Prateek Arora, PhD

+41 782136444 pratarora@gmail.com / prateek.arora@unibe.ch www.linkedin.com/in/pratarora/ https://github.com/pratarora https://orcid.org/0000-0003-0822-9240 Markircherstrasse 43, 4055 Basel, Switzerland



Bioinformatics Research Associate

SUMMARY

Passionate bioinformatician with expertise in single-cell transcriptomics, spatial omics, metabolomics, multiomics, shiny apps, and pipeline development using FAIR data principles. Proven track record in mining, analysing and effectively visualizing available information to facilitate target discovery. Known for deep understanding of biology, attention to details, collaborative projects, and strong written and oral communication skills. With experience in training people, leading teams, handling multiple projects and collaborations in academic and industrial research, I look forward to new challenging roles.

KEY SKILLS

Bioinformatics | Single-Cell RNAseq | Spatial omics | ATACseq |Methylome-Seq | Long-read scRNASeq | Multiomics | Lipidomics | Mass Spectroscopy | Machine Learning | Neural Networks |Network Theory | R | Bioconductor | Seurat | Python | scanPy | scGen | UNIX Shell | Bash | Shiny app | Docker | Conda | SLURM | JIRA | Clickup | HPC | AWS | EC2 | FAIR Data | Experiment Designing | Manuscript writing | Scientific Presentations | Project Management

EXPERIENCE

RESEARCH ASSOCIATE - BIOINFORMATICS

July 2023 - Present

University of Bern, Bern, Switzerland

- Long-read snRNAseq Analysis: First group in Switzerland to perform Long-read snRNASeq using Oxford Nanopore Sequencing; designed experiments and uncovered novel splice variants in regenerating zebrafish hearts; analysis was performed on HPC cluster using Seurat, Pseudobulk differential analysis, LIANA, scDblFinder, OmniPath on self-maintained Docker containers. Supervised PhD student.
- Proteomics Analysis: Explored mitochondrial proteome in zebrafish muscle and heart mutants, utilizing Limma for differential analysis, GO, GSEA for pathway analysis and NLP for literature review.
- **Spatial-transcriptomics**: Showed evidence for in situ vaccination in Nanostring panels in mice to study high dose X-ray microbeams using Pathways analysis with SingleR, Clusterprofiler, ComplexHeatMaps; collaboration between 2 research groups
- **Pipeline Development- Lipidomics**: Innovated a pipeline for Spatial Mass Spectrometry Imaging Lipidomics in zebrafish, incorporating statistical tests, libraries as Cardinal and MetaboAnnotation which reduced processing time from 3 months to 3 days
- **Single-cell Analysis**: Analysed developing mouse heart and mutants using 10X Genomics, presenting findings to collaborating groups and made user friendly shiny app.
- Methylation Analysis: Discovered methylation differences across generations in mouse after cardiac injury using Infinium Mouse Methylation BeadChip.

POSTDOCTORAL FELLOW - BIOINFORMATICS

University of Bern, Bern, Switzerland

- snRNAseq Analysis: Advanced autophagy model studies in zebrafish hearts using Seurat and LIANA (ligand receptor); explored inheritance patterns in mouse hearts. Pseudobulk analysis using Libra, shiny app with ShinyCell, Pathway analysis.
- ATACseq Studies: Investigated WT1 transcription factor's role in zebrafish and mouse sperm using pipeline tool snakemake and various bioinformatics tools- Bowtie, picardtools, MACS3, Samtools, Genrich, Bedtools. Found critical transcription factors using CHIPSeeker, DiffBind, MEME suite for transcription factor site discovery etc.
- Target Discovery Pipeline: Developed a Ligand Receptor Network pipeline using bulk RNAseq, DESeq2, Network theory, leading to 2 PhD projects.
- Meta-analysis: Conducted comprehensive meta-analysis of BulkRNAseq Data for regenerating hearts, uncovering conserved pathways and training PhD students.

SENIOR BIOINFORMATICIAN

Elucidata Data Consulting Pvt Ltd, New Delhi, India

- **Drug Target Discovery:** Led a team to develop a drug target discovery pipeline, combining bulk and scRNAseq datasets on AWS; 20 potential targets identified.
- **Team Leadership:** Line manager of a team of two, task assignment, oversaw internal product development, validated scientific products, and set departmental OKRs.

PUBLICATIONS/CONFERENCES

• Oral Presentations - Shiny Conf 2024, Swiss Zebrafish meeting 2023

• Selected publications:

Garcia-Poyatos, C., Arora, P.*, et al, Dev Cell, 2024- <u>https://doi.org/10.1016/j.devcel.2024.04.012</u>
Coppe et al, BiorXiv, 2024- <u>https://doi.org/10.1101/2024.02.09.579452</u>

oChavez, M. N., Arora, P.*, et al, BiorXiv, 2024- <u>https://doi.org/10.1101/2024.03.26.586825</u>

• Marques, I. J., Ernst, A^{.#}, Arora, P.[#]*, et al, Development, 2022- <u>https://doi.org/10.1242/dev.200375</u>

• Publications in Pipeline: 3

CERTIFICATIONS/TRAININGS

- Introduction to Machine Learning with Python (SIB Swiss Institute of Bioinformatics)
- Long-read sequence analysis (SIB Swiss Institute of Bioinformatics)

EDUCATION

PhD + MSc (Cellular and Molecular Biology)

Tata Institute of Fundamental Research, Mumbai, India

LANGUAGES

English - Proficient User (C1/C2 level) | German - B1 | Hindi - Mother Tongue

June 2019 – June 2020

2011 - 2020