

# Saksham Malhotra

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## EDUCATION

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### Master of Science, Applied Mathematics

Oct 2021 – Oct 2023

*Technical University of Munich*

*Munich, Germany*

- Relevant coursework: Machine learning, Introduction to deep learning, Deep generative models, Non-linear optimization, Probability theory, Computer vision, Math models in biology, Robotics.
- Thesis– Fast Eigensolvers for Koopman Operator Approximation: Developing an eigensolver algorithm that utilises the algebraic structure of Koopman eigenfunctions.

### Bachelor of Engineering, Electronics and Communication

April 2014 – April 2018

*Maharaja Surajmal Institute of Technology, GGSIPU*

*New Delhi, India*

## EXPERIENCE

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### Student Research Assistant (part-time)

June 2023 – Nov 2023

*Max Planck Institute for Dynamics of Complex Technical Systems*

*Remote, Germany*

- Reviewed 50 mathematical benchmark collections in numerical analysis and optimization, created a standardized database of their metadata using web scraping and APIs, and wrote a review paper on the state of mathematical benchmark collections.

### Software Developer (part-time)

June 2022 – May 2023

*Infineon Technologies*

*Munich, Germany*

- Developed an in-house microphone calibration database application using Vue and Openshift, with Rest APIs in Node js to interface with a MongoDB database, which streamlined the process of recording development projects for more than 200 customers.

### Data Scientist

June 2018 – June 2021

*Elucidata*

*New Delhi, India*

- Applied statistical methods on biological data such as hypothesis testing for differential gene expression analysis, bioinformatics methods for pathway analysis, dimensionality reduction and clustering methods on RNA sequencing data to aid three research labs and two therapeutic companies in understanding disease mechanisms and identifying cancer drug targets.
- Built a machine learning classifier to classify control and perturbation samples using text metadata. The classifier was trained on text metadata of 90k+ samples from the Gene Expression Omnibus repository, enabling multi-dataset discovery of differential genes.
- Created data analysis and processing pipelines in Python and R for public RNA-sequencing data repositories, transforming data and metadata to follow FAIR guidelines and providing 100k+ ML-ready datasets for the proprietary data platform–Polly. Packaged the pipelines using Docker for execution in AWS EC2.
- Created a Python pipeline for parallel processing single-cell reads from BAM files and automatic report generation for RNA counts.

## PROJECTS

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**Optimal race line for autonomous race car:** Solving an optimal control problem for path planning using IPOPT.

**Training ML models:** Training CNNs, variational autoencoders, and diffusion models in Pytorch for various tasks.

**Mercury:** DIY bioinformatics pipeline browser tool using Svelte, node js, and Tornado.

**Phantasus:** Open source contribution to data matrix analysis browser application built using jQuery and OpenCPU.

**cmappPy:** Open source contribution to Python package for parsing get files (popular format for biological data).

**Blog:** Various articles on mathematics topics.

## TECHNICAL SKILLS

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**Programming:** Python, R, Javascript, C++, Matlab, Git, Docker, SQL

**ML/DS frameworks:** Pytorch, Tensorflow, Scikit-learn, Numpy, Pandas