

VISHAL SARSANI

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Career Profile

Ph.D. in Statistics with ~4 years of industry experience in computational omics analysis and biostatistics, recognized for individual contributions through first-author papers and platform talks.

Postdoctoral Experience

2023-24 NOW	STATISTICAL GENETICS POSTDOC <i>Harvard T.H. Chan School of Public Health</i> <ul style="list-style-type: none">• Cross-tissue Phosphoproteomics & MS proteomics to study Alzheimer's Disease in Type 2 Diabetes subjects (IGES Talk, manuscript under preparation).
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Education

2018-23 4.5 YRS	PH.D. IN STATISTICS <i>University of Massachusetts Amherst</i> <ul style="list-style-type: none">• Multitrait PRS of T2D (currently working).• Multilevel analysis to study protein homeostasis network (Under review, CBI Chalk Talk).• Meta-analysis, fine-mapping, and gene prioritization of adiponectin (HGGA, ASHG Talk).• Model-based identification of conditionally-essential genes (PLoS Compbio, GLBIO Talk).• Jointly simulating correlated single-cell and bulk data (BMC Bioinfo, * co-first).
2013-15 2 YRS	Master of Science in BIOINFORMATICS <i>Indiana University (IU) School of Informatics and computing</i> <ul style="list-style-type: none">• As a research assistant, I was the primary bioinformatics analyst for 4 clinical publications.

Professional Experience

Biomedical

2015-18 3.5 YRS	APPLICATION COMPUTATIONAL SCIENTIST AT THE JACKSON LABORATORY, Bar Harbor <ul style="list-style-type: none">★ Computational Sciences Champion Award (for job performance).• Integrating long & optical reads for <i>de novo</i> assembly of the B6Eve (G3 Cover Paper).• Analysis and pipeline contributions collaboratively for resources like Collaborative Cross (CC), Patient-Derived Xenografts (PDX), and in Clinical Genomics.
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Biopharma

<i>Smr 2022</i> 3 MO	BIOSTATISTICS INTERN AT NOVARTIS, Cambridge <ul style="list-style-type: none">• Code contributions to add covariate selection methodologies to Nonlinear Mixed Effects Models (nlmixr) - an R package for Pharmacokinetic-Pharmacodynamic (PKPD) analysis.
<i>Smr 2019</i> 3 MO	BIOSTATISTICS INTERN AT ROCHE, Santa Clara <ul style="list-style-type: none">• Summer work resulted in New Development Record (NDR) for the biomarker identification from the digital pathology images of the colorectal cancer patients' clinical survival data.

Scientific Engagement

<i>Conference talks</i>	IGES 2023 - Platform Talk (Neel Award Finalist) ASHG 2022 - Platform Talk, Session: Using omics to dissect GWAS signals. GLBIO 2021 - Paper Talk, Session: Genotype to Phenotype in Model Organisms.
<i>Invited talks</i>	Rush University Medical Center, Aug 2023. MGH CTEU Research Seminar, Feb 2023. Chemistry-Biology Interface Chalk Talk, Dec 2022.
<i>Book Contributions</i>	Encyclopedia of Bioinformatics and Computational Biology: Chap on Genome Informatics.
<i>Peer Reviewer</i>	GENETICS (ECR in Statistical Genetics), Cell Reports, ICML, NeurIPS.
<i>Awards</i>	Ludmer Centre travel award for \$1000 Mathematics Fellowship of \$1500, University of Massachusetts Amherst
<i>Posters</i>	ASHG 2023
<i>Teaching</i>	My avg teaching rating was $4.8 \pm 0.42/5$. I taught discussions of STAT 240 & STAT 515.
<i>Competitions</i>	Nvidia TK1 CUDA contest, Island Story Slam.
<i>Software created</i>	R: rnbtn , nlmixr . Python: CTCDP .

Technical Engagement

$\frac{1}{3}$ Statistician + $\frac{1}{3}$ Engineer + $\frac{1}{3}$ Computational biologist. Dedicated to skill enhancement and transfer.

Core Competencies

<i>Statistics/ML</i>	<i>Regression:</i> Generalized linear mixed models, Logistic Regression, Survival Analysis. <i>Bayesian:</i> MCMC Sampling, Hierarchical (Multilevel) models, Longitudinal Analysis. <i>ML:</i> Nonparametric & latent models, Generative models, Deep Neural Networks.
<i>Engineering</i>	<i>Programming:</i> Skilled in Python & R. Rust learning enthusiast. Love Awk, Sed & Bash. <i>Pipelines:</i> Nextflow DSL2 (for analysis) & MLflow Recipes (for model dev). <i>Deployment:</i> Slurm (HPC), AWS (Cloud), Containers (Singularity and Docker).
<i>Comp Biology</i>	<i>Multiomics:</i> Phosphoproteomics & Proteomics, Metabolomics, Epigenetics. <i>Statistical Genetics:</i> GWAS, Polygenic risk scores, Mendelian Randomization. <i>Bioinformatics:</i> Whole Genome & Exome variant calling, Spatial & Single-cell RNAseq.

Workflow stack

<i>Planning</i>	I use Notion for project management, notes and documentation.
<i>Development</i>	I use VS Code , which has built-in support for Git , Jupyter Notebook (Python, R, Rust kernels) and Nextflow , within an Ubuntu development environment.
<i>Results</i>	Quarto (LaTeX, Markdown) for manuscript & documentation preparation.

Publications

First/Equal Author

- 1 **Sarsani, Vishal ***, Aldikacti*, B., Zhao, T., He, S., Chien, P., & Flaherty, P. (2023a). Discovering genetic modulators of the protein homeostasis system through multilevel analysis. *Under Review*.
- 2 **Sarsani, Vishal***, Brotman, S. M., Xianyong, Y., Silva, L. F., Laakso, M., & Cassandra, N. S. (2023b). A cross-ancestry genome-wide meta-analysis, fine-mapping, and gene prioritization approach to characterize the genetic architecture of adiponectin. *Human Genetics and Genomics Advances*, 100252.
- 3 **Sarsani, Vishal ***, Aldikacti, B., He, S., Zeinert, R., Chien, P., & Flaherty, P. (2022). Model-based identification of conditionally-essential genes from transposon-insertion sequencing data. *PLOS Computational Biology*, 18(3), e1009273.
- 4 Giguere, C., Dubey, H. V., **Vishal Kumar Sarsani ***, Saddiki, H., & Flaherty, P. (2020). Scsim: Jointly simulating correlated single-cell and bulk next-generation dna sequencing data. *BMC Bioinformatics*, 215(21).
- 5 **Sarsani, Vishal Kumar ***, Raghupathy, N., Fiddes, I. T., Armstrong, J., Thibaud-Nissen, F., Zinder, O., Bolisetty, M., Howe, K., Hinerfeld, D., Ruan, X., et al. (2019). The genome of c57bl/6j “eve”, the mother of the laboratory mouse genome reference strain. *G3: Genes, Genomes, Genetics*, 9(6), 1795–1805.

Second Author & Primary analysis

- 1 Parashette, K. R., **Sarsani, Vishal Kumar †**, Toh, E., Janga, S. C., Nelson, D. E., & Gupta, S. K. (2022). Esophageal microbiome in healthy children and esophageal eosinophilia. *Journal of Pediatric Gastroenterology and Nutrition*.
- 2 Kloepfer, K. M., **Sarsani, Vishal K †**, Poroyko, V., Lee, W. M., Pappas, T. E., Kang, T., Grindle, K. A., Bochkov, Y. A., Janga, S. C., Lemanske, R. F., et al. (2017). Community-acquired rhinovirus infection is associated with changes in the airway microbiome. *Journal of Allergy and Clinical Immunology*, 140(1), 312–315.

Colloborative papers

- 1 Wells, J., Srivastava, A., Maser, R. S., Kesharwani, R., **Sarsani, Vishal Kumar †**, Daigle, S. L., Lynch, R. P., Munger, H. J., Doty, R., Saxl, R. L., & Bult, C. J. (2022). Rna immunoprecipitation and sequencing of isolated rnas (rip-sir) identifies endogenous mirna-target interactions. *bioRxiv*. <https://doi.org/10.1101/2022.08.22.504764>
- 2 He, S., Schein, A., **Sarsani, V. †**, & Flaherty, P. (2021). A BAYESIAN NONPARAMETRIC MODEL FOR INFERRING SUBCLONAL POPULATIONS FROM STRUCTURED DNA SEQUENCING DATA. *Ann Appl Stat*, 15(2), 925–951.

- 3 Srivastava, A., **Kumar Sarsani, Vishal** [†] and Fiddes, I., Sheehan, S. M., Seger, R. L., Barter, M. E., Neptune-Bear, S., Lindqvist, C., & Korstanje, R. (2019). Genome assembly and gene expression in the american black bear provides new insights into the renal response to hibernation. *DNA Research*, *26*(1), 37–44.
- 4 Woo, X. Y., Srivastava, A., Graber, J. H., Yadav, V., **Sarsani, Vishal Kumar** [†], Simons, A., Beane, G., Grubb, S., Ananda, G., Liu, R., et al. (2019). Genomic data analysis workflows for tumors from patient-derived xenografts (pdxs): Challenges and guidelines. *BMC medical genomics*, *12*(1), 92.
- 5 Presa, M., Racine, J. J., Dwyer, J. R., Lamont, D. J., Ratiu, J. J., **Sarsani, Vishal Kumar** [†], Chen, Y.-G., Geurts, A., Schmitz, I., Stearns, T., et al. (2018). A hypermorphic nfkbid allele contributes to impaired thymic deletion of autoreactive diabetogenic cd8+ t cells in nod mice. *The Journal of Immunology*, *201*(7), 1907–1917.
- 6 Srivastava, A., Morgan, A. P., Najarian, M. L., **Sarsani, Vishal Kumar** [†], Sigmon, J. S., Shorter, J. R., Kashfeen, A., McMullan, R. C., Williams, L. H., Giusti-Rodriguez, P., et al. (2017). Genomes of the mouse collaborative cross. *Genetics*, *206*(2), 537–556.
- 7 Liang, T., Chalasani, N. P., Williams, K. E., **Sarasani, Vishal** [†], Janga, S. C., & Vuppalanchi, R. (2017). Differential expression of mirnas in nontumor liver tissue of patients with hepatocellular cancer caused by nonalcoholic steatohepatitis cirrhosis. *Clinical Gastroenterology and Hepatology*, *15*(3), 465–467.
- 8 De Abreu, F. B., Peterson, J. D., Deharvengt, S. J., Daber, R., **Sarsani, Vishal K** [†], Spotlow, V., Harrington, R. D., Lih, C.-J., Williams, P. M., Bouk, C. H., et al. (2017). Use of biosynthetic controls as performance standards for next-generation sequencing assays of somatic tumors: A multilaboratory study. *The Journal of Applied Laboratory Medicine*, *2*(2), 138–149.
- 9 Siddappa, M., Gandham, R. K., **Sarsani, Vishal** [†], Mishra, B. P., Mishra, B., Joshi, C., Sahoo, A., Tiwari, A., & Janga, S. C. (2014). Whole-genome sequence of sungri/96 vaccine strain of peste des petits ruminants virus. *Genome Announc.*, *2*(1), e00056–14.
- 10 Vuppalanchi, R., Liang, T., Goswami, C. P., Nalamasu, R., Li, L., Jones, D., Wei, R., Liu, W., **Sarasani, Vishal** [†], Janga, S. C., et al. (2013). Relationship between differential hepatic microrna expression and decreased hepatic cytochrome p450 3a activity in cirrhosis. *PloS one*, *8*(9).