Manan Chopra

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UC San Diego M.S. graduate with 3 years of academic research experience in bioinformatics building local and cloud-based pipelines for computational analysis as well as conducting data analysis. Strong ability to communicate with interdisciplinary teams due to training in molecular biology with wet-lab portions of experiments. Passionate about utilizing strong programming and data analysis skills to uncover biological stories and insights with data.

EDUCATION

UC San Diego | **La Jolla, CA**

B.S. Biology w/ Specialization in Bioinformatics | Major GPA: 3.97 **Sept. 2019 - June 2023**
M.S. Biology (Focus in Bioinformatics) | GPA: 4.0 **Sept. 2023 - Aug. 2024**

Master's Thesis: *Validation of Human Retinal Organoid Derived Photoreceptors through Single-cell RNA Sequencing*
Relevant Coursework: Adv. Data Structures & Algorithms, Applied Genomic Technologies, Adv. Bioinformatics Lab, Molecular Sequence Analysis, Probability & Statistics for Bioinformatics, Biological Databases

SKILLS

General Skills: Programming, Pipeline engineering, NGS/genomic data analysis, scientific writing
Lab Skills: DNA/RNA Purification/Quantification, NGS Library Prep Workflows (sc/bulk), Mammalian Cell Culture
Technologies: Nextflow, Snakemake, Python/Jupyter Notebook, AWS, Docker, Bash, Git, Anaconda/Miniconda, R/Rmd, WSL2/Linux, Java, C/C++, WSL2, Javascript/React
Processing Tools: Galaxy, FastQC, TrimGalore, HISAT2, STAR/STARsolo, featureCounts, DESeq2
NGS Formats: long-read RNA/DNAseq, Bulk RNAseq, Single-cell RNAseq, ATACseq, ChIPseq
NGS Analysis Stack: Excel, Scanpy, scvi-tools, pandas, seaborn, matplotlib, PyTorch, Seurat, ggplot2

EXPERIENCE

Wahlin Lab | *Graduate Researcher, Undergraduate Research Assistant* | La Jolla, California **June 2021 - Aug. 2024**
- Developed and implemented bioinformatic workflows for the processing, analysis and visualization of large NGS datasets on both Windows and Linux platforms using Nextflow, Snakemake, Python and R
- Tailored workflows with different tools and data filtering strategies to analyze datasets with unique needs
- Produced publication quality charts and graphs, and designed high quality figures for multiple publications in reputable journals that focused on conveying underlying biological stories and trends through data
- Created and maintained WahlinLab GitHub repository with the goal of making code accessible to scientists with varying levels of experience in computational biology (https://github.com/WahlinLab)
- Carried out wet-lab portions of experiments (RNA isolation, NGS library prep, stem cell work)
- Co-authored multiple peer-reviewed research articles/reviews in reputable journals, demonstrating proficiency in scientific writing and creation of publication-quality figures

UC San Diego | Teaching Assistant for Recombinant DNA Lab (BIMM101) | La Jolla, California **Jan 2024 - June 2024**

SELECTED PUBLICATIONS & PROJECTS

- *NGS Bulk Processing Pipeline with Nextflow* (https://github.com/recursivelymanan/NGS-bulk-pipeline)
- *Human Retinal Ganglion Cell Neurons Generated by Synchronous BMP inhibition and Transcription Factor Mediated Reprogramming*, npj Regenerative Medicine (https://github.com/WahlinLab/Human_RGC-iN)
- *Chromatin Accessibility and Transcriptional Differences in Human Stem Cell-Derived Early-Stage Retinal Organoids*, MDPI Cells, Nov 2022 (https://www.mdpi.com/2073-4409/11/21/3412)
- *Early Transcriptional Dynamics of Retinal Ganglion Cells Generated by Direct Conversion*, ARVO Research Conference Poster, April 2023 (https://iovs.arvojournals.org/article.aspx?articleid=2786985)