Piyush Nanda

Ph.D. Candidate, Harvard University
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Biologist using theory, molecular genetics, and microscopy to dissect how biochemical circuits control metabolic state and growth in fluctuating environments.

Education

Harvard University, Cambridge, USA 2020–Present
Ph.D. Candidate in Biological and Biomedical Sciences Program
Advisor: Andrew W. Murray
Thesis: Mechanisms controlling single-cell heterogeneity in fluctuating environments

IIT Kharagpur, Kharagpur, India 2015–2020
B.Tech & M.Tech in Biotechnology and Biochemical Engineering
Thesis: Cell-to-cell heterogeneity in lipid droplet accumulation
CGPA: 9.31/10; Institute Silver Medal; Best Thesis Award

Publication List

1. Alpay, B. A., **Nanda, P.**, Nagy, E., and Desai, M. M. (2026). Amino acid exchangeability and surface accessibility underpin the effects of single substitutions. *Genetics*, 233(2), iyag104.
2. **Nanda, P.**, Barrere, J., LaBar, T., and Murray, A. W. (2024). A dynamic network model predicts the phenotypes of multicellular clusters from cellular properties. *Current Biology*, 34(12), 2672–2683.
3. Barrere, J., **Nanda, P.**, and Murray, A. W. (2023). Alternating selection for dispersal and multicellularity favors regulated life cycles. *Current Biology*, 33(9), 1809–1817.
4. Evans-Yamamoto, D., Rouleau, F. D., **Nanda, P.**, Makanae, K., Liu, Y., Després, P. C., *et al.* (2022). Barcode fusion genetics–protein-fragment complementation assay (BFG-PCA): Tools and resources that expand the potential for binary protein interaction discovery. *Nucleic Acids Research*, 50(9), e54.
5. **Nanda, P.**, and Ghosh, A. (2021). Genome Scale–Differential Flux Analysis reveals deregulation of lung cell metabolism on SARS-CoV-2 infection. *PLOS Computational Biology*, 17(4), e1008860.
6. **Nanda, P.**, Patra, P., Das, M., and Ghosh, A. (2020). Reconstruction and analysis of genome-scale metabolic model of weak Crabtree-positive yeast *Lachancea kluyveri*. *Scientific Reports*, 10, 16314.

Manuscript in Review

1. **Nanda, P.**, and Murray, A. W. (2026). Translational antagonism enables bet-hedging in yeast via mitochondrial bistability. *bioRxiv* [preprint]. doi:10.64898/2026.03.30.715437.

Research Experience

Ph.D. project, Murray Lab, Harvard University – Metabolic bistability in yeast 2020–Present

- Combined single-cell metabolic imaging with physiological perturbations to identify a mitochondrial bistable switch controlling yeast energy metabolism.
- Developed theory and computational pipelines for long-term cell tracking.

Rotation project, Murray Lab, Harvard University – Multicellular cluster size distributions 2020

- Built a dynamic network model linking cell-level properties to multicellular cluster size distributions and composition in yeast.
- Established high-throughput microscopy and image analysis workflows for quantification of absolute cluster size.

Metabolic Engineering Laboratory, IIT Kharagpur – Genome-scale differential flux analysis 2018–2020

- Designed a statistical framework for genome-scale differential flux analysis integrating metabolic networks with transcriptomics.
- Applied this framework to computationally identify altered metabolic reactions in SARS-CoV-2 infected lung cells.

Research Internships

Dept. of Systems Biology, Harvard Medical School (Johan Paulsson) 2019

- Constructed and characterized combinatorial promoter–RBS libraries in *Vibrio natriegens* to study the effect of fast growth on gene expression noise.
- Used microfluidic single-cell assays and multiplexed fluorescent barcoding to quantify transcriptional dynamics.

Yachie Lab, University of Tokyo (Nozomu Yachie) 2018

- Established a high-throughput barcode-based pipeline (BFG-PCA) to detect binary protein interaction networks in *S. cerevisiae*.
- Ran large-scale BFG-PCA screens on proteasome and nucleoporin complex proteins under different environmental perturbations.

Great Lakes Bioenergy Research Center, Michigan State University (Michaela TerAvest) 2017

- Performed metabolic gap-filling in *Zymomonas mobilis* glycolysis with Embden–Meyerhof–Parnas pathway genes from *E. coli*.
- Quantified extracellular fluxes in engineered strains by HPLC under aerobic and anaerobic conditions.

Teaching and Mentoring

Head Laboratory Instructor, LS50 Integrated Life Sciences, Harvard University 2023–Present

- Independently supervised student-led projects on understanding the ligand specificity of yeast GPCR sensing (2023 and 2026) and signal processing through the yeast MAPK pheromone pathway (2024).
- Delivered lectures and hands-on labs on molecular biology, fluorescence microscopy, and quantitative data analysis.

Graduate Student Mentor, Harvard iGEM, School of Engineering and Applied Sciences 2022–2023

- Mentored undergraduate students on synthetic biology projects (GPCR-based sensing, inducible lysis circuits in bacteria).
- Guided teams through project scoping, experimental roadmapping, and troubleshooting; the 2023 team received a Silver Medal at the iGEM Grand Jamboree in Paris, France.

Teaching Assistant, Quantitative Modeling in Cell Biology, EMBL, Heidelberg 2025

- Prepared course material for quantitative biology topics for EMBL graduate students.
- Gave lectures and demonstrations on modeling bistable switching and gene expression noise.

Talks

- Winter Quantitative Biology (QBio) Retreat, Hawaii, 2026 – Metabolic bistability in yeast.
- Gordon Research Conference, *Molecular Mechanisms in Evolution*, 2025 – Metabolic bistability in yeast.
- 129th International Titisee Conference (Germany), 2024 – Metabolic bistability in yeast.
- American Society for Cell Biology Minisymposium, 2023 – Metabolic bistability in yeast.

Competitions and Awards

- Merck Innovation Cup 2022 (Merck KGaA, Seeheim, Germany) – Selected in top 7 teams; proposed integrating real-world data into clinical trial design.
- Khorana Scholar 2019 (Department of Biotechnology, Government of India) – Fully funded summer internship at Harvard University.
- Honda Young Engineers and Scientists Award 2018 (Honda Foundation, Japan). Awarded a fully sponsored summer internship at the University of Tokyo and attended the International Symposium on Eco Technology in Cambodia 2019.

Skills

Experimental: molecular biology in bacteria and yeast; mammalian cell culture; FACS and high-throughput flow cytometry; fluorescence microscopy; NGS library preparation; single-cell RNA-seq.
Programming & analysis: Python, R, MATLAB; single-cell and image analysis; metabolic modeling; COBRA; ordinary differential equations; NGS analysis.
Tools & platforms: Fiji, COPASI, Cytoscape, GSEA, O2 cluster, Amazon AWS.