

Contact Information	Broad Institute of MIT and Harvard 75 Ames Street, 6080C Cambridge, MA 02142 ORCID: 0000-0003-2872-2307 LinkedIn: /in/ayushraman; Twitter: aayushraman Website: araman.rbind.io		(412) 614-9490 araman@broadinstitute.org aayushraman09@gmail.com
Bio	Statistical epigenomics postdoctoral associate interested in computational biology, single-cell (epi)genomics, machine learning and diseases such as cancer and autism.		
Education and Training	Broad Institute of MIT and Harvard , Cambridge, MA Statistical Epigenomics Postdoc Associate, Epigenomics Program Dec 2018 - Present <ul style="list-style-type: none"> • Advisors: Martin Aryee, Ph.D., Alexander Meissner, Ph.D. and Andreas Gnirke, Ph.D. Baylor College of Medicine , Houston, TX Ph.D., Quantitative and Computational Biosciences Sept 2013 - Sept 2018 <ul style="list-style-type: none"> • Thesis Topic: <i>Decoding Big Genomic Datasets: Biases, hypotheses & regulation</i> • Advisors: Zhandong Liu, Ph.D. and Kunal Rai, Ph.D. • Advisory Committee: Zhandong Liu, Ph.D. (Chair), Huda Y. Zoghbi, M.D., Aleksandar Milosavljevic, Ph.D., Olivier Lichtarge, M.D., Ph.D., Mirjana Maletić-Savatić, M.D., Ph.D., Kunal Rai, Ph.D. Carnegie Mellon University , Pittsburgh, PA M.S., Computational Biology Aug 2007 - Dec 2008 <ul style="list-style-type: none"> • Academic Achievement Fellowship (2007 - 2009) Vellore Institute of Technology , Vellore, India B. Tech, Bioinformatics Aug 2002 - May 2006 <ul style="list-style-type: none"> • Thesis Topic: <i>Study of Host Protein Mimicry of M. tuberculosis proteins in H. sapiens</i> • Distinction with highest honors (equivalent to <i>Summa Cum Laude</i>) 		
Selected Publications (* CO-FIRST AUTHORS)	<ol style="list-style-type: none"> 1. H Gu*, AT Raman*, X Wang, AW Mohammad, A Arczewska, ZD Smith, DA Landau, MJ Aryee, A Meissner, A Gnirke. Smart-RRBS for single cell methylome and transcriptome analysis. <i>Nature Protocols</i> (2021) (PMID: 34244697) 2. E Orouji*, AT Raman*, AK Singh*, ..., S Kopetz, K Rai. Chromatin state dynamics confers specific therapeutic strategies in enhancer subtypes of colorectal cancer. <i>Gut</i> (2021) (PMID: 34059508) 3. V Kochat*, AT Raman*, ..., K Rai, KE Torres. PRC2 loss-mediated epigenomic reprogramming induces an aggressive neural crest-like phenotype in malignant peripheral nerve sheath tumors. <i>Acta Neuropathologica</i> (2021) (PMID: 34283254) 4. AT Raman*, AE Pohodich*, YW Wan, HK Yalamanchili, HY Zoghbi, Z Liu. Apparent bias towards long gene misregulation in MeCP2 syndromes disappears after controlling for baseline variations. <i>Nature Communications</i> (2018) (PMID: 30104565) 5. H Yi*, AT Raman*, H Zhang, G Allen and Z Liu. Detecting hidden batch factors through data-adaptive adjustment for biological effects. <i>Bioinformatics</i> (2018) (PMID: 29617963) 		

Honors And Distinctions	<ul style="list-style-type: none"> • Hechter Memorial Travel Award, Broad Institute (2020) • Junior Research Parasite Award for Rigorous Secondary Data Analysis (2020) • MCBIOS Young Scientist Excellence Postdoc Award (Third place; 2020) • Gigascience Travel Award to attend the Pacific Symposium on Biocomputing Conference (2020) • GSBS Scholarship, Baylor College of Medicine (2013 - 2014) • Academic Achievement Fellowship, Carnegie Mellon University (2007-2009) • Undergraduate thesis awarded highest grade at School of Chemical Engineering and Biotechnology, Vellore Institute of Technology (2006) • Distinction with highest honors (equivalent of Dean's List), Vellore Institute of Technology, Vellore (2002-2006) • Awarded Distinction in Mathematics Delhi Olympiad (2000-2001) • Awarded Distinction in New South Wales Mathematics Olympiad for three consecutive years (1996-1999) 	
Research Experience	<p>Statistical Epigenomics Postdoc Associate Dec 2018 - Present Epigenomics Program Cambridge, MA Broad Institute of MIT and Harvard, Massachusetts General Hospital & Dana Farber Cancer Institute Advisor: Martin Aryee, Ph.D., Alexander Meissner, Ph.D. and Andreas Gnirke, Ph.D. Collaborator: Bradley Bernstein</p> <p>Research Assistant May 2014 - Sept 2018 Jan and Duncan Neurological Research Institute Houston, TX Baylor College of Medicine Advisor: Zhandong Liu, Ph.D.</p> <p>Research Assistant July 2015 - Sept 2018 Genome Medicine Department Houston, TX MD Anderson Cancer Center Advisor: Kunal Rai, Ph.D.</p> <p>Research Assistant Jan 2014 - June 2015 Genome Medicine Department Houston, TX MD Anderson Cancer Center Advisor: Lynda Chin, M.D.</p> <p>Bioinformatics Scientist July 2010 - July 2013 Institute for Systems Biology Seattle, WA Supervisors: Ilya Shmulevich, Ph.D.</p> <p>Programming Analyst/ Statistician April 2009 - July 2010 University of Pittsburgh Pittsburgh, PA</p> <p>Research Assistant Oct 2007 - August 2008 Carnegie Mellon University Pittsburgh, PA</p>	
Complete list of Publications (* CO-FIRST AUTHORS)	<ol style="list-style-type: none"> 1. E Orouji, AT Raman. Computational methods to explore chromatin state dynamics. <i>Briefings in Bioinformatics</i> (2022) (PMID: 36208178) 2. SC Callahan, V Kochat, Z Liu, AT Raman, J Schulz, C Terranova, M Divenko, A Ghosh, M Tang, C Pickering, J Myers, K Rai. High Enhancer Activity is an Epigenetic Feature of HPV Negative Atypical Head and Neck Squamous Cell Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> (2022) (PMID: 35927986) 	

3. CJ Terranova*, KM Stemler*, P Barrodia, SL Jeter-Jones, Z Ge, M de la Cruz Bonilla, **A Raman**, KL Allton, E Arslan, OH Yilmaz, MC Barton, K Rai, H Piwnica-Worms. Reprogramming of H3K9bhb at Regulatory Elements is an Epigenetic Feature of Fasting in the Small Intestine. *Cell Reports* (2021) (PMID: 34818540)
4. C Terranova*, M Tang*, M Maitituoheti*, **A Raman**, ..., K Rai. Bivalent and Broad Chromatin Domains Regulate Pro-metastatic Drivers in Melanoma. *Cell Reports* (2021) (PMID: 34289358)
5. V Kochat*, **AT Raman***, ..., K Rai, KE Torres. PRC2 loss-mediated epigenomic reprogramming induces an aggressive neural crest-like phenotype in malignant peripheral nerve sheath tumors. *Acta Neuropathologica* (2021) (PMID: 34283254)
6. H Gu*, **AT Raman***, X Wang, AW Mohammad, A Arczewska, ZD Smith, DA Landau, MJ Aryee, A Meissner, A Gnirke. Smart-RRBS for single cell methylome and transcriptome analysis. *Nature Protocols* (2021) (PMID: 34244697)
7. E Orouji*, **AT Raman***, AK Singh*, ..., S Kopetz, K Rai. Chromatin state dynamics confers specific therapeutic strategies in enhancer subtypes of colorectal cancer. *Gut* (2021) (PMID: 34059508)
8. S Shareef, S Bevil, **AT Raman**, M Aryee, P Galen, V Hovestadt, B Bernstein. Expanded representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. *Nature Biotech* (2021) (PMID: 33958785)
9. **AT Raman**. A research parasite's perspective on establishing a baseline to avoid errors in secondary analyses. *GigaScience* (2021) (PMID: 33710326)
10. M Maitituoheti, EZ Keung, M Tang, L Yan, H Alam, G Han, **AT Raman et al.** Enhancer Reprogramming Confers Dependence on Glycolysis and IGF Signaling in KMT2D Mutant Melanoma. *Cell Reports* (2020) (PMID: 33086062)
11. T Manzo, B Prentice, K Anderson, **A Raman et al.** Accumulation of Long-chain fatty acids in the tumor microenvironment drives dysfunction in intra-pancreatic CD8+ T cells. *Journal of Exp. Medicine* (2020) (PMID: 32491160)
12. CA Chen, W Wang, SE Pedersen, **A Raman**, ML Seymour, FR Ruiz, ME van der Heijden, L Wang, J Yin, J Lopez, ME Rech, RA Lewis, SM Wu, Z Liu, FA Pereira, RG Pautler, HY Zoghbi, CP Schaaf. Nr2f1 heterozygous knockout mice recapitulate neurological phenotypes of Bosch-Boonstra-Schaaf optic atrophy syndrome and show impaired hippocampal synaptic plasticity. *Hum Mol Genet.* (2019) (PMID: 31600777)
13. S Adhikary*, D Chakravarti*, C Terranova*, I Sengupta, M Maitituoheti, A Dasgupta, D Srivastava, J Ma, **A Raman**, E Tarco, A Sahin, R Bassett, F Yang, C Tapia, S Roy, K Rai, C Das. Atypical PHD Domain of UBR7 Functions as an H2BK120Ub Ligase and Breast Cancer Tumor Suppressor. *Nature Communications* (2019) (PMID: 30923315)
14. **AT Raman**, K Rai. Loss of Histone Acetylation and H3K4 methylation promotes melanocytic malignant transformation. *Molecular & Cellular Oncology* (2018) (PMID: 30250885)
15. **AT Raman***, AE Pohodich*, YW Wan, HK Yalamanchili, HY Zoghbi, Z Liu. Apparent bias towards long gene misregulation in MeCP2 syndromes disappears after controlling for baseline variations. *Nature Communications* (2018) (PMID: 30104565)
 - Recommended by the Faculty of 1000
 - Synopsis in Texas Children's Hospital website: Long genes are not preferentially altered in Rett and MeCP2 duplication syndromes
16. C Terranova, M Tang, E Orouji, M Maitituoheti, **A Raman**, S Amin, Z Liu, K Rai. An Integrated Platform for Genome-wide Mapping of Chromatin States using High-Throughput ChIP-sequencing in Tumor Tissues. *J Vis Exp.* (2018) (PMID: 29683440)

17. H Yi*, **AT Raman***, H Zhang, G Allen and Z Liu. Detecting hidden batch factors through data-adaptive adjustment for biological effects. *Bioinformatics* (2018) (PMID: 29617963)
18. A Pohodich, HK Yalamanchili, **AT Raman**, YW Wan, M Gundry, S Hao, H Jin, J Tang, Z Liu, H Zoghbi. Forniceal deep brain stimulation induces gene expression and splicing changes that promote neurogenesis and synaptic plasticity. *elife* (2018) (PMID: 29570050). *Computational and Integrative analysis lead (equal contributor)*
 - Featured in TheScientist. Press release - Deep Brain Stimulation Affects the Activity of Hundreds of Genes
19. U Oleksiewicz*, M Gladych*, **AT Raman*** *et al.* KRAB/TRIM28 preserve self-renewal of human pluripotent stem cells through epigenetic repression of pro-differentiation genes. *Stem Cell Reports* (2017) (PMID: 29198826)
20. TCGA Network. Genomic classification of cutaneous melanoma. *Cell* (2015) (PMID: 26091043)
21. V Litvak, A Ratushny, A Lampano, F Schmitz, A Huang, **A Raman**, A. Rust, A. Berghaler, J. Aitchison, A. Aderem. A FOXO3/IRF7 gene regulatory circuit limits inflammatory sequelae of antiviral responses. *Nature* (2012) (PMID: 22982991)
 - Recommended by the Faculty of 1000
22. S Ramachandran, A Katiyar, A Sinha, A Bharadwaj, A Dutta, **A Raman** *et al.* Mycobacterium tuberculosis systems biology data in R. *Biobytes* (2009)

**Manuscripts in
Peer-Review**
(* CO-FIRST
AUTHORS)

1. M Maitituoheti*, E Arslan*, **AT Raman***, ..., JN Myers, and K Rai. Pan-cancer Chromatin Landscape Reveals Principles of Epigenetic Heterogeneity and Dependencies in Cancer Cells. *In revision, Nature Cell Biology (NCB-R44336)* (2022)

**Invited
Presentations &
Seminars**

1. Amplification-based expression data show bias towards long gene misregulation in synaptic disorders in MeCP2 syndrome. Virtual/oral presentation for the Young Scientist Award session, *Annual Conference Of The Midsouth Computational Biology & Bioinformatics Society (MCBIOS) and MAQC Annual Meeting* (2020)
2. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *IGIB, New Delhi*. Host: Debasis Dash, Ph.D. and Anurag Agrawal, M.D., Ph.D. (2019)
3. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *Harvard Medical School, Boston*. Host: Steven McCarroll, Ph.D. (2018)
4. Deciphering epigenomic landscape in colorectal cancer at *Genome Medicine Science Day, MD Anderson Cancer Center, Houston, TX* (2018)
5. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *Broad Institute of MIT and Harvard, Cambridge*. Host: Evan Macosko, M.D., Ph.D. and Aviv Regev, Ph.D. (2018)
6. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *Broad Institute of MIT and Harvard, Cambridge*. Host: Martin Aryee, Ph.D., Alexander Meissner, Ph.D. and Andreas Gnirke, Ph.D. (2018)
7. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *University of Toronto, Toronto*. Host: Mathieu Lupien, Ph.D. (2018)
8. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *University of California, San Diego*. Host: Bing Ren, Ph.D. (2018)

9. Decoding Big Genomic Datasets: Biases, hypotheses & regulation at *University of California, Los Angeles*. Host: Daniel Geschwind, M.D., Ph.D. (2018)
10. ChIP-seq Analysis: Pipelines and Data Interpretations at *ISB Nucleic Acid Course*, Seattle, WA (2013)
11. Identification of Foxo3/IRF7 circuits that limits inflammatory sequel of antiviral response at *ISB Retreat*, Seattle, WA (2012)

Teaching Experience

- Teaching Assistant for Bioinformatics Workshop, MD Anderson Cancer Center (Dec. 2017)
– Supervised by Kunal Rai, Ph.D.
- Teaching Assistant for Computational Math for Quantitative Biomedicine, BCM
– Supervised by Zhandong Liu, Ph.D. and Aleksandar Milosavljevic, Ph.D.
– Evaluation from the students: **6/7** (Fall 2017)
- Taught a course on ChIP-seq analysis at ISB Nucleic Acid Course (2013)

Academic Services and Memberships

- **Ad Hoc Peer Review** – IUBMB Life, Stem Cell Research & Therapy, Frontiers in Genetics, PLOS Computational Biology, Computational and Structural Biotechnology Journal
- **Guest Editor** – Frontiers in Pharmacology
- **Professional Societies and Memberships**
– Core RSG India Member, ISCB (2016-2017)
– Contributors of SysBorgTB & Open Source Drug Discovery by CSIR, India
- **Wikipedia articles**
– **Tumor Metabolism** for Cancer Biology course (Spring 2014)

Posters (* CO-FIRST AUTHORS)

1. **AT Raman**, A Pohodich, YW Wan, HK Yalamanchili, HY Zoghbi, Z Liu. Amplification-based expression data show bias towards long gene misregulation in synaptic disorders in Rett syndrome. Poster at *Pacific Symposium on Biocomputing (PSB)*, The Big Island of Hawaii (2020)
2. **AT Raman***, Elias Orouji*, Kunal Rai. Deciphering epigenomic landscape in colorectal cancer. Poster at *Genome Medicine Science Day, MD Anderson Cancer Center*, Houston, TX (2018)
3. Elias Orouji*, **AT Raman***, et al. Colorectal cancer epigenomic landscape. In: *Proceedings of the American Association for Cancer Research Annual Meeting 2018*; 2018 Apr 14-18; Chicago, IL. Philadelphia (PA): AACR; Cancer Res 018;78(13 Suppl):Abstract nr 4315.
4. **AT Raman***, Elias Orouji*, Kunal Rai. Deciphering epigenomic landscape in colorectal cancer. Poster at *Chromatin Architecture and Chromosome Organization (Keystone Conference)*, Whistler, British Columbia, Canada (2018)
5. **AT Raman**, A Pohodich, YW Wan, HK Yalamanchili, HY Zoghbi, Z Liu. Amplification-based expression data show bias towards long gene misregulation in synaptic disorders in Rett syndrome. Poster at *Quantitative and Computational Biosciences Annual Retreat*, Houston (2018) – **Second Best Poster Award**
6. **Veena Kochat***, **AT Raman***, et al. Oncogenic Role of EZH2 in the Pathogenesis of Malignant Peripheral Nerve Sheath Tumors with Functionally Inactive Polycomb Repressor Complex 2. Poster at *Cancer Epigenetics: New Mechanisms, New Therapies (Keystone Conference)*, Breckenridge, Colorado (2018)
7. **CA Chen**, S Pedersen, **A Raman**, L Wang, J Yin, H Zoghbi, Z Liu, R Pautler, CP Schaaf. NR2F1 mutations: Human phenotypes and investigation of a mouse model. Poster at *ASHG*, Vancouver, Canada (2016)

8. **A Raman** et al. Existence of gene-regulatory network in Macrophages. Poster at *International Conference on Systems Biology and Microbiome*, Seattle (2012)
9. **A Raman** et al. Activation states of genes in Toll Like Receptor induced macrophages. Poster at *International Conference on Systems Biology and Microbiome* (2012), Seattle
10. **A Raman** et al. Strategies in Systems Biology to predict and confirm the existence of gene-regulatory network. Poster at *BioC* (2011), Seattle
11. **A Raman**, Vladimir Litvak, et al. Strategies in systems biology to improve the prediction of gene regulatory network involving the dynamic interaction among the transcription factors. Poster at *Systems Biology in Human Diseases*, Boston (2011)

Skill-Set Summary

- Experience in Next Gen-Sequencing Data Analysis:
Proficiency in RNA-seq (5+ years), ChIP-seq (5+ years), Microarray (7+ years)
Intermediate in NanoString (1+ years), ATAC-seq (1+ years)
Familiarity scRNA-seq (3+ months)
- Programming Languages:
Proficiency in R, Perl
Intermediate in C/C++, MATLAB, Java, Shell Scripting
Familiarity in Python, Octave
- High Performance Computing: Load Sharing Facility (LSF), Condor
- Operating Systems: Linux, Windows, Mac OS X, Unix

Research Experience – Details

- | | |
|---|--|
| <p>Statistical Epigenomics Postdoc Associate</p> <p>Aryee, Meissner and Gnirke Groups, Broad Institute and MGH</p> <ul style="list-style-type: none"> • Understanding the dynamics of gene regulation using single-cell genomics and long read sequencing | <p>Dec 2018 - Present
Cambridge, MA</p> |
| <p>Research Assistant</p> <p>Liu's Lab (in collaboration with Zoghbi's lab), BCM</p> <ul style="list-style-type: none"> • Amplification-based expression data show bias towards long gene misregulation in synaptic disorders (Published in <i>Nature Comm.</i>) • Developed batch detection algorithm in gene expression datasets (Published in <i>Bioinformatics</i>) • Mechanism behind the effects of deep brain stimulation in Rett syndrome, meta-analysis of activity dependent genes and intellectual disorders (Published in <i>elife</i> and <i>Hum Mol Genet.</i>) | <p>July 2015 - Sept 2018
Houston, TX</p> |
| <p>Research Assistant</p> <p>Rai Lab, Genome Medicine, MD Anderson Cancer Center</p> <ul style="list-style-type: none"> • Studying epigenomic landscape in colorectal tumors (Published in <i>Gut</i>) • Oncogenic Role of EZH2 in the pathogenesis of MPNST tumors (Published in <i>Acta Neuropathologica</i>) • Role for the TRM28/KRAB repressors during early development, with a particular emphasis in nuclear reprogramming (Published in <i>Stem Cell Reports</i>) • Integrative analysis of ChIP-seq and RNA-seq datasets | <p>July 2015 - Sept 2018
Houston, TX</p> |
| <p>Research Assistant</p> <p>Lynda Chin's Lab, Genome Medicine, MD Anderson Cancer Center</p> <ul style="list-style-type: none"> • Genome wide analysis of non-coding regulatory mutations in cancer • Lymphocytic Infiltration as a basis of response in melanoma tumors (Published in <i>Cell</i>) | <p>July 2014 - June 2015
Houston, TX</p> |
| <p>Graduate Rotation Student</p> <p>Baylor College of Medicine</p> | <p>Sept 2013 - May 2014
Houston, TX</p> |

- Han Liang's Lab: Analyzed RNA-seq Data for various TCGA Datasets for the potential unique transcription factors per subtype
- Lynda Chin's Lab: Analyzed known mutations in leukemia dataset for Apollo Project and the reported somatic mutations in COSMIC
- Zhandong Liu's Lab: Correlation network for 90,000 samples from Affymetrix Human Genome U133 Plus 2.0 Array

Bioinformatics Scientist

July 2010 - July 2013

Shmulevich Lab, Institute for Systems Biology

Seattle, WA

- Rhinovirus vs Influenza Virus Project: Analyzing the similarities and differences between the two viruses using microarray datasets
- Tol-II Receptors Project: Analysis 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*)
- Poised Genes Project: Predicting poised genes in the macrophages using machine learning algorithms
- In-House ChIP-seq Pipeline: Development and integration of various functionalities within the pipeline

Statistician

Nov 2009 - July 2010

Computational Genetics Lab, WPIC-UPMC

Pittsburgh, PA

- Palau Project: Analyzed GWAS datasets for the detection of causal genes in psychotic disorders and schizophrenia and
- Implemented genomic distance based multivariate regression model for the estimation of Identity by Descent (IBD) in the haplotype datasets
- Worked on the detection of IBD for the use of the population based linkage analysis among the case and control pairs

Research Assistant Programmer

Apr 2009 - Oct 2009

Department of Biomedical Informatics, University of Pittsburgh

Pittsburgh, PA

- Feature/covariates selection from comparative and high-throughput data for the prediction of protein-protein interaction pairs
- Computational prediction and accuracy of different statistical based algorithms such as discriminative and generative algorithms, and clustering based algorithms

Research Assistant

Sept 2007 to Dec 2007

Murphy Lab, Carnegie Mellon University

Pittsburgh, PA

- Development of database using PostgreSQL and JSP as back-end and front-end respectively

Research Trainee

Dec 2005 to Nov 2006

Institute of Genomics and Integrative Biology

New Delhi, India

Advisers: Dr. S. Ramachandran and Dr. Vani Brahmachari

- B.Tech Thesis: "Study of Host Protein Mimicry of *M. tuberculosis* proteins in *H. sapiens*"
- Comparative genomic analysis of *M. tuberculosis* H37Rv with *H. sapiens* using sequence and structural based approaches

Course Projects

- [Loan Default Prediction - Imperial College London \(Kaggle dataset\)](#). A. Raman and M. Chen. (Comp 540, Spring 2014; Prof. Devika Subramanian)
- [Analysis and Forecast of Start-Up Companies](#). A. Raman, Y. Miao and G. Breternitz (Stat 405, Fall 2013; Dr. Roberto Bertolusso) - Our project was used as a reference for Spring/Fall 2014-2015 class
- CMBMS Final Project: B-cell HIV Epitope Predictor (B-HIVE P). S Garimalla, A Raman,

V Pillalamarri (03-712 Course Project, Fall 2008; Prof. Russell Schwartz, CMU)

- Developed ORF and Gene Prediction Tool in prokaryotes in Perl and HTML (Genomics & Computational Molecular Biology Course Project, Spring 2005; Prof. Ghosh, VIT) – Awarded as the best class project

Relevant Courses

- *Massive Open Online Courses*: Machine Learning ([Coursera](#)), RNA-seq data analysis ([edX](#))
- *Baylor College of Medicine (Ph.D. course work)*: Computational Mathematics for Quantitative Biomedicine, Methods and Logic in Molecular Biology
- *Rice University (Ph.D. course work)*: Molecular Biophysics, Statistical Computing & Graphics, Statistical Machine Learning, Cancer Biology, Probability & Statistics
- *Carnegie Mellon University (M.S. course work)*: Data Mining, Applied Machine Learning, Computational Biology, Computational Methods for Biological Modeling & Simulation, Mathematical Models, Advanced Molecular & Cell Biology, Data Structure & Algorithms
- *Vellore Institute of Technology (B.Tech course work)*: Biochemistry, Cell Biology, Immunology, Probability and Biostatistics, Discrete Math, Genomics, Proteomics, Systems Biology, Programming Languages, Databases, Machine Learning, Structure and Molecular Modeling, Molecular Evolution and Phylogeny, Artificial Intelligence, Data Mining and Warehousing

References

Martin Aryee, Ph.D.

Merkin Institute Fellow at the Broad Institute of MIT and Harvard

Assistant Professor, Department of Pathology, Massachusetts General Hospital

Assistant Professor in the Department of Biostatistics, Harvard School of Public Health

Associate Member, Broad Institute of Harvard and MIT

Charlestown, Massachusetts 02129

Alexander Meissner, Ph.D.

Director and Scientific member, Department of Genome Regulation,

Max Planck Institute for Molecular Genetics, Berlin, Germany

Visiting Scientist and Professor, Department of Stem Cell and Regenerative Biology,

Harvard University and Broad Institute of MIT and Harvard

Berlin, Germany 14195

Zhandong Liu, Ph.D.

Assistant Professor, Department of Pediatrics

Jan and Dan Duncan Neurological Research Institute

Baylor College of Medicine

Houston, TX 77030

Huda Zoghbi, M.D.

Professor, Departments of Neuroscience, Molecular and Human Genetics,

Pediatrics, and Neurology

Investigator, Howard Hughes Medical Institute

Jan and Dan Duncan Neurological Research Institute

Baylor College of Medicine

Houston, TX 77030

Kunal Rai, Ph.D.
Associate Professor, Dept. of Genome Medicine
MD Anderson Cancer Center
Houston, TX 77054
✉ krai@mdanderson.org; ☎ +1 (617) 697-3491

Additional references available upon request.