Ayush Raman, Ph.D.

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EDUCATION

Broad Institute of MIT and Harvard Cambridge, MA
Postdoc Associate, Epigenomics Program *December 2018 – April 2024*

Baylor College of Medicine Houston, TX
Ph.D. in Quantitative and Computational Biosciences *September 2013 – September 2018*

Carnegie Mellon University Pittsburgh, PA
M.S. in Computational Biology *August 2007 - December 2008*

Vellore Institute of Technology Vellore, India
B.Tech in Bioinformatics *August 2002 - May 2006*

EXPERIENCE

Staff Scientist April 2024 – Present
National Cancer Institute, NIH *Bethesda, MD*

- Worked on computational pipeline for calling of C>T modification in RNA sequencing reads due to $NaBH_4$ and $NaCNBH_3$ treatment
- Compared SNP calling software, including GATK and Deepvariant
- Compared peak calling methods in RIP-seq datasets and applied Gaussian Mixture Models for estimating background noise and signal accurately
- Studying the exonization of transposon elements as a source of the neo-tumor antigens in myeloid malignancies

Statistical Epigenomics Postdoc Associate Dec 2018 – April 2024
Broad Institute / MGH Pathology / Data Science, Dana Farber Cancer Center *Cambridge, MA*

- Studied the dynamics of gene regulation using single-cell genomics (co-developed SMART-RRBS assay) and long-read sequencing (Published in *Nature Protocol* and *Nature Biotechnology*)
- Elucidated regulatory mechanisms of tumor suppressor genes, including CDKN2A (p14/p16) in cellular senescence (*Calico* funded project; submitted to *Cell Genomics*)
- Analyzed the role of DNA methylation and its writers in diseases in development and aging

Research Assistant and Graduate Student Sept 2013 – Sept 2018
Baylor College of Medicine / MD Anderson Cancer Center *Houston, TX*

- Discovered the epigenomic subtypes in colon cancer for effective combinatorial therapy (Published in *Gut*)
- Developed statistical method to show that the "preferential misregulation of long genes" observed in gene expression (GE) datasets in Rett syndrome is due to PCR amplification (Published in *Nature Communications*)
- Co-developed machine learning algorithm for detection of batch effects in GE-data (Published in *Bioinformatics)*
- Showed the role of TRM28/KRAB repressors during development (Published in *Stem Cell Reports*)
- Estimated lymphocytic infiltration in melanoma heterogeneous tumors (TCGA project; Published in *Cell*)

Bioinformatics Scientist July 2010 – July 2013
Institute for Systems Biology *Seattle, WA*

- Enumerated GE trajectories between the rhinovirus and influenza viruses (*P&G* funded project)
- Elucidated gene regulatory network due to anti-viral or anti-bacterial responses (Published in *Nature*)

Previous Employments April 2009 – July 2010; Jan 2007 – July 2007; Dec 2005 – Nov 2006
UPMC; IIT Delhi; CSIR-IGIB *Pittsburgh, PA; New Delhi; New Delhi, India*

- Analyzed GWAS datasets for the detection of causal genes in psychotic disorders and schizophrenia
- Implemented genomic distance based multivariate regression model for the estimation of Identity by Descent (IBD) in the haplotype datasets
- Computational prediction and accuracy of different statistical algorithms, such as discriminative and generative algorithms, and clustering algorithms
- Comparative genomic analysis of *M. tuberculosis* H37Rv with *H. sapiens* using sequence and structural based approaches

TECHNICAL SKILLS

- **Languages**: R, Python, Perl, Bash, LaTeX; Working Knowledge of C, C++, SQL
- **Next Gen Data Analysis**: Bulk ATAC-/ChIP-/RNA-seq, single-cell ATAC-/RNA/RRBS-seq/multi-omic, Long-read sequencing (ONT, PacBio), NanoString nCounter, Microarray, Detection & correction of Batch Effects, GWAS & Fine-mapping analysis (PLINK, SuSie), Variant Calling (GATK, DeepVariant), RIP-/Ribo-/GRO-/PRO-seq
- **General 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/Shrinkage Methods (LASSO (L1), Ridge (L2), Elastic-net)
- **Deep Learning Algorithms**: Variational Autoencoder, Convolutional and Recurrent Neural Networks
- **Libraries**: tidyverse, Bioconductor, ggplot2, DESeq2, edgeR, Seurat, ArchR, pandas, NumPy, Matplotlib
- **Developer Tools**: Git, Docker, Google Cloud, Visual Studio, Workflow manager (Snakemake, WDL)
- **High Performance & Cloud Computing**: LSF, Slurm, Google Cloud Computing, Terra

SELECTED PUBLICATIONS (** denotes (co-) first authorship*)

- E Orouji*, **AT Raman***, AK Singh* et al. Chromatin state dynamics confers specific therapeutic strategies in enhancer subtypes of colorectal cancer. ***Gut*** (2022)
- H Gu*, **AT Raman*** et al. Smart-RRBS for single cell methylome and transcriptome analysis. ***Nature Protocols***(2021) [Code]
- **AT Raman**. A research parasite's perspective on establishing a baseline to avoid errors in secondary analyses. ***GigaScience*** (2021)
- **AT Raman***, AE Pohodich* et al. Apparent bias towards long gene misregulation in MeCP2 syndromes disappears after controlling for baseline variations. ***Nature Communications*** (2018) [Code]
- H Yi*, **AT Raman*** et al. Detecting hidden batch factors through data-adaptive adjustment for biological effects. ***Bioinformatics*** (2018) [Code]

All publications are listed in **Google Scholar**

AWARDS AND HONORS

- Hechter Memorial Award, Broad Institute ($500; 2020)
- Junior Research Parasite Award for Rigorous Secondary Data Analysis (2020)
- MCBIOS Young Scientist Excellence Postdoc Award ($500; 2020)
- Gigascience Award for Pacific Symposium on Biocomputing ($3,500; 2020)
- GSBS Scholarship, Baylor College of Medicine ($35,000; 2013-2014)
- Academic Achievement Fellowship, Carnegie Mellon University ($30,000; 2007-2009)
- Undergraduate thesis awarded highest grade, Vellore Institute of Technology (2006)
- Distinction with highest honors, Vellore Institute of Technology (2002-2006)

MISCELLANEOUS 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)
- **Teaching Assistant or Co-Instructor**: Co-Instructor for Introduction to Data Science, HBKU Qatar (Jan-March,2025); Teaching Assistant for Bioinformatics, MD Anderson Cancer Center (Dec. 2017); Teaching Assistant for Computational Math for Quantitative Biomedicine, Baylor College of Medicine (Fall 2017)
- **Soft-skills**: Communication, collaboration, honesty, adaptability, creativity, conflict management, punctuality, critical thinking, goal setting
- **References**: Zhandong Liu, Ph.D.; Huda Zoghbi, M.D.; Kunal Rai, Ph.D. and Martin Aryee, Ph.D.