

Pratibha Jagannatha, PhD

Computational Biologist

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SUMMARY

Computational biologist with expertise in RNA biology, next-generation sequencing, and high-throughput screening, combining computational proficiency, experimental wet lab experience, and a proven record of scientific leadership. Extensive experience in both academic research and venture capital. Excels in collaborative environments and passionate about operationalizing basic science for disease-relevant technology development.

SKILLS

Technical: Python, R, Linux, Snakemake, AI/ML, bioinformatics and biostatistics, next-generation sequencing (NGS), long-read and short-read sequencing analysis, single-cell and bulk transcriptomics, multi-omics analysis, data visualization, HPC cluster, Github, AWS, cell culture, high-throughput screening, library preparation, molecular biology experimental techniques, technology development, project management

Analytical: scientific due diligence, market analysis, strategic planning

EDUCATION AND TRAINING

University of California San Diego, San Diego, CA

2019 — 2024

Ph.D. Bioinformatics and Systems Biology

Advisor: Dr. Gene Yeo

University of California Santa Cruz, Santa Cruz, CA

2015 — 2018

B.S. in Bioengineering, Minor in Bioinformatics

Cum laude, Member of Tau Beta Pi the Engineering Honor Society

RESEARCH EXPERIENCE

Postdoctoral Scholar, University of California, San Diego

2025 — Present

Yeo Lab

- Evaluating and implementing AI/ML approaches to design RNA therapeutics for splicing modulation

Graduate Student Researcher, University of California, San Diego

2020 — 2024

Yeo Lab

- Developed a long-read sequencing-based method leveraging RNA editing for profiling transcriptome-wide protein-RNA interactions
- Developed a long-read sequencing-based method for translation profiling at mRNA isoform resolution
- Designed a high-throughput screen to characterize RNA binding proteins in alternative polyadenylation
- Implemented machine learning models to predict RNA binding protein domains important for mRNA processing mechanisms
- Analyzed single-cell long-read and multiplexed CRISPR knockdown data to profile single-cell perturbations

Junior Specialist, University of California Santa Cruz

2018 — 2019

Brooks Lab and Carpenter Lab

- Implemented gold-standard computational pipelines for systematic, high-throughput analysis of RNA-seq data to characterize the innate immune response
- Developed a computational pipeline for the comprehensive analysis of Frac-seq data

UCSC iGEM Co-captain, University of California Santa Cruz

2016 — 2017

<http://2017.igem.org/Team:UCSC>

- Engineered cyanobacteria to produce essential medicines and supplements using principles and methods of synthetic biology and metabolic pathway modeling

Undergraduate Researcher, University of California Santa Cruz, Brooks Lab and Carpenter Lab

2016 — 2018

- Identified and quantified novel alternative splicing events relevant to the innate immune response and chronic inflammation using advanced computational tools
- Authored grant proposals, securing funding for ongoing research initiatives

PROFESSIONAL EXPERIENCE

Vida Ventures Fellow, Vida Ventures

2022 — 2023

- Executed detailed scientific and business due diligence on biotech companies, evaluating their potential for investment
- Evaluated market trends and therapeutic landscapes, contributing to key investment decisions that align with life science advancements

Process Science Intern, Boehringer Ingelheim

2018

- Collaborated with cross-functional teams to design and implement a data verification tool for regulatory compliance and enhancing process efficiency

LEADERSHIP

Nucleate Bio San Diego, Co-Director of Sponsorship and Partnership

2021 — 2022

- Established and developed the San Diego chapter of a nonprofit bioentrepreneurship program supporting the formation of local life science ventures
- Secured local and national sponsorships valued over \$30,000
- Forged partnerships with key members of the San Diego biotech ecosystem
- Conducted due diligence on team technologies to assess alignment of market needs and scientific potential
- Facilitated lab-to-market workshops to guide participants in the commercialization of their technologies

Bioinformatics and Systems Biology Diversity, Equity, and Inclusion Committee Member

2020 — 2023

- Partnered with faculty to establish programs to advance diversity, equity, and inclusion efforts within the program

Graduate Diversity and Science Lecture Series Organizer

2021

- Organized and hosted weekly speaker sessions, facilitated discussions to enhance diversity, equity, and inclusion amongst the scientific community

Co-Captain of UCSC iGEM

2016 — 2017

- Recruited and co-led a team of fifteen undergraduate researchers competing in the International Genetic Engineering Machine (iGEM) competition, driving innovation in synthetic biology

TEACHING

Teaching Assistant, CMM 262: Quantitative Methods in Genetics and Genomics

2020 — 2022

- Designed lectures, structured and created class material, and assisted students enrolled in CMM 262

Synbio School Course Creator and Course Instructor

2019

- Designed and developed an online synthetic biology course, equipping professionals from various industries with skills to develop, design, and complete a synthetic biology project

- Created engaging course content and facilitated discussions about the ethics of genetic engineering

Group Tutor, Research Programming for the Life Sciences, Department of Biomolecular Engineering, University of California Santa Cruz

2018

- Tutored undergraduate students in writing programs with Python for biological applications using active learning methods

Learning Support Services Tutor, University of California Santa Cruz

2017

- Tutored students enrolled in BME 5: Introduction to Biotechnology using active learning methods

VOLUNTEERING

College Town Tutor, Reality Changers

2020 — 2021

- Mentored and tutored high school students from underserved backgrounds in the greater San Diego area, empowering them to overcome academic challenges

San Diego Tutor Tree

2020 — 2021

- Established and coordinated a network of graduate student tutors to provide free academic support to children during COVID-19 lockdown, ensuring continued learning

PUBLICATIONS

Jagannatha, P., Yoon, Y., Landry, S., Naritomi, J.T., Zhan, L., Olson, S., Wei, X., Street, L. A., Jovanovic, M., Graveley, B. R., Yeo, G.W., Large-scale discovery of RNA-binding proteins that directly modulate poly(A) site selection (*in preparation*)

Zampa, F., Sison, L. S., Kofman, E. R., Choi, S. Y., **Jagannatha, P.**, Nguyen, G. G., Naritomi, J. T., Shin, A., Khorgade, A., Jin, W., Chen, C., Sievert, D. M., Mukhopadhyay, S., Mizrahi, O., Blue, S. M., Marina, R. J., Yang, D., Wang, C. C., Pang, Z., Brannan, K. W., Ye, Li., Stowers, L., Al' Khafaji, A. M., Lippi, G., Yeo, G. W. Single cell and isoform-specific translational profiling of the mouse brain. (*submitted*)

Liang, Q., Yu, T., Kofman, E., **Jagannatha, P.**, Rhine, K., Yee, B. A., Corbett, K. D., Yeo, G. W.. High-sensitivity in situ capture of endogenous RNA-protein interactions in fixed cells and primary tissues. *Nat Commun* 15, 7067 (2024). <https://doi.org/10.1038/s41467-024-50363-4>

Jagannatha, P., Tankka, A. T., Lorenz, D. A., Yu, T., Yee, B. A., Brannan, K. W., Zhou, C. J., Underwood, J. G., & Yeo, G. W. (2024). Long-read Ribo-STAMP simultaneously measures transcription and translation with isoform resolution. *Genome research*, gr.279176.124. Advance online publication. <https://doi.org/10.1101/gr.279176.124>

Medina-Munoz, H. C., Kofman, E., **Jagannatha, P.**, Boyle, E. A., Yu, T., Jones, K. L., Mueller, J. R., Lykins, G. D., Doudna, A. T., Park, S. S., Blue, S. M., Ranzau, B. L., Kohli, R. M., Komor, A. C., & Yeo, G. W. (2024). Expanded palette of RNA base editors for comprehensive RBP-RNA interactome studies. *Nature communications*, 15(1), 875. <https://doi.org/10.1038/s41467-024-45009-4>

Schmok, J. C., Jain, M., Street, L. A., Tankka, A. T., Schafer, D., Her, H. L., Elmsaouri, S., Gosztyla, M. L., Boyle, E. A., **Jagannatha, P.**, Luo, E. C., Kwon, E. J., Jovanovic, M., & Yeo, G. W. (2024). Large-scale evaluation of the ability of RNA-binding proteins to activate exon inclusion. *Nature biotechnology*, 10.1038/s41587-023-02014-0. Advance online publication. <https://doi.org/10.1038/s41587-023-02014-0>

Boyle, E. A., Goldberg, G., Schmok, J. C., Burgado, J., Izidro Layng, F., Grunwald, H. A., Balotin, K. M., Cuoco, M. S., Chang, K. C., Ecklu-Mensah, G., Arakaki, A. K. S., Ahmed, N., Garcia Arceo, X., **Jagannatha, P.**, Pekar, J., Iyer, M., DASL Alliance, & Yeo, G. W. (2023). Junior scientists spotlight social bonds in seminars for diversity, equity, and inclusion in STEM. *PloS one*, 18(11), e0293322. <https://doi.org/10.1371/journal.pone.0293322>

Brannan K. W., Chaim I. A., Marina R. J., Yee B. A., Kofman E. R., Lorenz D. A., **Jagannatha .P**, Dong K. D., Madrigal A. A., Underwood J. G. & Yeo G. W. (2021). Robust single-cell discovery of RNA targets of RNA-binding proteins and ribosomes. *Nat Methods* 18, 507–519. <https://doi.org/10.1038/s41592-021-01128-0>

Robinson, E. K.*, **Jagannatha, P.***, Covarrubias, S., Cattle, M., Smaliy, V., Safavi, R., Shapleigh, B., Abu-Shumays, R., Jain, M., Cloonan, S. M., Akesson, M., Brooks, A. N., & Carpenter, S. (2021). Inflammation drives alternative first exon usage to regulate immune genes including a novel iron-regulated isoform of *Aim2*. *eLife*, 10, e69431. <https://doi.org/10.7554/eLife.69431>

PRESENTATIONS

- 2023, “STAMPing Protein-RNA Networks,” Cold Spring Harbor Eukaryotic mRNA Processing, *Talk*
2023, “High-throughput RBP-wide screen to characterize the effect of RBP binding on poly(A) site selection,” Cold Spring Harbor Eukaryotic mRNA Processing, *Poster presentation*
2022, “Long-read STAMP: mapping RBP-RNA interactions in an isoform aware manner”, Advances in Genomic Technology Development, *Talk*
2022, “Long-read STAMP: mapping RBP-RNA interactions in an isoform aware manner”, PacBio Discoveries Roadshow, Farmer & the Seahorse, La Jolla, CA, *Invited Talk*
2017, “High Throughput Analysis of the Role of Alternative Splicing Regulation in the Innate Immune Response”, Northern California Computational Biology (NCCB) Student Symposium, University of California, Santa Cruz, CA, *Talk*
2017, “Bugs Without Borders”, iGEM Giant Jamboree, Hynes Convention Center, Boston, MA, *Talk*
2017, “The Role of Alternative Splicing Regulation in the Innate Immune Response”, Biomedical Computation Conference at Stanford, Stanford University, CA, *Poster Presentation*

HONORS, AWARDS, AND FELLOWSHIPS

Merit Scholarship, University of California, Santa Cruz	2015 — 2018
Crown College Undergraduate Research Fellowship, University of California, Santa Cruz	2017
Dean’s Award	2018
NSF GRFP Honorable Mention	2020
ARCS Scholar	2021— 2024