Ayshwarya Subramanian **Updated April 26, 2019**

CONTACT INFORMATION
Kidney Disease Initiative and Klarman Cell Observatory
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AREAS OF EXPERTISE
Computational Biology (Kidney disease, Cancer, Inflammatory Bowel Disease, RNA Biology), Genomic Data Analysis (Single-cell and Bulk-RNAseq, Metagenomics, Exome and single-nucleus DNA sequencing), Machine Learning, Probabilistic modeling, Phylogenetics, Applied Statistics

EDUCATION

2013 **Ph.D., Biological Sciences**
Carnegie Mellon University, Pittsburgh, PA USA
Doctoral Advisor: Russell Schwartz, Ph.D.
Dissertation: Inferring tumor evolution using computational phylogenetics

2007 **M.Sc. (Hons), Biological Sciences** (*Undergraduate degree*)
Birla Institute of Technology and Science (BITS–Pilani), Rajasthan, India
CGPA 9.21/10, Major GPA 10/10, with Distinction
Undergraduate Honors Thesis: A mathematical model for phototactic responses in *Halobacterium salinarium*, Max Planck Institute for Complex Technical Systems, Germany.

CURRENT APPOINTMENT

Computational Scientist, Cambridge MA 2017–Present
Mentors: Anna Greka, M.D., Ph.D. & Aviv Regev, Ph.D.
Research Summary: Single-cell portraits of disease and normal states using human data, mouse and organoid models
Kidney Disease Initiative and Klarman Cell Observatory
Broad Institute, Cambridge, MA 02142

PUBLICATIONS

Pre-prints/Under review

[1] Baryawno N, Przybylski D, Kowalczyk MS, Kfoury Y, Severe N, Gustafsson K, Kokkaliaris KD, Mercier F, Tabaka M, Hofree M, Dionne D, Ashenberg O, **Subramanian A**, Vaishnav ED, Papazian A, Lee D, Rozenblatt-Risen 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 *accepted*.

[2] 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 *in press*.

[3] **Subramanian A**[†], Sidhom EH[†], Emani M[†], 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). Kidney organoid reproducibility across multiple human iPSC lines and diminished off target cells after transplantation revealed by single cell transcriptomics. bioRxiv. doi: https://doi.org/10.1101/516807

[4] Korthauer K[†], Kimes PK[†], Duvallet C [‡], Reyes A[‡], **Subramanian A**[‡], Teng M, Shukla C, Alm EJ, Irizarry RA, Hicks SC. (2018). A Practical Guide to Methods Controlling False Discoveries in Computational Biology. *bioRxiv*. doi: https://doi.org/10.1101/458786

Peer-reviewed Journal Articles

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

[†]co-first
[‡]co-second, CD, AR, AS contributed equally and are listed alphabetically

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 Chapter

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

Papers in progress

1. **Subramanian A**, et al. Single-cell portraits of human kidney disease.*in preparation*

2. **Subramanian A**, Schwartz R and Lee AV. Genomic variation among MCF-7 cancer cell lines grown in different laboratories: a phylogenetic analysis.*in preparation*

3. **Subramanian A**, Eric Franzosa, Dirk Gevers, Ramnik Xavier, Huttenhower C. Computational prediction of novel secreted bioactive microbial gene products from microbial shotgun sequencing studies.*in preparation*

4. **Subramanian A**, Irizarry RA. Creating a transcript expression barcode using RNA-Seq Data.*in preparation*

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 *Co-Investigator* The Broad Institute Chemical Biology and Therapeutics Science (CBTS) Shark Tank Program, ($200,000 direct costs)

2016 *Principal Investigator* 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) *(declined).*

2001 Ford Environment and Conservation grant awarded to only 3 high-school science projects, Ford Motors, USA.

Awards and Honors

2018 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

2015 Stellar Abstract Award for poster 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)

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 Only Invited Student Panelist, ACM Women in Bioinformatics, ACM-BCB

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)

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

Talks

Invited Talks

[1] An introduction to single-cell transcriptomics. Broad Institute Data Sciences Program. 2018 November. Cambridge, MA.

[2] An introduction to single-cell transcriptomics. Broad Institute Cancer Program Bootcamp. 2018 May. Cambridge, MA.

[3] 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

[4] 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

[5] Defining transcriptional activity states by leveraging massive, public RNAseq datasets. Bioinformatics Meeting, Division of Immunology, Harvard Medical School. 2017 May 11. Boston, MA.

[6] *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.

[7] Computational Screens for identifying bioactive microbial compounds in Inflammatory Bowel Disease. Novartis Institute for Biomedical Research (NIBR). 2015 July 13. Cambridge, MA.

[8] 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

[9] 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 **Postdoctoral Research Associate**
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	**Bridge Postdoctoral Research Associate**
08/07–12/13	**Graduate Research and Teaching Assistant**. Department of Biological Sciences, Carnegie Mellon University, Pittsburgh
Summer 2011	**Summer Research Intern** (Mentor: Dr. Peter Haverty). Department of Bioinformatics and Computational Biology, Genentech, South San Francisco
01/07–06/07	**Undergraduate Honors Thesis Advisee** (Mentor: Dr. Wolfgang Marwan) Molecular Network Analysis Group, Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany
2005–2007	**Undergraduate Research Assistant** (Mentor: Dr. A.K. Das). Birla Institute of Technology & Science (BITS Pilani), India
Summer 2006	**Indian Academy of Science Summer Research Fellow** (Mentor: Dr. M.S. Shaila). Indian Institute of Science (IISc), Bangalore, India
Summer 2005	**Undergraduate Summer Research Intern** (Mentor: Dr. Krishnakumar Subramanian). Sankara Nethralaya Eye Hospitals, Chennai, India
2002	**High School Term project**. Childs Trust Hospital, Human Genetics Department, Chennai, India

Technical Skills

Programming: Stan, R, Python, Git, Perl, LaTeX, Matlab, Shell scripting, Java (basic), C(basic)
Operating Systems: Mac OS X, Unix, Linux
Relevant Graduate coursework: 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

Program Committee

2017, 2019	International Conference on Machine Learning (ICML) Workshop on Computational Biology

Grant reviewing

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

Ad hoc Peer-Review

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)

Research Mentoring

2019	Mikhail Alperovich, MIT Primes
2011–2012	Titas Banerjee, Carnegie Mellon University

STEM Outreach

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

06/14–07/17	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