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*

- Understanding the dynamics of gene regulation using single-cell genomics (Published in *Nature Protocol* and *Nature Biotechnology*) and long read sequencing
- Understanding the role of DNA methylation and its writers in diseases in development and aging
- Elucidating 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*

- Amplification-based expression data show bias towards long gene misregulation (Published in *Nature Comm.*)
- Developed batch detection algorithm in gene expression datasets (Published in *Bioinformatics*)
- Mechanism behind the effects of deep brain stimulation in Rett syndrome, meta-analysis of activity-dependent genes and intellectual disorders (Published in *elife* and *Hum Mol Genet.*)

Research Assistant, MD Anderson Cancer Center — Houston, TX
Lynda Chin and Kunal Rai Lab, Genome Medicine — *Sept '13 - Sept '18*

- Elucidated epigenomic landscape in colorectal tumors (Published in *Gut*)
- Oncogenic Role of EZH2 in the pathogenesis of MPNST tumors (Published in *Acta Neuropathologica*)
- Role for the TRM28/KRAB repressors during early development (Published in *Stem Cell Reports*)
- Lymphocytic Infiltration as a basis of response in melanoma 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*

- Analyzing the gene expression similarities and differences between the rhinovirus and influenza viruses using microarray datasets (P&G project)
- Analyses of Pol-II, Transcription Factor, HDAc ChIP-seq datasets, Integrative analysis with gene Expression data for the discovery of gene regulatory network that gets activated in the presence of Tol-II receptors (Published in *Nature*)
- Predicting poised genes in the macrophages using machine learning algorithms

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
- Computational prediction and accuracy of different statistical based algorithms such as 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)
- 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