zhang M, Avraham-Davidi 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. doi: 10.1038/s41592-021-01264-7. PMID: 34711971.
6. 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. doi: 10.1016/j.xcrm.2020.100137. PMID: 33294858.
5. 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. doi: 10.1016/j.ccell.2020.06.012. PMID: 32707077.
4. 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 Jul 9. doi: 10.1161/CIRCULATIONAHA.118.038362. PMID: 31146585.
3. 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 Jun 13. doi: 10.1016/j.cell.2019.04.040. PMID: 31130381
2. 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. doi: 10.1038/s41564-017-0096-0. PMID: 29335554.
1. Adithi M, Kandalam M, Ramkumar HL, **Subramanian A**, Venkatesan N, Krishnakumar S. Retinoblastoma: expression of HLA-G. **Ocul Immunol Inflamm**. 2006 Aug. doi: 10.1080/09273940600826497. 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 (ICCBAS), 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** 2021 Aug 5. doi: 10.1186/s13059-021-02433-9. PMID: 34353350.
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.

## Ph.D. Dissertation

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

## PROVISIONAL PATENT

Regev A, Anderson AC, **Subramanian A**, Rozenblatt-Rosen O. Compositions and methods targeting complement component 3 for inhibiting tumor growth. Provisional US Patent App. 16/442,348

## 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.

## TALKS

### Invited Talks

- [1] Comparative transcriptomics of mouse and human kidneys to study disease altered cell states. [Harvard Program in Quantitative Genomics \(PQG\) Working group](#), Harvard T.H. Chan School of Public Health, Boston MA, 26 April 2022.
- [2] 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.
- [3] Insights into kidney disease from single-cell genomics. KidneyNext6 international conference, The Broad Institute of MIT and Harvard, Cambridge MA, 30 September 2021
- [4] Introduction to Perturb-seq analysis. Medical and Populations Genetics Program Primer series, The Broad Institute of MIT and Harvard. 2021 June 17. Cambridge, MA
- [5] Data Science: An alternative path for biomedical scientists. Postdoctoral Association and Career Development, Boston Children's Hospital. 2019 October 15. Boston, MA.
- [6] An introduction to single-cell transcriptomics. Broad Institute Data Sciences Program. 2018 November. Cambridge, MA.
- [7] An introduction to single-cell transcriptomics. Broad Institute Cancer Program Bootcamp. 2018 May. Cambridge, MA.

- [8] 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
- [9] 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
- [10] Defining transcriptional activity states by leveraging massive, public RNAseq datasets. Bioinformatics Meeting, Division of Immunology, Harvard Medical School. 2017 May 11. Boston, MA.
- [11] *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.
- [12] Computational Screens for identifying bioactive microbial compounds in Inflammatory Bowel Disease. Novartis Institute for Biomedical Research (NIBR). 2015 July 13. Cambridge, MA.
- [13] 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
- [14] 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.

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| OTHER<br>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)   |
| PROFESSIONAL<br>EXPERIENCE | 2022–<br>05/14-10/17 | <b>Ad hoc consultant in computational genomics</b><br><b>Postdoctoral Research Associate</b><br>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).<br>Department of Bioinformatics and Computational Biology, Genentech, South San Francisco   |
|                            | 01/07–06/07          | <b>Undergraduate Honors Thesis Advisee</b> (Mentor: Dr. Wolfgang Marwan)<br>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  |
|                            |                      |  |



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|                  | 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)<br><b>Operating Systems:</b> Mac OS X, Unix, Linux<br><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><br>2017, 2019 International Conference on Machine Learning (ICML) Workshop on Computational Biology<br><b>Grant reviewing</b><br>2018 Florida Department of Health William G. "Bill" Bankhead, Jr., and David Coley Cancer Research Program.<br>2016 Medical Research Council (MRC) UK<br>2015 Florida Department of Health<br><b>Ad hoc Peer-Review</b><br>Journals Bioinformatics, PLOS Computational Biology, Nature, BMC Genomics<br>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 and Management</b>   |
|                  | 2022–       | Yuyang Han, Data Manager, Evergrande Center for Immunologic Diseases, Brigham Women's Hospital and Harvard Medical School  |
|                  | 2022–       | Adriana Payan-Medina, Broad Institute BSRP Program   |
|                  | 2021–       | Alexander Young, Brown University  |
|                  | 2021–       | Anish Mudide, MIT PRIMES   |
|                  | 2021–       | Yufan Wu, Associate Computational Biologist  |
|                  | 2021        | Brad Fortunato, Boston University Masters in Bioinformatics intern   |
|                  | 2021        | Neha Gupta, Boston University Masters in Bioinformatics intern   |
|                  | 2021        | Conner Lambden, Associate Computational Biologist  |
|                  | 2019–       | Mikhail Alperovich, MIT Primes   |
|                  | 2019        | Sam Nitz, MIT UROP   |
|                  | 2011–12     | Titas Banerjee, Carnegie Mellon University   |
|                  |             | <b>STEM Outreach</b>   |
|                  | 2020–21     | Selection Committee, Broad Institute Summer Research Program (BSRP)  |
|                  | 2019, 2021  | Session Chair, MIT PRIMES Fall Conference for high-school students   |
|                  | 2016–18     | 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  |
|                  |             | <b>Community</b>   |
|                  | 06/14–      | 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   |