Samuel Bharti

Doctoral Researcher, Biomedical Engineering and Bioinformatics, University of Alabama at Birmingham

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Summary

I'm a doctoral researcher in Biomedical Engineering and Bioinformatics at the University of Alabama at Birmingham. My research integrates single-nuclei and multi-omics data to find better ways to diagnose and treat Neurofibromatosis Type 1 (NF1) and its associated cancers.

Alongside the research I own six open-source packages for omics data across R, Python, and TypeScript, and I build the apps and agentic AI tools scientists use to explore their own results. I wrote five of those packages in 2026 at Posit (formerly RStudio). The year before, at Genentech, I built MOLV, a locus-first multi-omics visualization platform for Alzheimer's disease.

Skills

Programming & scripting	R, Python, Bash, SQL, TypeScript, JavaScript, PHP, Git, GitHub
Data products & publishing	R Shiny, Quarto, Streamlit, Jupyter, ggplot2, Plotly, D3, Leaflet, interactive reporting
Bioinformatics & multi-omics	single-cell & spatial transcriptomics, bulk RNA-seq, variant & clinical analysis, multi-omics integration, quality control, Seurat, DESeq2, CellChat, Bioconductor, nf-core / Nextflow
Workflows & infrastructure	reproducible workflows, modular development, workflow automation, Docker, REST APIs, Posit publishing, AWS, GCP, HPC / SLURM
Agentic AI & ML	agent systems, tool calling, MCP, A2A, Google ADK, OpenAI APIs, LangChain, LLM apps, Neo4j knowledge graphs, machine learning, network analysis

Education

Ph.D., Biomedical Engineering & Bioinformatics *Birmingham, AL · Expected 2027*
University of Alabama at Birmingham

Certificate, Translation of Biomedical Innovation to Clinical Practice *Birmingham, AL*
University of Alabama at Birmingham

B.Tech., Bioinformatics *Noida, India*

Amity University

Experience

PhD Candidate, Center for Genomics and Data Science, UAB *Birmingham, AL · Aug 2022 - Present*

- Own the single-nuclei and multi-omics analysis of NF1-associated tumor models, from quality control to the shortlist of drugs worth testing.
- Built and deployed 5+ Shiny applications and internal tools on UAB research infrastructure for visualization, sample tracking, QC review, and multi-omics exploration.
- Caught sample contamination in 3' datasets that quality control had passed, and had it confirmed by the platform vendor.

Software Engineering Intern, Posit *Boston, MA (remote) · May 2026 - Aug 2026*

- Owned five packages end to end, from API design through release: biobouncer, biohttp, bioclients, biocohort, and plotomics.
- Contributed seven merged pull requests upstream to the Shiny ecosystem, and the first shinyreact release credits me as a New Contributor.
- Built more than ten apps across R, Python, and JavaScript, mostly for computational biology and bioinformatics.

Human Genetics gRED Intern, Genentech *South San Francisco, CA · Jun 2025 - Aug 2025*

- Built MOLV, a Shiny platform and R package for locus-first visualization across 11,000+ GWAS, eQTL, pQTL, single-cell, and ATAC-seq datasets in Alzheimer's disease.
- Built its components and workflows so the same locus view worked across every dataset.
- Integrated it into Genentech's secure internal systems alongside the scientists and engineers who use it, then presented the work to the Human Genetics department.

Software

apps (21)

tahoe-explorer	Subset 100.6M rows and leave with a pull recipe.	live app	github
recount-explorer	Browse, QC, and export 18,998 recount3 studies.	live app	github
variant-reviewer	One gene, one variant, one page.	live app	github
Plotomics Live	Twenty-six GPU-rendered pages in 476 lines of R.	live app	github
DE Explorer	Differential expression on TCGA and airway RNA-seq.	live app	github
Drug Perturbation	Connectivity scoring against a perturbation panel.	live app	github
Signature Scoring	Scores TCGA-BRCA samples on 50 Hallmark pathways.	live app	github
Genome Explorer	Recurrent TCGA breast drivers on hg19 via igv.js.	live app	github
gene-list-builder	Seven gene-disease sources, one row per gene.	live app	github
draft-reviewer	Markdown review with comments that survive edits.		github
genescout	An agentic evidence-review workbench.	live app	github
MOLV	Locus-first views across 11,000+ Alzheimer's datasets.	INTERNAL	

RAPTOR	Phenotype, ontology, and disease-relation records.	INTERNAL
PTC Explorer	Exome and RNA-seq review of pediatric thyroid cancer.	
SEAS	Finds clinotypes enriched in a sample subset.	
NF1 scRNA-seq App	nf-core, Seurat, and CellChat in one single-cell app.	INTERNAL
NF1 Rat Exome	Whole-exome variants from NF1-associated rat tumors.	INTERNAL
sMAP	Teaches a transcriptomics pipeline, QC to biomarkers.	
PAGER 3.0	Pathway repository with enrichment and networks.	github
BioDivPortal	Maps species occurrences across Poland over time.	
ondemand-html-renderer	Restores HTML report viewing in OnDemand v2+.	github

packages (6)

plotomics	Seventeen plots from one core, wrapped three ways.	github docs
biobouncer	A gate for biological inputs.	github doi
bioclients	One client per database, parsers testable offline.	github docs
biohttp	Normalized HTTP transport.	github docs
peacock	Project scaffolding for R and Python.	github docs
biocohort	Holds a study's subjects and samples in one object.	github docs

templates (1)

R Shiny Template	Starter kit for reproducible Shiny data apps.

teaching (2)

R for Beginners	Interactive R lessons and decks, built on Gapminder.	github doi
AWS Shiny Workshop	Deploying a Dockerized Shiny app on AWS EC2.	github

databases (3)

GlucoKinaseDB	1,700+ curated glucokinase modulators, 3D and API.
PepEngine	Synthetic peptide structures containing ΔF and Aib.
VIRdb 2.0	Vitiligo genes, targets, compounds, and networks.

Publications

Siddharth Yadav, Samuel **Bharti**, Puniti Mathur (2023). GlucoKinaseDB: A comprehensive, curated resource of glucokinase modulators for clinical and molecular research. Computational Biology and Chemistry
doi.org/10.1016/j.compbiolchem.2023.107818

Samuel **Bharti**, Nikita Krishnan, Arian Veyssi, Maryam Momeni, Sneha Raj (2022). sMAP: An interactive microarray data analysis tool for early-stage researchers. bioRxiv
doi.org/10.1101/2022.05.27.492984

Zongliang Yue, Radomir Slominski, Samuel **Bharti** and Jake Y Chen (2022). PAGER Web APP: An Interactive, Online Gene Set and Network Interpretation Tool for Functional Genomics. Frontiers in Genetics
doi.org/10.3389/fgene.2022.820361

Siddharth Yadav, Samuel **Bharti**, Priyansh Srivastava & Puniti Mathur (2022). PepEngine: A Manually Curated Structural Database of Peptides Containing α, β-Dehydrophenylalanine (ΔPhe) and α-Amino Isobutyric Acid (Aib). International Journal of Peptide Research and Therapeutics.
doi.org/10.1007/s10989-022-10362-9

Nguyen, T. M., **Bharti**, S., Yue, Z., Willey, C. D., & Chen, J. Y. (2021). Statistical Enrichment Analysis of Samples: A General-Purpose Tool to Annotate Metadata Neighborhoods of Biological Samples. Frontiers in Big Data, 4, 725276.
doi.org/10.3389/fdata.2021.725276
Corrigendum: doi.org/10.3389/fdata.2021.804141

Srivastava, P., Talwar, M., Yadav, A., Choudhary, A., Mohanty, S., **Bharti**, S., Narad, P., & Sengupta, A. (2021). VIRdb 2.0: Interactive analysis of comorbidity conditions associated with vitiligo pathogenesis using co-expression network-based approach. F1000Research, 9, 1055.
doi.org/10.12688/f1000research.25713.2

Bharti, S., Sengupta, A., Chugh, P., & Narad, P. (2020). PluriMetNet: A dynamic electronic model decrypting the metabolic variations in human embryonic stem cells (hESCs) at fluctuating oxygen concentrations. Journal of Biomolecular Structure and Dynamics, 1-9.
doi.org/10.1080/07391102.2020.1860822

Bharti, S., Narad, P., Chugh, P., Choudhury, A., Bhatnagar, S., & Sengupta, A. (2020). Multi-parametric disease dynamics study and analysis of the COVID-19 epidemic and implementation of population-wide intrusions: The Indian perspective. medRxiv, 2020.06.02.20120360.
doi.org/10.1101/2020.06.02.20120360

Presentations

Mapping the Genomic Landscape and Tumor Heterogeneity of NF1-Associated Breast Cancer Using Novel Rat Models.
Children's Tumor Foundation NF Conference 2026, Denver, CO (Jun 2026).

Application of a Multi-Omics Approach in NF1-Deficient Tumors and Controls can Highlight Novel Associations and Therapeutic Targets.
CCTS Translational Training Symposium, Biloxi, MS (Sep 2023).

Exploratory Analysis of Cancer Clinical Samples using the new Web-based SEAS Software.
O'Neal Research Retreat, UAB (Oct 2022).

Exploratory Analysis of Cancer Clinical Samples using the new Web-based SEAS Software.
CCTS Translational Training Symposium, Mobile, AL (Sep 2022).

PluriMetNet: A dynamic electronic model deciphering the metabolic profiling of human embryonic stem cells (hESCs) and its applications.
RECOMB 2020, Italy (Jun 2020).

Honors and awards

- Claude Science Hackathon, one of 500 participants selected globally (2026)
- Google Cloud Research Credit Award, Google (2026)
- Elected Member, Tau Beta Pi Engineering Honor Society, UAB (2025)
- Blazer Graduate Research Fellowship, UAB (2022 - 2023)
- Professional Development & Travel Awards, UAB CCTS & UAB GSG (2022 - 2024)

Professional memberships

- American Association for Cancer Research (AACR), Student Member (2024 - Present)

Teaching and leadership

- **Certified Instructor**, The Carpentries (2024 - Present). Taught workshops on R, Git, Bash, and Python at UAB's Biological Data Science Core.
- **President**, Informatics Club, UAB (2023 - 2025). Grew computational training across departments through workshops, peer-learning sessions, and professional-development seminars.
- **Mentor**, STEM-Away. Gave a talk and live demo on containerized bioinformatics and deploying R Shiny apps on AWS.