

Chaarvi Bansal

Portfolio: [chaarvii.github.io](https://github.com/chaarvii)
Github: github.com/chaarvii

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EDUCATION

- Birla Institute of Technology and Science, Pilani** Rajasthan, India
• *Master of Science - Biological Sciences and Bachelor of Engineering - Computer Science* Aug 2018 - May 2023
GPA: 8.60
Courses Data Structures & Algorithms, Neural Networks & Fuzzy Logic, Design & Analysis of Algorithms, Bioinformatics, Object Oriented Programming, Genetics, Cell Biology, Recombinant DNA Technology, Probability & Statistics, Multivariate Calculus

SKILLS SUMMARY

- **Languages:** Python, C++, JAVA, C, SQL
- **Frameworks:** Scikit, TensorFlow, Keras
- **Tools:** GIT, MySQL, SQLite

UPCOMING POSITIONS

- **Thesis Student, University of New South Wales** Sydney, Australia
• *Five month long thesis project fully funded by NHRMC MRFF and paid by UNSW* Aug 2022

EXPERIENCE

- **Bloomberg LP** Pune, Maharashtra
• *Software Engineering Intern* May 2022 - Jul 2022
 - **Project Overview:** Enhancing Bloomberg's Exchange Information Service This service is a centralized location to query normalized information about electronic trading connectivity protocols used by different exchanges and trading venues around the globe.
 - Improved performance of the service by reducing response time.
 - Redesigned modules to make the service more scalable to handle increasing traffic.
 - Implemented a utility to record performance statistics.
- **University of New South Wales, Australia** Remote
• *Research Intern* Dec 2022 - May 2022
 - **Supervisors:** Dr. Rohitash Chandra and Prof. S.S. Vasani
 - **Project Overview:** Design of Experiments for COVID-19 drug testing using a Bayesian Optimisation approach
 - Designed bayesian optimisation frameworks with random walk and genetic algorithm as acquisition functions to select a design that maximises confidence in posterior predictive model.
 - Analysing high-throughput multi-omics dataset using multi-variate and machine learning methods to identify useful signatures of ex vivo disease progression and drug efficacy.
- **North Eastern Space Application Center** Remote
• *Research Intern* May 2020 - Jun 2020
 - **Project Overview:** Designed a QGIS Plugin for automating Machine Learning based Land Cover Classification
 - Developed three advanced land cover classification models for integration with QGIS through a plugin (QAI Toolbox).
 - Achieved a kappa score of 0.81 on pixel-based models and accuracy of 94.46% on CNN-based image segmentation models.
 - QAI Toolbox was selected amongst the top 30 worldwide for presentation at QGIS North America 2020, an annual international conference conducted by OSGeo.

PUBLICATIONS

- **Hardik A. Jain, Chaarvi Bansal et al., CoviRx: A user-friendly interface for systematic down-selection of repurposed drug candidates for COVID-19:** Submitted for peer-review to MDPI Data Journal (May 2022)

HONORS AND AWARDS

- **MITACS Globalink Scholar:** Awarded MITACS Globalink Research Internship Scholarship to undertake a three month long fully funded research internship at Queen's University, Kingston - Dec 2021 (Declined)
- **INSPIRE-SHE Scholar:** Secured the coveted scholarship by The Department of Science and Technology (Govt. of India) for finishing in the top 1% in All India Senior School Certificate Examination 2018 - May 2019

PROJECTS

- **Lexical Analyser and Parser Construction (Jan 2022 - May 2022):** Implemented a lexical analyser and parser for provided custom language from scratch. Designed all the necessary data structures in C. Implemented and tested the complete pipeline for the given language to parse tree.
- **Surviving strategies of drug-tolerant tumor cells - a comparative with drug resistance (Jan 2022 - May 2022):** Studied the epigenetic modifications responsible for drug resistance in cancer cells. Identified markers responsible for the transition of cancer cells from a drug tolerant to drug resistance state. Identified epigenetic differences between drug tolerance and drug resistant state.
- **De-Novo Genome Assembler (Mar 2021 - Dec 2021):** Designed a module in C for assembling reads into contigs using paired-end information and generalised genomic signatures. Implemented a two-level hash table structure to make the algorithm easy to parallelize and distribute. Designed an algorithm to increase the intermediate assembly length by 30%.