

Supriya Bidanta

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Professional Summary

Ph.D. Student in Bioengineering with a strong focus on computational biology and bioinformatics. Skilled in developing scalable pipelines for sequencing data, analyzing high-dimensional single-cell and spatial transcriptomics datasets, and applying machine learning to biological systems. Experienced in integrating multi-omics and imaging data for translational research in cancer, immunology, and aging. Adept at communicating complex analyses and contributing to interdisciplinary biomedical research teams.

Education

Ph.D. in Bioengineering (Minor in Bioinformatics)

Aug 2022–Dec 2026(expected)

Indiana University, Bloomington, IN, US

Master of Science in Bioinformatics

Aug 2021 – May 2023

Indiana University, Bloomington, IN, US

Bachelor of Technology in Biotechnology

Aug 2011 – May 2015

OUTR, Odisha, India

Skills

- **Programming & Scripting:** Python, R, C++, Shell, SQL, HTML/CSS
- **Bioinformatics Tools:** CellRanger, Bowtie2, minimap2, IGV, HMMER, SOAPdenovo2
- **Multiscale Modeling Tools:** PhysiCell, CompuCell3D
- **Machine & Deep Learning:** CNNs, GANs, GNNs, SVM, Reinforcement Learning, PyTorch, TensorFlow
- **Data Analysis & Integration:** RNA-seq, single-cell (sc/snRNA-seq), spatial transcriptomics, imaging data, multi-omics integration
- **Cloud & Workflow Management:** AWS, Azure, Apache Airflow
- **Visualization & Reporting:** Dash, Plotly, Adobe Illustrator, TIBCO Spotfire
- **Versioning & Reproducibility:** Git, Docker

Presentations

- Invited Speaker, CTSI Modeling & Simulation Symposium (CTSI M&S 2025) – *Functional Tissue Units in the Human Reference Atlas*
- Lighting Talk - 60 sec Presentation at CIFAR MacMillan Multiscale Human Meet 2024 - *Functional Tissue Units in the Human Reference Atlas*
- Invited Speaker, The Spatial Biology Revolution 2023 - Mapping The Human Body At Single Cell Resolution: Developing The Human Reference Atlas
- Poster, Spatial Biology- Boston, 2022 - *Mapping The Human Body At Single Cell Resolution: Developing The Human Reference Atlas*

Publication

- Bidanta, S., Börner, K., Herr II, B.W. et al. Functional tissue units in the Human Reference Atlas. Nat Commun 16, 1526 (2025). <https://doi.org/10.1038/s41467-024-54591-6>
- Bergman D, Marazzi L, Chowkwale M, Maheshvare M D, Bidanta S, Mapder T, Li J. PhysiPKPD: A pharmacokinetics and pharmacodynamics module for PhysiCell. GigaByte. 2022 Nov 30;2022:gigabyte72. doi: 10.46471/gigabyte.72. PMID: 36950142; PMCID: PMC10027063.

Projects

Cell-Cell Communication Analysis Using Omics Data

Oct 2025 – Present

- Analyzing cell-cell communication in cell types using scRNA-seq and spatial transcriptomics data.
- Applied tools including CellChat, CellPhoneDb, and Liana+ to identify ligand-receptor interactions and signaling networks.
- Integrated pathway enrichment and receptor-ligand network analysis to uncover context-specific communication patterns in aging and inflammation.

Enhancing Breast Cancer Classification via Deep Learning and Synthetic Data

*Sep 2023 – Dec 2024
(merged project)*

- Improved diagnostic accuracy to 86% by combining **CNN-ResNet** and **SVD**-based feature extraction.
- Addressed data imbalance using **DC-GAN** to generate synthetic histopathology and mammography images.
- Optimized preprocessing, augmentation, and model tuning for high-precision tumor classification.

Single-nucleus RNA-sequencing of polyploid senescent cells in Drosophila

May 2024 - Dec 2024

- Built a pipeline to convert snRNA-sequenced FASTQ files to a gene expression matrix using **CellRanger**, **scVI**, and **scanpy** to harmonize snRNA-seq data.
- Visualized clusters using UMAP and t-SNE; identified regulatory pathways with SCENIC.
- Discovered Toll and JAK-STAT signaling activation in inter-epithelial cells via pathway enrichment.
- Integrated imaging and transcriptomic data to characterize senescence-related immune responses.

The Effects of Vaping Liquid on Zebrafish Gene Expression

Feb 2024 - May 2024

- Analyzed scRNA-seq data from **zebrafish embryos** exposed to flavored vaping liquids to assess developmental toxicity and DNA damage.
- Identified **>2,700 differentially expressed genes** related to cartilage, bone, vascular, and metabolic development.
- Performed gene enrichment using **DAVID**, **g:Profiler**, and **Reactome**, revealing downregulation of mitochondrial and lipid metabolism pathways.
- Constructed **signaling networks** using **Cytoscape**, highlighting disruptions in redox signaling, transmembrane transport, and extracellular matrix remodeling.
- Findings suggested increased oxidative stress, impaired detoxification, and potential analogs to human developmental and metabolic disorders.

Cancer Drug Synergy Prediction using Graph Neural Networks.

Mar 2022 - July 2022

- Developed a deep learning framework to predict synergistic cancer drug combinations using **graph neural networks (GNNs)**.
- Integrated drug descriptors (TPSA, molecular weight, MACCS keys) and cancer cell line gene expression data.
- Modeled synergy scores using **GNN**, with comparisons to **SVM**, **Random Forest**, and **DeepSynergy** baselines.
- Incorporated **protein-protein interaction networks** and pathway-level gene expression to improve biological relevance.
- Achieved improved predictive accuracy (**Pearson correlation**, **RMSE**) in leave-one-drug-out (**LODO**) validation.
- Proposed CNN-based feature image encoding for spatial modeling of molecular features.

Simulation of Iron and Glucose's effect on cancer cells.

Apr 2022 - May 2022

- Developed an **ODE-based model** to simulate breast tumor and healthy cell dynamics under varying iron, glucose, and oxidative stress conditions.
- Modeled iron transport across blood and tissue compartments to explore metabolic regulation in **pre- vs. post-menopausal contexts**.
- Implemented simulations in **Python** using **SciPy**, **NumPy**, and **Matplotlib** to visualize growth patterns and nutrient flux.
- Identified metabolic conditions promoting tumor proliferation, offering insights into nutrient-driven cancer progression.

Work Experience

Indiana University, Bloomington | Teaching Assistant,

Jan 2024 – May 2024, Jan 2025 – Present

Information Visualization E438/538, IUB

- Introduced a module on **Large Language Models (LLMs)** to demonstrate real-time data visualization using the Data Visualisation Literacy framework.
- Delivered a live demo on **TIBCO Spotfire** to **130+ students**; supported learners with advanced visualization tools.
- Collaborated on course design and provided individualized academic support to improve student performance.

Indiana University, Bloomington | Research Assistant,

Jan 2022 – Dec 2023, May 2024 – Dec 2024

Human Reference Atlas, IUB

- Curated and analyzed data from 180+ transcriptomic, proteomic, and lipidomic datasets to define **Functional Tissue Units (FTUs)** across human organs.
- Integrated **omics** data and anatomical illustrations into an interactive online portal for tissue-level exploration.
- Automated 2D segmentation pipelines using **OpenCV and the Watershed** algorithm, improving efficiency by 95%.
- Collaborated with biologists and illustrators to maintain 80%+ **data annotation** accuracy through quality control.

Divergene LLC | NGS Bioinformatics Data Analyst, Co-op

Sept 2022 - May 2023

- Built scalable NGS pipelines for short-read (Illumina) and long-read (Oxford Nanopore Technologies) data using **trimmomatic, bowtie2, BWA-MEM, minimap2, SAMTools, bamtools, IGV and AWS S3, EC2**, reducing manual processing time by 80%.
- Developed secure cloud workflows for genomic data storage and access, improving speed and security by 99%.
- Designed interactive dashboards using **Dash and Plotly**, enhancing data accessibility and real-time visualization by 80%.
- Conducted multi-modal sequencing analysis to support minimal residual disease detection and viral vector (AAV) integration profiling.

Tata Consultancy Services, India | Data Engineer | Application Support Engineer

May 2015 – June 2021

- Automated data workflows using **Apache Airflow and Python-based APIs**, with real-time monitoring dashboards for performance tracking.
- Created dynamic **TIBCO Spotfire** reports and dashboards for enterprise **analytics**.
- Managed production applications and supported server infrastructure using **UNIX/Linux scripting**.
- Documented engineering processes in **Confluence**, tracked workflows in **JIRA**, and maintained code via **Git**.
- Received “**Best Employee of the Month**” and “**On-the-Spot**” awards for operational excellence.

Award: On-the-spot award and Best Employee of the Month

Imgenex Pvt Ltd, India | Bioinformatics Intern

May 2014 – Jun 2014

- Implemented predictive models for Ebola virus clinical outcomes using Python and R.

Imgenex Pvt Ltd, India | Genomic-Proteomics Biotechnology Intern

May 2013 - Jun 2013

- Developed and implemented research studies and assisted with developing and implementing novel research methodologies.
- Collected and tested cells, tissues, and blood samples to conduct studies.
- Maintained the integrity of the laboratory through weekly lab cleaning and maintenance procedures.

Certifications

Bioinformatics Specialization (Coursera), Neural Networks and Deep Learning (Coursera), Genetics and Next Generation Sequencing (Udemy), UcanCRISPR: CRISPR/Cas9 Master Class (Udemy), Deep Learning with PyTorch: Image Segmentation (Coursera), Hypothetical Protein Annotation by Laura Harris, 5 day - Generative AI Intensive Course By Google