Shraddha Puntambekar, Ph.D.

+(91) 9637435293 | shraddha.puntambekar@gmail.com |
https://www.linkedin.com/in/shraddhapuntambekar | https://github.com/shraddhapuntambekar

SUMMARY

- 10+ years of experience in bioinformatics, multi-omics data analysis, and systems biology, with a Ph.D. in Computational Biology, resulting in 5 impactful peer-reviewed publications.
- Designed and implemented end-to-end bioinformatics pipelines for NGS analysis workflows (including bulk RNA-seq, small-RNAseq, WGS, ChIP-seq, ATAC-seq) across diverse interdisciplinary projects using cloud computing, R, python, and bash.
- Experience in using mathematical modeling and network analysis to test data-driven hypotheses, identify therapeutic targets, and elucidate disease mechanisms.
- Strong project management experience, including leading a remote team in a startup environment with a focus on delivering high-quality results that resulted in the discovery of novel cancer biomarkers.

SKILLS

Data analysis	RNA-seq analysis (bulk and small RNAseq, denovo and reference-based assembly), ChIP-seq, WGS, ATAC-seq, Comparative transcriptomics, nf-core's Nextflow pipelines, ENCODE pipelines
Bioinformatics	Variant annotation analysis, Evolutionary rate analysis, Survival analysis, Functional annotation analysis, Pathway enrichment analysis, Designing siRNAs & qPCR primers, In-silico drug screening, AWS services (batch and OMICS)
Mathematical modeling	Deterministic modeling, Boolean modeling, Analytical, and Numerical steady-state analysis, Data fitting and optimization, Sensitivity Analysis, Parameters estimation
Scripting	R, Bash, Python, Nextflow, MATLAB
Project management	Led and mentored interdisciplinary team in a remote settings, Project scoping, and planning, Managed computational resources to optimize cost-effective solutions, Technical documentation, and reporting

PROFESSIONAL EXPERIENCE

Project Scientist II, CSIR-National Chemical Laboratory 2023 – 2024

- Led the initiation and development of a research project, and facilitated collaborative discussions to share knowledge, identify key research gaps, and explore new research opportunities.
- Evaluated different ChIP-seq analysis tools and workflows (ENCODE, nf-core/nextflow) to perform alignment, peak detection, and de novo motif analysis.
- Implemented pipelines to analyze ATAC-seq, ChIP-seq, and RNA-seq data to understand the role of GATA3 in breast cancer.
- Integrated multi-omics data to construct gene regulatory network and study molecular mechanisms underlying breast cancer.

Head of Computational Biology, NonExomics LLP 2021 - 2023

- Mentored and managed a fully remote team, in different time zones, to deliver an on-time analysis of proprietary WGS and RNAseq data for identifying novel cancer biomarkers.
- Extensive hands-on experience in storing, retrieving, and analyzing sequenced data using Illumina's BaseSpace platform.

- Implemented and maintained nf-core’s RNAseq and WGS Nextflow pipelines using AWS cloud computing services to analyze proprietary and publicly available expression datasets.
- Designed siRNAs and qPCR primers for the bioinformatically predicted cancer targets.
- Presented on behalf of NonExomics at the startup’s meetup organized by VCR Park, Vizag, India

Research Associate, Indian Institute of Science Education & Research, Pune 2018 - 2019

- Evaluated read alignment and assembly tools and developed an optimal pipeline for comparative transcriptomics of two cichlid fish species.
- Analyzed publicly available RNA-seq and Ribo-seq datasets to systematically characterize novel peptides and evaluate their use as cancer biomarkers.
- Pan-cancer analysis of novel transcripts and their association with overall patient survival.
- Predicted the structure of the novel peptides and carried out their functional analysis.
- Identified novel genetic variants using variant calling methods like GATK, and FreeBayes and, identified the effects of variants using VEP.
- In-silico screening for inhibitors against novel peptides.

Doctoral Researcher, CSIR-National Chemical Laboratory 2011 - 2017

- Reconstructed the signaling and metabolic networks for melanosome transport, melanogenesis, and sumoylation by literature-based manual curation.
- Developed and analyzed boolean and ODE-based mathematical models to propose mechanistic understanding underlying the clinical and experimental observations of the pigmentation and post-translational modification systems.
- Worked in collaboration with three wet labs to routinely analyze and interpret experimental data and present the modeled simulation and prediction results.
- Served as a research mentor to undergraduate and summer students to help them meet their project objectives and deadlines.
- Received an International Travel Grant awarded by DBT, Govt. Of India, to present my findings at the International Conference on Systems Biology (ICSB -2016) in Barcelona, Spain.
- Received Bioinformatics National Certification (DBT-BINC) Ph.D. Fellowship

Research Assistant, CSIR-National Chemical Laboratory 2010 - 2011

- Analyzed confocal images of keratinocytes to observe nuclear capping phenomena.
- Analyzed FACS and microarray data to study the uptake of melanosomes by the melanocytes.
- Collaborated with three academic labs to manually curate and reconstruct the signaling and metabolic pathways involved in skin pigmentation.

EDUCATION

Ph.D. in Biological Sciences (Computational Biology) 2011 - 2017
CSIR-National Chemical Laboratory (NCL), Pune, India

M.Sc. Bioinformatics 2008 – 2010
Bioinformatics Centre, University of Pune, India

B.Sc. Biotechnology 2005 - 2008
University of Pune, India

PROFESSIONAL DEVELOPMENT

Course, ‘Data scientist with R’, a 22 courses skill track	*datacamp.com*
Course, ‘Machine Learning’ *by Andrew Ng*	*coursera.org*
Course, ‘Case Studies in Personalized Medicine’	*coursera.org*
Course, ‘Numerical Techniques and Programming’	*NCL*
Organizing Member, 2015 NNMCB National Meeting	*IISER, Pune*
Volunteer, Research Scholar Meet, Annual event	*NCL*
Student Representative, Students Committee, Department of Bioinformatics	*University of Pune*

PRESENTATIONS

Talk, Represented NonExomics at the conference ‘Vision Meets Action: 2022’	*VCR Park, Vizag*
Poster, International Conference on Systems Biology (ICSB - 2016)	*Barcelona, Spain*
Poster, 1st IBSE International Symposium 2018 – From Genotype to Phenotype	*IIT Madras*
Poster, Genomic Medicine in Skin Research (GENMEDSKIN 2016)	*IGIB, Delhi*
Talk, BioPhysics Paschim 8, 2015	*IIT Bombay*
Talk, International Conference on Mathematical & Computational Biology (ICMCB 2015)	*IIT Kanpur*
Poster, 2015 NNMCB National Meeting	*IISER Pune*
Talk, Symposium on Systems Biology, 2012	*IIT Bombay*

PUBLICATIONS

- Puntambekar, S., Newhouse, R., ... & Prabakaran, S. (2020). Evolutionary divergence of novel open reading frames in cichlid speciation. *Scientific Reports*, *10*(1), 1-18.
- Erady, C.*, Boxall, A.*, Puntambekar, S.*, Jagannathan, N. S.*, Chauhan, R.*, ... ,& Prabakaran, S. (2021). Pan-cancer analysis of transcripts encoding novel open reading frames (nORFs) and their potential biological functions. *NPJ genomic medicine*, 6(1), 4. (* contributed equally to work)
- Puntambekar, S. S., Nyayanit, D., Saxena, P., & Gadgil, C. J. (2016). Identification of Unintuitive Features of Sumoylation through Mathematical Modeling. *Journal of Biological Chemistry*, *291*(18), 9458-9468.
- Natarajan, V. T., Ganju, P., Singh, A., Vijayan, V., Kirty, K., Yadav, S., Puntambekar, S., ... & Gokhale, R. S. (2014). IFN-γ signaling maintains skin pigmentation homeostasis through regulation of melanosome maturation. *Proceedings of the National Academy of Sciences*,*111*(6), 2301-2306.
- Dnyane, P. A., Puntambekar, S. S., & Gadgil, C. J. (2018). Method for identification of sensitive nodes in Boolean models of biological networks. *IET Systems Biology*,*12*(1), 1-6.