ARUSHI VARSHNEY, PHD

varshney.arushi@gmail.com
Google Scholar
Orcid
github.com/arushiv

HIGHLIGHTS & SKILLS

- **PhD plus 6 years experience in leading functional genomics research** – Integrating multi-modal data spanning genomics, bulk and single-cell epigenomics and transcriptomics in relevant human/model organism tissues to understand metabolic disease mechanisms. Mentoring high-school, undergraduate, MS, and PhD level trainees.
- **Computational Biology** – GWAS, genotype imputation, molecular quantitative trait locus mapping (QTL), statistical finemapping, signal colocalization, mediation and Mendelian Randomization. Bulk and single-cell (sc) / single-nucleus (sn) multi-omics profiling and NGS data analysis including RNA/scRNA/snRNA-seq, ATAC/snATAC-seq, ChIP-seq, CAGE-seq. Utilizing large datasets such as the UK Biobank (UKBB), Genotype-Tissue Expression (GTEx), ENCODE, Roadmap epigenomics.
- **Bioinformatics reproducibility** – Git, Nextflow, Snakemake, Docker/Singularity.
- **Computing** – High Performance Computing (HPC), Slurm, pbs, Google Cloud Platform, Amazon Web Services (AWS).
- **Languages** – Python, R, Shell, LaTeX.

EDUCATION

2014-2019 **University of Michigan**, Ann Arbor, MI, USA
Doctor of Philosophy, Human Genetics
Thesis Advisor: Prof. Stephen C. J. Parker
Thesis: Understanding the Genetics of Gene Regulation Using Multi-Omics Profiling[a]

---

[a] `https://deepblue.lib.umich.edu/handle/2027.42/151691`

2012-2014 **École Polytechnique Fédérale de Lausanne (EPFL)** (Swiss Federal Institute of Technology), Lausanne, Switzerland
Master of Science, Bioengineering

2008-2012 **Indian Institute of Technology (IIT)**, Guwahati, Assam, India
Bachelor of Technology, Biotechnology

POSITIONS

Assistant Research Scientist *University of Michigan*, Ann Arbor, MI *August 2024-present*

- Lead highly collaborative research projects integrating genomics, epigenomics, and transcriptomics to understand complex disease mechanisms.
- Leverage genetics and single-nucleus/single-cell multi-omics to identify gene regulatory mechanisms and their relevant cell types.
- Collaborate across academia and industry as part of AMP-CMD, FUSION consortia.
- Mentor PhD level trainees in their research projects.
- Grant writing.

Research Investigator *University of Michigan*, Ann Arbor, MI *April 2021-present*

- Leading highly collaborative research projects using single-nucleus multi-omics profiling to identify the cell-type, regulatory element, target gene and causal variant in gaining mechanistic insights underlying GWAS signals.
- Analyzed single-nucleus RNA and ATAC data across >400 human skeletal muscle samples to understand context-specific gene regulation. Identified gene expression and chromatin accessibility QTLs (eQTLs, caQTLs) and performed statistical finemapping and colocalization with GWAS signals.
- Relevant preprint: ***Varshney A***, *Manickam N, Orchard P, Tovar A, et al.*, Population-scale skeletal muscle single-nucleus multi-omic profiling reveals extensive context specific genetic regulation, **BioRxiv**, 2023, `https://doi.org/10.1101/2023.12.15.571696`
- Mentor high-school, undergraduate, masters and PhD level trainees in research projects.

Senior Computational Biologist *University of Michigan*, Ann Arbor, MI *June 2019-March 2021*

- Leading research projects towards understanding gene regulatory mechanisms underlying complex diseases.
- Lead analyst in the large Accelerated Medicines Partnership - Common Metabolic Disorders (AMP-CMD) consortium which spans academia and industry.
- Identified effector-transcripts underlying GWAS signals using eQTL colocalizations.
- Optimized analyses procedures for molecular QTL signal identification, finemapping and colocalization while analyzing single and multi-ancestry datasets.

GRANTS

- Integrating multi-omics data to identify underlying disease mechanisms in metabolic dysfunction. Co-Investigator (Principal Investigator: Stephen Parker) Pfizer, Inc.
  11/2021 - 11/2023
  $1,253,000

FELLOWSHIPS

- Rackham Predoctoral Fellowship 2018-19
- **[2x]** Rackham Travel Grant, University of Michigan, United States
- Barbour International Doctoral Scholarship 2017-18
- American Association for University Women (AAUW) International Doctoral Fellowship 2016-17
- Zeno Karl Schindler Grant for Master's thesis project at Massachusetts Institute of Technology (MIT), 2013-14
- Women in Science and Humanities (WISH) Fellowship, EPFL, 2013-14
- **[3x]**Institute Merit Scholarship, IIT Guwahati, 2009-12

HONORS AND AWARDS

- Employment-based first preference (EB1) US visa under the "Outstanding Researchers" category granted by the USCIS.
- ProQuest Distinguished Dissertation Awards - Honorable Mention, 2019.

- Best Poster Award, University of Michigan - Dept. of Human Genetics Retreat, 2016.
- Mention d'excellence (Award for Academic Excellence), EPFL, 2014.
- Institute Silver Medal, IIT Guwahati, 2012.

PUBLICATIONS & TALKS

Preprints under peer-review

1. ***Varshney A***, *Manickam N, Orchard P, Tovar A, et al.*, Population-scale skeletal muscle single-nucleus multi-omic profiling reveals extensive context specific genetic regulation, **BioRxiv**, 2023, `https://doi.org/10.1101/2023.12.15.571696`

2. *Tovar A, Kyono Y, Nishino K, Bose M,* ***Varshney A***, *Parker, SCJ, Kitzman JO*, Using a modular massively parallel reporter assay to discover context-specific regulatory grammars in type 2 diabetes, **BioRxiv**, 2023, `https://doi.org/10.1101/2023.10.08.561391`

3. *Albanus RDO, Tang X, Taylor HJ, Manickam N, Erdos M, Narisu N, Han Y, Orchard P,* ***Varshney A***, *Liu C, Naji A, HPAP Consortium, Collins FS, Chen S, Parker SCJ*, Single-cell gene expression and chromatin accessibility profiling of human pancreatic islets at basal and stimulatory conditions nominates mechanisms of type 1 diabetes genetic risk, **BioRxiv**, 2023, `https://doi.org/10.1101/2022.11.12.516291`

4. *Zhao Z, Albanus RDO, Taylor H, Tang X, Han Y, Orchard P,* ***Varshney A***, *Zhang T, Manickam N, Erdos M, et al.*, An integrative single-cell multi-omics profiling of human pancreatic islets identifies T1D associated genes and regulatory signals, **Research Square**, 2023, `https://doi.org/10.21203/rs.3.rs-3343318/v1`

Peer-reviewed journal

1. *Walker J*[1], *Saunders D*[1], *Rai V*[1], *Dai C, Orchard P, Hopkirk A, Reihasmann C, Tao Y, Fan S, Shrestha S,* ***Varshney A***, *Wright J, Pettway Y, Ventresca C, Agarwala S, Aramandla R, Poffenberger G, Jenkins R, Hart N, Greiner D, Shultz L, Bottino R, Human Pancreas Analysis Program, Liu J, Parker SCJ*[1], *Powers A*[1], *Brissova M*[1], Genetic risk converges on regulatory networks mediating early type 2 diabetes, **Nature**, 2023, `https://doi.org/doi:10.1038/s41586-023-06693-2`

2. *Tenney AP, Di Gioia SA, Webb BD, Chan W-M, de Boer E, Garnai SJ, Barry BJ, Ray T, Kosicki M, Robson CD, Zhang Z, Collins TE, Gelber A, Pratt BM, Fujiwara Y,* ***Varshney A***, *Lek M, Warburton PE, Van Ryzin C, Lehky TJ, Zalewski C, King KA, Brewer CC, Thurm A, Snow J, Facio FM, Narisu N, Bonnycastle LL, Swift A, Chines PS, Bell JL, Mohan S, Whitman MC, Staffieri SE, Elder JE, Demer JL, Torres A, Rachid E, Al-Haddad C, Boustany R-M, Mackey DA, Brady AF, Fenollar-Cortés M, Fradin M, Kleefstra T, Padberg GW, Raskin S, Sato MT, Orkin SH, Parker SCJ, Hadlock TA, Vissers LELM, van Bokhoven H, Jabs EW, Collins FS, Pennacchio LA, Manoli I, Engle EC*, Noncoding variants alter GATA2 expression in rhombomere 4 motor neurons and cause dominant hereditary congenital facial paresis, **Nature Genetics**, 2023, `https://doi.org/10.1038/s41588-023-01424-9`

3. *Li JH, Brenner LN, Kaur V, Figueroa K, Schroeder P, Huerta-Chagoya A,* ***MAGIC Investigators***, *Diabetes Prevention Program (DPP) Research Group, Udler MS, Leong A, Mercader JM, Florez JC*, Genome-wide association analysis identifies ancestry-specific genetic variation associated with acute response to metformin and glipizide in SUGAR-MGH, **Diabetologia**, 2023, `https://doi.org/10.1007/s00125-023-05922-7`

4. _Broadaway KA, Yin X, Williamson A, Parsons VA, Wilson EP, Moxley AH, Vadlamudi S, **Varshney A**, Jackson AU, Ahuja V, Bornstein SR, Corbin LJ, Delgado GE, Dwivedi OP, Fernandes Silva L, Frayling TM, Grallert H, Gustafsson S, Hakaste L, Hammar U, Herder C, Herrmann S, Højlund K, Hughes DA, Kleber ME, Lindgren CM, Liu C-T, Luan J, Malmberg A, Moissl AP, Morris AP, Perakakis N, Peters A, Petrie JR, Roden M, Schwarz PE H, Sharma S, Silveira A, Strawbridge RJ, Tuomi T, Wood AR, Wu P, Zethelius B, Baldassarre D, Eriksson JG, Fall T, Florez JC, Fritsche A, Gigante B, Hamsten A, Kajantie E, Laakso M, Lahti J, Lawlor DA, Lind L, März W, Meigs JB, Sundström J, Timpson NJ, Wagner R, Walker M, Wareham NJ, Watkins H, Barroso I, O'Rahilly S, Grarup N, Parker SC, Boehnke M, Langenberg C, Wheeler E, Mohlke KL_, Loci for insulin processing and secretion provide insight into type 2 diabetes risk, **American Journal of Human Genetics**, 2023, `https://doi.org/10.1016/j.ajhg.2023.01.002`

5. _DiCorpo D, Gaynor SM, Russell EM, Westerman KE, Raffield LM, Majarian TD, Wu P, Sarnowski C, Highland HM, Jackson A, Hasbani NR, de Vries PS, Brody JA, Hidalgo B, Guo X, Perry JA, O'Connell JR, Lent S, Montasser ME, Cade BE, Jain D, Wang H, D'Oliveira Albanus R, **Varshney A**, Yanek LR, Lange L, Palmer ND, Almeida M, et al._, Whole genome sequence association analysis of fasting glucose and fasting insulin levels in diverse cohorts from the NHLBI TOPMed program, **Communications Biology**, 2022, `https://doi.org/10.1038/s42003-022-03702-4`

6. _Orchard P, Manickam N, Ventresca C, **Varshney A**, Rai V, Kaplan J, Lalancette C, Gallagher K, Burant CF, Parker SCJ_, Human and rat skeletal muscle single-nuclei multi-omic integrative analyses nominate causal cell types, regulatory elements, and SNPs for complex traits, **Genome Research**, 2021, `https://doi.org/10.1101/gr.268482.120`

7. _**Varshney A**, Kyono Y, Venkateswaran E, Wang C, Erdos M, Narisu N, Albanus R, Orchard P, Stitzel M, Collins F, Kitzman J, Parker S_, A Transcription Start Site Map in Human Pancreatic Islets Reveals Functional Regulatory Signatures, **Diabetes**, 2021, `https://doi.org/10.2337/db20-1087`

8. _Chen J_[1], _Spracklen CN_[1], _Marenne G_[1], _**Varshney A**_[1], _Corbin LJ, et al._, The Trans-Ancestral Genomic Architecture of Glycaemic Traits, **Nature Genetics**, 2021, `https://doi.org/10.1038/s41588-021-00852-9`

9. _Albanus RDO, Kyono Y, Hensley J, **Varshney A**, Orchard P, Kitzman JO, Parker SCJ_, Chromatin information content landscapes inform transcription factor and DNA interactions, **Nature Communications**, 2021, `https://doi.org/10.1038/s41467-021-21534-4`

10. _Viñuela A_[1], _**Varshney A**_[1], _van de Bunt M_[1], _Prasad RB_[1], _Asplund O, Bennett A, Boehnke M, Brown AA, Erdos MR, Fadista J, Hansson O, Hatem G, Howald C, Iyengar AK, Johnson P, Krus U, MacDonald PE, Mahajan A, Manning Fox JE, Narisu N, Nylander V, Orchard P, Oskolkov N, Panousis NI, Payne A, Stitzel ML, Vadlamudi S, Welch R, Collins FS, Mohlke KL, Gloyn AL, Scott LJ, Dermitzakis ET_[1], _Groop L_[1], _Parker SCJ_[1], _McCarthy MI_[1], Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D, **Nature Communications**, 2020, `https://doi.org/10.1038/s41467-020-18581-8`

11. _**Varshney A**, VanRenterghem H, Orchard P, Boyle AP, Stitzel ML, Ucar D, Parker SC J_, Cell specificity of human regulatory annotations and their genetic effects on gene expression, **Genetics**, 2019, `https://doi.org/10.1534/genetics.118.301525`

12. _Lawlor N, Marquez E, Orchard P, Narisu N, Shamim MS, Thibodeau A, **Varshney A**, Kursawe_

R, Erdos MR, Kanke M, Gu H, Pak E, Dutra A, Russell S, Li X, Piecuch E, Luo O, Chines PS, Fuchsberger C, Sethupathy P, Aiden AP, Ruan Y, Aiden EL, Collins FS, Ucar D, Parker SC J, Stitzel ML, Multiomic profiling identifies cis-regulatory networks underlying human pancreatic β cell identity and function, **Cell Reports**, 2019, `https://doi.org/10.1016/j.celrep.2018.12.083`

13. *Zou LS, Erdos MR, Taylor DL, Chines PS,* ***Varshney A****, McDonnell GI, Parker SC J, Collins FS, Didion JP*, BoostMe accurately predicts DNA methylation values in whole-genome bisulfite sequencing of multiple human tissues, **BMC Genomics**, 2018, `https://doi.org/10.1186/s12864-018-4766-y`

14. *Taylor DL, Knowles DA, Scott LJ, Ramirez AH, Casale FP, Wolford BN, Guan L,* ***Varshney A****, Albanus RD, Parker SC J, Narisu N, Chines PS, Erdos MR, Welch RP, Kinnunen L, Saramies J, Sundvall J, Lakka TA, Laakso M, Tuomilehto J, Koistinen HA, Stegle O, Boehnke M, Birney E, Collins FS*, Interactions between genetic variation and cellular environment in skeletal muscle gene expression, **PLoS One**, 2018, `https://doi.org/10.1371/journal.pone.0195788`

15. *Pacelli S, Basu S, Whitlow J, Chakravarti A, Acosta F,* ***Varshney A****, Modaresi S, Berkland C, Paul A*, Strategies to develop endogenous stem cell-recruiting bioactive materials for tissue repair and regeneration, **Advanced Drug Delivery Reviews**, 2017, `https://doi.org/10.1016/j.addr.2017.07.011`

16. *Roman TS, Cannon ME, Vadlamudi S, Buchkovich ML, Wolford BN, Welch RP, Morken MA, Kwon GJ,* ***Varshney A****, Kursawe R, Wu Y, Jackson AU, National Institutes of Health Intramural Sequencin, Erdos MR, Kuusisto J, Laakso M, Scott LJ, Boehnke M, Collins FS, Parker SC J, Stitzel ML, Mohlke KL*, A Type 2 Diabetes-Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the ADCY5 Locus, **Diabetes**, 2017, `https://doi.org/10.2337/db17-0464`

17. ***Varshney A***[1]*, Scott LJ*[1]*, Welch RP*[1]*, Erdos MR*[1]*, Chines PS, Narisu N, Albanus RD, Orchard P, Wolford BN, Kursawe R, Vadlamudi S, Cannon ME, Didion JP, Hensley J, Kirilusha A, NISC Comparative Sequencing Program, Bonnycastle LL, Taylor DL, Watanabe R, Mohlke KL, Boehnke M*[1]*, Collins FS*[1]*, Parker SCJ*[1]*, Stitzel ML*[1], Genetic regulatory signatures underlying islet gene expression and type 2 diabetes, **Proc Natl Acad Sci USA**, 2017, `https://doi.org/10.1073/pnas.1621192114`

18. *Niederriter AR,* ***Varshney A****, Parker SC J, Martin DM*, Super Enhancers in Cancers, Complex Disease, and Developmental Disorders, **Genes**, 2015, `https://doi.org/10.3390/genes6041183`

Selected oral presentations

1. Epigenetic profiling at high resolution reveals genetic regulatory signatures underlying islet gene expression and type 2 diabetes, ***American Society for Human Genetics (ASHG) Meeting***, 10/2016

2. Single nuclei resolution chromatin and gene expression profiling in skeletal muscle across 287 genotyped individuals reveals cell-specific genetic regulatory architectures, ***American Society for Human Genetics (ASHG) Meeting***, 10/2020

---

[1] Equal contribution

3. Context-specific genetic regulation of skeletal muscle biology, ***The Biology of Genomes Meeting***, 05/2021
4. Context-specific genetic regulation of skeletal muscle biology, ***American Diabetes Association (ADA) Meeting***, 06/2021
5. Context-specific genetic regulation of skeletal muscle biology, ***American Society of Human Genetics (ASHG) Meeting***, 10/2021

JOURNAL AND ABSTRACT REVIEWS

- 2019 PLoS ONE
- 2019 - 2020 Nature Communications
- 2019 - 2022 Gene
- 2020 PLoS Genetics
- 2020 eLife
- 2020 Diabetes
- 2021 - 2020 PLoS ONE
- 2021 Human Molecular Genetics
- 2021 Bioinformatics
- 2021 Science Advances
- 2023 Nucleic Acids Research
- 2023 American Diabetes Association (ADA), Meeting abstracts reviewer

MENTORSHIP

Graduate Student

- 08/2019-04/2020 Nuha Mahmood, University of Michigan, Master's thesis.
- 11/2020-04/2021 Breanna McBean, University of Michigan, PhD rotation project.
- 03/2021-04/2021 Kinsey Van Deynze, University of Michigan, PhD rotation project.
- 03/2022-04/2021 Jianhui Gong, University of Michigan, PhD rotation project.
- 09/2022-Present Avery Mitchell Maddox, University of Michigan, MSTP program, First prize at the AMP-CMD Parliament Meeting poster session, 27-28 March, 2023, Boston MA. Ongoing PhD project.
- 01/2023-Present Benjamin Li, University of Michigan, MSTP program, Work selected for platform talk at the ASHG meeting 2023 and ADA meeting 2024
- 10/2023-01/2024 Alice Wang, University of Michigan, PhD project. Work selected for platform talk at the ADA meeting, 2024.
- 02/2024-Present Maya Bose, University of Michigan, PhD project.

Undergraduate Student

- 06/2018-08/2018 Stephanie Laureano, University of Puerto Rico at Humacao, University of Michigan UM-SMART Program
- 09/2018-04/2019 Prashit Parikh, Vassar College, University of Michigan, UM-SMART Program

- 09/2018-04/2019 Nicole Kim, University of Michigan
- 12/2021-04/2021 Fateema Bazzi, University of Michigan

Highschool Student

- 06/2015-09/2015 Hadley VanRenterghem, Ann Arbor Huron High School. Publication: *Varshney A, VanRenterghem H, Orchard P, Boyle AP, Stitzel ML, Ucar D, Parker SC J*, Cell specificity of human regulatory annotations and their genetic effects on gene expression, **Genetics**, 2019, `https://doi.org/10.1534/genetics.118.301525`
- 06/2018-12/2018 Collin Wang, Detroit Country Day Upper School, Publication: *Varshney A, Kyono Y, Venkateswaran E, Wang C, Erdos M, Narisu N, Albanus R, Orchard P, Stitzel M, Collins F, Kitzman J, Parker S*, A Transcription Start Site Map in Human Pancreatic Islets Reveals Functional Regulatory Signatures, **Diabetes**, 2021, `https://doi.org/10.2337/db20-1087`