Ayush Raman, Ph.D.

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STATISTICAL EPIGENOMICS POSTDOC ASSOCIATE, BROAD INSTITUTE OF MIT AND HARVARD

EDUCATION		
	Broad Institute of MIT and Harvard, Cambridge, MA	*Dec' 18 - Present*
	Statistical Epigenomics Postdoc Associate, Epigenomics Program	
	Baylor College of Medicine, Houston, TX	*Sept' 13 - Sept' 18*
	Ph.D., Quantitative and Computational Biosciences	
	Dissertation: Decoding Big Genomic Datasets: Biases, hypotheses & regulation	
	Carnegie Mellon University, Pittsburgh, PA	*Aug' 07 - Dec' 08*
	M.S., Computational Biology; *Academic Achievement Fellowship*	
	Vellore Institute of Technology, Vellore, India	*Aug' 02 - May' 06*
	Bachelor of Technology, Bioinformatics; *Distinction with highest honors*	

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*, **AT Raman*** et al. Smart-RRBS for single cell methylome and transcriptome analysis. ***Nature Protocols***(2021) (PMID: 34244697) [Code]

📄 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*, **AT Raman***, AK Singh* et al. Chromatin state dynamics confers specific therapeutic strategies in enhancer subtypes of colorectal cancer. ***Gut*** (2021) (PMID: 34059508)

📄 **AT Raman**. A research parasite's perspective on establishing a baseline to avoid errors in secondary analyses. ***GigaScience*** (2021) (PMID: 33710326)

📄 **AT Raman***, AE Pohodich* et al. Apparent bias towards long gene misregulation in MeCP2 syndromes disappears after controlling for baseline variations. ***Nature Communications*** (2018) (PMID: 30104565) [Code]

📄 H Yi*, **AT Raman*** et al. Detecting hidden batch factors through data-adaptive adjustment for biological effects. ***Bioinformatics*** (2018) (PMID: 29617963) [Code]

* denotes (co-) first authorship; All publications are listed in **Google Scholar**

SKILL-SET SUMMARY

- **Languages**: R (tidyverse & Bioconductor), Perl, Python, Bash, LaTeX, SQL

- **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 (k-means, hierarchical clustering, NMF, semi-NMF), Dimensionality reduction methods (PCA, ICA, t-SNE, UMAP, MDS), Classification Algorithms (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 manager (Snakemake, WDL)

WORK AND RESEARCH EXPERIENCE

	Statistical Epigenomics Postdoc Associate, Broad Institute	**Cambridge, MA**
	Martin Aryee, Alex Meissner and Andi Gnirke Labs	*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 — Houston, TX
Zhandong Liu's Lab in collaboration with Huda Zoghbi's Lab, NRI — *Sept '13 - Sept '18*

- 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 — *Sept '13 - Sept '18*

- 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

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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)
- 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