

- CONTACT INFORMATION** Department of Biostatistics
Harvard T. H. Chan School of Public Health
Department of Biostatistics and Computational Biology
Dana-Farber Cancer Institute
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- AREAS OF EXPERTISE** Computational Biology (Genomics, Cancer, Microbiome, RNA Biology), Machine Learning, Probabilistic modeling, Phylogenetics, Statistics
- RESEARCH SUMMARY** I am primarily interested in the design, development, and applications of computational data analyses methods for the understanding of human health and disease, its prevention and treatment. During my PhD, I developed computational methods to discern cancer subtypes from whole genome datasets to determine tumor evolution, infer heterogeneity and novel marker discovery. Understanding tumor evolution is critical to preventing remission, predicting disease trajectories and planning appropriate care. My current research focuses on modeling human gene expression states using publicly available RNA sequencing data. This work deals with both the challenges of working with massive genomics datasets being made public via federal funding and the benefits to answer fundamental biological questions, not possible with experiments from a single lab or group. I also work on computational prioritization of microbial gene products in Inflammatory Bowel Disease from gut metagenomic data. Leveraging the human microbiome for healthcare presents a modifiable alternate path to tackle complex diseases.
- CURRENT APPOINTMENT** **Postdoctoral Research Associate**, Boston MA 2015–Present
Department of Biostatistics, Harvard T.H. Chan School of Public Health
Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute
Cancer Program, The Broad Institute (*Affiliate*)
Mentor: Rafael Irizarry, Ph.D.
- 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, Top 5% in graduating class
Undergraduate Honors Thesis: A mathematical model for phototactic responses in *Halobacterium salinarium*, Max Planck Institute for Complex Technical Systems, Germany.
- PUBLICATIONS** **Peer-reviewed Journal Articles**
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. 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 (2017+). Stability of the Human Gut Microbiome in Population-based Studies. under review at *Nature Microbiology.*
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**, 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

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.

TALKS

Invited Talks

- [1] Defining transcriptional activity states by leveraging massive, public RNAseq datasets. Bioinformatics Meeting, Division of Immunology, Harvard Medical School. 2017 May 11. Boston, MA.
- [2] *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.
- [3] 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
- [4] Inferring tumor progression using computational phylogenetics. MIT-Computer Science and Artificial Intelligence Laboratory (CSAIL). 2013 August 22. Boston, MA.

Contributed Talks

- [1] 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.

GRANTS AND FELLOWSHIP

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| 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 to set up vermicomposting in high-school, Ford Motors, USA. |

AWARDS AND HONORS	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 (All India rank 1 = 487/500) in AISSCE Grade 12 examinations
TEACHING EXPERIENCE	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)
PROFESSIONAL EXPERIENCE	05/14–10/15	Postdoctoral Research Associate (PI: Dr. Curtis Huttenhower). Department of Biostatistics, Harvard T.H.Chan School of Public Health, Boston, MA & Medical and Population Genetics Program, The Broad Institute, Cambridge, MA
	08/07–05/14	Bridge Postdoctoral Research Associate 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, C
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 International Conference on Machine Learning (ICML) Workshop on Computational Biology

Grant reviewing

2016 Medical Research Council (MRC) UK
2015 Florida Department of Health

Ad hoc Peer-Review

Journals 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

2011–2012 Titus Banerjee, Carnegie Mellon University

STEM Outreach

2016, 2017 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

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