## Ayush Raman, Ph.D.

STATISTICAL EPIGENOMICS POSTDOC ASSOCIATE, BROAD INSTITUTE OF MIT AND HARVARD

Education	<b>Broad Institute of MIT and Harvard</b> , Cambridge, MA Statistical Epigenomics Postdoc Associate, Epigenomics Program	Dec' 18 - Present	
	<b>Baylor College of Medicine</b> , Houston, TX <i>Ph.D.</i> , Quantitative and Computational Biosciences <i>Dissertation</i> : Decoding Big Genomic Datasets: Biases, hypotheses & reg	Sept' 13 - Sept' 18 ulation	
	Carnegie Mellon University, Pittsburgh, PA M.S., Computational Biology; Academic Achievement Fellowship	Aug' 07 - Dec' 08	
	Vellore Institute of Technology, Vellore, India Bachelor of Technology, Bioinformatics; Distinction with highest honors	Aug' 02 - May' 06	
Research Interests	Computational Biology, epigenetics and gene expression, single-cell (epi)-genomics, ONT long- read seq, multi-omic integration & analyses, machine learning		
Selected Publications	H Gu*, <b>AT Raman</b> <sup>*</sup> et al. Smart-RRBS for single cell methylome and <i>Nature Protocols</i> (2021) (PMID: 34244697) [Code]	transcriptome analysis.	
	➡ V Kochat*, AT Raman* et al. PRC2 loss-mediated epigenomic reprogramming induces an aggressive neural crest-like phenotype in malignant peripheral nerve sheath tumors. Acta Neuropathologica (2021) (PMID: 34283254) [Code]		
	E Orouji <sup>*</sup> , AT Raman <sup>*</sup> , AK Singh <sup>*</sup> et al. Chromatin state dynamics peutic strategies in enhancer subtypes of colorectal cancer. $Gut$ (2021) (	s confers specific thera- PMID: 34059508)	
	<b>AT Raman</b> . A research parasite's perspective on establishing a baseline to avoid errors in secondary analyses. <i>GigaScience</i> (2021) (PMID: 33710326)		
	■ AT Raman*, AE Pohodich* et al. Apparent bias towards long MeCP2 syndromes disappears after controlling for baseline variations. <i>cations</i> (2018) (PMID: 30104565) [Code]	gene misregulation in Nature Communi-	
	➡ H Yi*, AT Raman* et al. Detecting hidden batch factors through data-adaptive adjustment for biological effects. <i>Bioinformatics</i> (2018) (PMID: 29617963) [Code]		
	* denotes (co-) first authorship; All publications are listed in <b>Google Sc</b>	holar	
Skill-Set	• Languages: R (tidyverse & Bioconductor), Perl, Python, Bash, ${\rm IAT}_{\rm E} {\rm X}$	, SQL	
Summary	• Next Gen Data Analysis: Bulk ATAC-/ChIP-/RNA-seq, single-cell ATAC-/RNA-seq, Long-read seq (1+ year), NanoString nCounter, Microarray, Detection & correction of Batch Effects		
	• Machine Learning Algorithms: Clustering ( <i>k</i> -means, hierarchical clustering, NMF, semi- NMF), Dimensionality reduction methods (PCA, ICA, t-SNE, UMAP, MDS), Classification Al- gorithms (Naive Bayes, Linear Discriminant Analysis, Decision Trees, Random Forest, SVM, Logistic Regression), Regression (Linear, GLM), Regularization (LASSO, Ridge, Elastic-net)		
	• High Performance Computing: Load Sharing Facility (LSF), Condor		
	• Cloud Computing: Google Cloud Computing, Terra		
	• Pipeline Development Tools: Version control (Git), Workflow manag	er (Snakemake, WDL)	
Work and Research Experience	Statistical Epigenomics Postdoc Associate, Broad Institute Martin Aryee, Alex Meissner and Andi Gnirke Labs	Cambridge, MA Dec '18 - Present	

- Studying the dynamics of gene regulation using single-cell genomics (Published in Nature Protocol and *Nature Biotechnology*) and long read sequencing

- Studying the role of DNA methylation and its writers in diseases in development and aging
- Studied regulatory mechanisms of tumor suppressor genes in senescence (Calico project)

## Research Assistant, Baylor College of Medicine

Zhandong Liu's Lab in collaboration with Huda Zoghbi's Lab, NRI

- Showed that the "preferential misregulation of long genes" observed in transcriptomic datasets of Rett syndrome can occur due to PCR amplification (Published in Nature Communications)

- Developed machine learning algorithm for detection of batch effects in transcriptomic datasets (Published in *Bioinformatics*)

- Illuminated the mechanism behind the effects of deep brain stimulation in Rett syndrome (Published in eLife)

## Research Assistant, MD Anderson Cancer Center Houston, TX

Lynda Chin and Kunal Rai Lab, Genome Medicine

- Elucidated the epigenomic landscape in colorectal cancer (Published in Gut)
- Showed the oncogenic role of EZH2 in the pathogenesis of MPNST tumors (Published in Acta *Neuropathologica*)
- Showed the role of TRM28/KRAB repressors during development (Published in Stem Cell Reports)
- Estimated lymphocytic infiltration in melanoma heterogeneous tumors (Published in Cell)

Bioinformatics Scientist, Institute for Systems Biology	Seattle, WA
Shmulevich Lab in collaboration with Alan Aderem's and Leeroy Hood's Lab	Jul '10 - Jul '13

- Enumerated gene expression similarities and differences between the rhinovirus and influenza viruses using time-course microarray datasets (P&G project)

- Analyzed different types of ChIP-seq datasets, including Pol-II, Transcription Factor & HDAc and performed integrative analyses with gene expression data to elucidate gene regulatory network that gets activated due to anti-viral or anti-bacterial responses (Published in Nature)

Statistician/Research Programmer, University of Pittsburgh Pittsburgh, PA Computational Genetics Lab and Department of Biomedical Informatics Apr '09 - Jul '10

- Implemented genomic distance-based multivariate regression model for the estimation of Identity by Descent (IBD) in the haplotype datasets between the case and control pairs

- Performed computational prediction and accuracy of different types of discriminative and generative algorithms

Awards & Honors	• Hechter Memorial Award, Broad Institute (2020)	
	• Junior Research Parasite Award for Rigorous Secondary Data Analysis (2020)	
	• MCBIOS Young Scientist Excellence Postdoc Award (2020)	
	• Gigascience Award for Pacific Symposium on Biocomputing (2020)	
	• GSBS Scholarship, Baylor College of Medicine (2013-2014)	
	• Academic Achievement Fellowship, Carnegie Mellon University (2007-2009)	
	$\bullet$ Undergraduate thesis awarded highest grade, Vellore Institute of Technology (2006)	
Misc. Information	• Peer Review (ad hoc): Nature Communications, PLOS Computational Biology, IUBMB Life, Stem Cell Research & Therapy, Frontiers in Genetics, Frontiers in Immunology, Frontiers in Molecular Biosciences, Frontiers in Pharmacology (Guest Editor)	
	• Professional Societies and Memberships: Core RSG India Member, ISCB (2016-2017)	
	• Soft-skills: Communication, collaboration, honesty, adaptability, creativity, conflict management, punctuality, critical thinking, goal setting	

## Houston, TX Sept '13 - Sept '18

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