BIOGRAPHICAL SKETCH

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NAME: Moudgil, Arnav

eRA COMMONS USER NAME (credential, e.g., agency login): ARNAVMOUDGIL

POSITION TITLE: Postdoctoral Scholar

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
Stanford University, Stanford, CA	BS	06/2010	Biology
Stanford University, Stanford, CA	MS	06/2011	Biology
Washington University in St. Louis, St. Louis, MO	PHD	05/2022	Computational Biology
Washington University in St. Louis, St. Louis, MO	MD	05/2022	Medicine
Stanford Health Care, Stanford, CA	Resident	06/2023	General Surgery Preliminary Year
Stanford University School of Medicine, with Drs. Sui Wang and Alistair Boettiger, Stanford, CA	Postdoctoral Fellow	present	Developmental Genomics
Stanford Health Care, Stanford, CA	Resident	present	Ophthalmology Resident

A. Personal Statement

I am a physician-scientist and ophthalmology resident with expertise in genomics and computational biology who plans to lead a basic science research laboratory studying cell fate in retinal development and disease. As a graduate student, I developed one of the first methods to map transcription factor binding in single cells from complex tissues such as the brain. This introduced me to the field of gene regulation and sparked my passion for uncovering the mechanistic basis of cell fate decisions. I am currently a research-track resident in the Department of Ophthalmology at Stanford University and postdoctoral scholar jointly working with Drs. Sui Wang and Alistair Boettiger. In addition to building a broad clinical foundation, I am gaining additional expertise in mouse models of retinal development and cutting-edge microscopy-based techniques to understand genome regulation. Together, these experiences will expand my expertise in gene regulatory dynamics and help prepare me for an independent research career. After residency I will pursue subspecialty training in vitreoretinal surgery as well as ocular oncology. After completing clinical training, I aim to join an academic medical center with joint appointments in ophthalmology and genetics. In addition to seeing patients, I plan to lead an independent, competitively funded lab focusing on the molecular etiologies of cell fate decisions with specific applications toward engineering nuanced genetic circuits for gene therapies and regenerative medicine.

1. Yen A, Mateusiak C, Sarafinovska S, Gachechiladze MA, Guo J, Chen X, Moudgil A, Cammack AJ, Hoisington-Lopez J, Crosby M, Brent MR, Mitra RD, Dougherty JD. Calling Cards: A Customizable Platform to Longitudinally Record Protein-DNA Interactions Over Time in Cells and Tissues. Curr Protoc. 2023 Sep;3(9):e883. PubMed Central PMCID: PMC10627244.
2. Lalli M, Yen A, Thopte U, Dong F, Moudgil A, Chen X, Milbrandt J, Dougherty JD, Mitra RD. Measuring transcription factor binding and gene expression using barcoded self-reporting transposon calling cards and transcriptomes. NAR Genom Bioinform. 2022 Sep;4(3):lqac061.

PubMed Central PMCID: PMC9428926.

3. Moudgil A, Wilkinson MN, Chen X, He J, Cammack AJ, Vasek MJ, Lagunas T Jr, Qi Z, Lalli MA, Guo C, Morris SA, Dougherty JD, Mitra RD. Self-Reporting Transposons Enable Simultaneous Readout of Gene Expression and Transcription Factor Binding in Single Cells. Cell. 2020 Aug 20;182(4):992-1008.e21. PubMed Central PMCID: PMC7510185.
4. Cammack AJ, Moudgil A, Chen J, Vasek MJ, Shabsovich M, McCullough K, Yen A, Lagunas T, Maloney SE, He J, Chen X, Hooda M, Wilkinson MN, Miller TM, Mitra RD, Dougherty JD. A viral toolkit for recording transcription factor-DNA interactions in live mouse tissues. Proc Natl Acad Sci U S A. 2020 May 5;117(18):10003-10014. PubMed Central PMCID: PMC7211997.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2023 -	Postdoctoral Scholar, Laboratories of Drs. Sui Wang and Alistair Boettiger, Stanford University School of Medicine, Stanford, CA
2023 -	Stanford Ophthalmology Advanced Research (SOAR) Resident, Stanford Health Care, Palo Alto, CA
2022 -	Member, American Academy of Ophthalmology, San Francisco, CA
2022 - 2023	General Surgery Preliminary Year, Stanford Health Care, Stanford, CA
2017 - 2018	Organizer, Genome Analysis Training Program's Annual Guest Speaker, Washington University in St. Louis School of Medicine, St. Louis, MO
2016 - 2016	Graduate Teaching Assistant, "Medical Genetics", Washinton University in St. Louis School of Medicine, St. Louis, MO
2015 - 2020	Graduate Student Researcher (Laboratory of Dr. Robi Mitra), Washington University in St. Louis School of Medicine, St. Louis, MO
2014 - 2022	Organizer, Washington University in St. Louis MSTP Class of 2013 Journal Club, Washington University in St. Louis School of Medicine, St. Louis, MO
2013 - 2022	Member, Washington University in St. Louis MSTP Student Committee, Washington University in St. Louis School of Medicine, St. Louis, MO
2011 - 2013	Life Sciences Research Assistant (Laboratory of Dr. Peter Parham), Stanford University School of Medicine, Stanford, CA
2010 - 2011	Undergraduate Student Researcher (Laboratory of Dr. Marcus Feldman), Department of Biology, Stanford University, Stanford, CA
2009 - 2009	Undergraduate Teaching Assistant ("The Technical Aspects of Photography"), Stanford University, Stanford, CA

Honors

2024 - 2025	Career-Starter Research Grant, Knights Templar Eye Foundation
2018 - 2021	Ruth L. Kirschstein National Research Service Award F30 Individual Fellowship (HG009986), National Institute's of Health
2017 - 2018	National Human Genome Research Institute T32 Predoctoral Fellowship, Washington University in St. Louis School of Medicine
2014 - 2016	National Institute of General Medical Sciences T32 Predoctoral Fellowship, Washington University in St. Louis School of Medicine
2023	National Eye Institute T32 Postdoctoral Fellowship, Stanford University
2021	Spencer T. and Ann W. Olin Medical Science Fellow, Washington University in St. Louis School of Medicine
2008	BIO 44Y Laboratory Class Award Winner, Stanford University

C. Contribution to Science

1. RNA calling cards and single cell calling cards. During my graduate work, I developed RNA calling cards and its evolution into single cell calling cards, one of the first scalable techniques to assay transcription factor (TF) binding at single cell resolution. This work grew out of transposon calling cards, a method for genome-wide mapping of TF binding sites by fusing a TF to a transposase. As the TF visits binding sites, the transposase inserts a transposon marker nearby. We discovered a way to map these transposons using run-on transcription and bulk RNA-seq. We were subsequently able to combine this approach with droplet-based single cell RNA-seq platforms to perform simultaneous deconvolution of cell types and TF binding in heterogeneous samples. We have used these methods to map transcription factor binding in a variety of cell lines, during cell state transitions, and in complex tissues such as the mouse brain.
    a. Yen A, Mateusiak C, Sarafinovska S, Gachechiladze MA, Guo J, Chen X, Moudgil A, Cammack AJ, Hoisington-Lopez J, Crosby M, Brent MR, Mitra RD, Dougherty JD. Calling Cards: A Customizable Platform to Longitudinally Record Protein-DNA Interactions Over Time in Cells and Tissues. Curr Protoc. 2023 Sep;3(9):e883. PubMed Central PMCID: PMC10627244.
    b. Lalli M, Yen A, Thopte U, Dong F, Moudgil A, Chen X, Milbrandt J, Dougherty JD, Mitra RD. Measuring transcription factor binding and gene expression using barcoded self-reporting transposon calling cards and transcriptomes. NAR Genom Bioinform. 2022 Sep;4(3):lqac061. PubMed Central PMCID: PMC9428926.
    c. Moudgil A, Wilkinson MN, Chen X, He J, Cammack AJ, Vasek MJ, Lagunas T Jr, Qi Z, Lalli MA, Guo C, Morris SA, Dougherty JD, Mitra RD. Self-Reporting Transposons Enable Simultaneous Readout of Gene Expression and Transcription Factor Binding in Single Cells. Cell. 2020 Aug 20;182(4):992-1008.e21. PubMed Central PMCID: PMC7510185.
    d. Cammack AJ, Moudgil A, Chen J, Vasek MJ, Shabsovich M, McCullough K, Yen A, Lagunas T, Maloney SE, He J, Chen X, Hooda M, Wilkinson MN, Miller TM, Mitra RD, Dougherty JD. A viral toolkit for recording transcription factor-DNA interactions in live mouse tissues. Proc Natl Acad Sci U S A. 2020 May 5;117(18):10003-10014. PubMed Central PMCID: PMC7211997.
2. Novel genomic data formats, visualizations, and algorithms. While developing single cell calling cards, I anticipated needing new approaches to share, browse, and analyze such data. I developed a new genomics data format, the quantized BED (qBED), to encode discrete, quantitative genomic data. While initially developed for transposon insertions, I also showed that it was possible to encode other data types, such as SNPs from GWAS studies or CADD scores for predicting mutation effects. I also created an accompanying visualization track on the WashU Epigenome Browser to readily examine such data. To analyze qBED data, which is inherently point-based, I adapted the Bayesian blocks algorithm (used in astrophysics) and created an open source software package for the greater genomics community. In the process I was able to dramatically accelerate the algorithm and analyze massive data sets that are shedding new light on genome organization (manuscript in preparation).
    a. Moudgil A, Li D, Hsu S, Purushotham D, Wang T, Mitra RD. The qBED track: a novel genome browser visualization for point processes. Bioinformatics. 2021 May 23;37(8):1168-1170. PubMed Central PMCID: PMC8150125.
    b. Moudgil A, Wilkinson MN, Chen X, He J, Cammack AJ, Vasek MJ, Lagunas T Jr, Qi Z, Lalli MA, Guo C, Morris SA, Dougherty JD, Mitra RD. Self-Reporting Transposons Enable Simultaneous Readout of Gene Expression and Transcription Factor Binding in Single Cells. Cell. 2020 Aug 20;182(4):992-1008.e21. PubMed Central PMCID: PMC7510185.
    c. Cammack AJ, Moudgil A, Chen J, Vasek MJ, Shabsovich M, McCullough K, Yen A, Lagunas T, Maloney SE, He J, Chen X, Hooda M, Wilkinson MN, Miller TM, Mitra RD, Dougherty JD. A viral toolkit for recording transcription factor-DNA interactions in live mouse tissues. Proc Natl Acad Sci U S A. 2020 May 5;117(18):10003-10014. PubMed Central PMCID: PMC7211997.
3. Computational models of protein evolvability. As an undergraduate, I sought to understand how evolutionary processes choose which trajectories to follow, and whether they do so in a replicable manner. I developed a computational model of evolvability using “lattice proteins,” which were 12-mer receptors constrained to fold onto the points of grid. I measured fitness by calculating how strong

these peptides bound a specific 6-mer ligand protein, with the fittest receptors being allowed to replicate. These proteins were segregated into distinct populations (demes), each with a different ligand, but individual sequences could migrate between demes. We were surprised to find that the same receptor starting sequences would tend to overtake the population despite every replicate following different sets of mutations and migration. This model has gone to inform subsequent work on evolutionary theory.
   a. Palmer ME, Moudgil A, Feldman MW. Long-term evolution is surprisingly predictable in lattice proteins. J R Soc Interface. 2013 May 6;10(82):20130026. PubMed Central PMCID: PMC3627087.

4. Software to genotype individuals at immunogenomic loci. Major histocompatibility complex (MHC) class I and killer cell immunoglobulin-like receptors (KIRs) are the most polymorphic genes in the human genome. As a research technician, I developed new software to efficiently genotype individuals at these loci from geographically diverse populations. We collaborated with Illumina to generate sequencing strategies for the regions but our ability to process and catalog sequence diversity lagged behind. I wrote code to store compressed representations of known sequences, assemble short reads from a single individual at KIR loci, and rapidly output a list of that person's most likely genotypes. This program offered the only automated solution to a task that otherwise had to be carried out manually. The core of this program has been transferred to a software company for further development.
   a. De Santis D, Dinauer D, Duke J, Erlich HA, Holcomb CL, Lind C, Mackiewicz K, Monos D, Moudgil A, Norman P, Parham P, Sasson A, Allcock RJ. 16(th) IHIW : review of HLA typing by NGS. Int J Immunogenet. 2013 Feb;40(1):72-6. PubMed Central PMCID: PMC4793271.
5. Assembled the orangutan major histocompatibility complex (MHC) -B and -C loci. The MHC-B and -C loci have undergone significant selection and expansion in primates, with MHC-C unique to great apes. The individual sequenced for the orangutan genome project showed unique copy number variation at these loci; specifically, she appeared to have three copies of MHC-B and a single copy of MHC-C. These loci were not finished as part of the orangutan genome, so their spatial and ancestral relationships to each other were unclear. I assembled these loci by culturing unassembled bacterial artificial chromosomes (BACs) from the orangutan genome project. I prepared long-read sequencing libraries and sequenced them on the Pacific Biosciences RSII platform, which let us physically link specific B and C alleles on the same chromosome. As a result, 11 unassembled BACs were stitched together into a long-range haplotype. These data are in preparation for publication.