# MAYANK MURALI

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#### **EDUCATION**

# The Pennsylvania State University

# University Park, PA

**Expected graduation May 2022** 

- Master of Science, Computer Science.
- Selected Coursework: Algorithm Design and Analysis, Fundamentals of Computer Architecture, Digital Image Processing II, Pattern Recognition and Machine Learning, Computational Biology, Algorithms and Data Structures in Bioinformatics.
- *Thesis*: Benchmarking and analyzing different de novo metagenome-assembly tools on NGS long-read metagenome datasets (both synthetic and real), to understand how different algorithms use the assembly graphs to resolve strains.

### **Vellore Institute of Technology**

# Chennai, India

2015 - 2019

• Bachelor of Technology, Computer Science and Engineering.

#### **EXPERIENCE**

#### Graduate Teaching Assistant The Pennsylvania State University

Jan 2020 - Dec 2021

• Facilitated cognitive learning on 'Introduction to System Programming (CMPSC 311)' course for B.S. (Engineering) students for 20 credit hours which included tutoring sessions, grading as well as counselling students in need.

#### **Full Stack Developer Intern**

# Agrometrics Analytics & Technology Pvt.Ltd.

Jan 2019 - April 2019

• Part of the team which developed a software product "FarmPro" which is an ARP system for agri-business. Helped in building backend software modules that capture data related to farm operations from SQL database and relay them to the front-end website interface using Python, PHP and SQL.

# **TECHNICAL PROJECTS**

• Drug-Disease Prediction and its Feature Selection Analysis | Python 3 | Code

Developed a predictive model using binary classification algorithms to identify potent drug candidates for a given disease using the existing knowledge of drugs. Applied feature selection on the dataset obtained from Kaggle having features like drug chemical structures, drug-drug and drug-disease correlations.

Understanding FOXC1 mouse gene regulation

Implemented a bioinformatics pipeline on Galaxy. The pipeline for ChIP-exo and RNA-seq analysis was used to identify where the transcription factor protein Forkhead box C1 binds to the mouse genome and understand possible FOXC1 regulation.

A study on k-mer counting methods using different data structures | C++

The performance of data structures such as unordered map, suffix array, hash table and bloom filter were analysed to implement *k*-mer counting operation on the human genome GRCh38 and the *Staphylococcus aureus* bacterium dataset. The benchmarking was performed with respect to the KMC 2 algorithm based on the memory usage and runtime.

### **LANGUAGES AND TECHNOLOGIES**

- Programming/Scripting Languages: C, C++, Python, Java, SQL, HTML, PHP, JavaScript, R.
- Framework and tools: Hadoop, Pandas, MATLAB, LaTeX, Git, Visual Studio, Anaconda, Galaxy.

#### ADDITIONAL EXPERIENCE AND AWARDS

- Microsoft, Networking Fundamentals Certification: received 'Microsoft Technology Associate 2018' certificate.
- **TEDx Event Management**: Executive member of Organization Committee of TEDx VIT Chennai hosted by the English Literary Association.
- **ENACTUS** for Social Uplift, Project Lead: Student Member of Enactus VIT Chennai (2017-2018), took part in implementation of community outreach projects for economic upliftment of the underprivileged in India.

#### **RESEARCH PUBLICATIONS**

- M. Murali, M. Bhargava, G. Snehaa, A. Anand, Md. A. Haque and V.R. Sarobin, "Data Analytics on IoT-based Health monitoring system", International Journal of Recent Technology & Engineering (Scopus- indexed) ISSN:2277-3878, Volume-8, Issue-1, pp. 220-223, 2019.
- B. Sahoo, A. Maharana, **M. Murali**, L. Shivani, G. Suganya and M. Premalatha, "Low-Cost Air Sensing System," In *Proceedings of 3rd International Conference on Computing and Communications Technologies (ICCCT)*, pp. 258-267. IEEE, 2019. doi: 10.1109/ICCCT2.2019.8824890