Amartya Achin Mandal

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EDUCATION

Georgia Institute of Technology

Atlanta, Georgia

Master of Science (MS) in Bioinformatics (GPA: 4.0/4.0)

Aug 2021 - Dec 2022

Relevant Coursework: Medical Image Processing, Machine Learning in Computational Biology, Computer Vision

Indian Institute of Technology Guwahati (IITG)

Guwahati, India

Bachelor of Technology (B. Tech) in Biotechnology

Jul 2013 - Jun 2017

PROFESSIONAL EXPERINCE

McGrath Lab - Georgia Institute of Technology

Aug 2021 - Present

Graduate Research Assistant

Atlanta, Georgia

- Applying **Object Detection** and **Tracking** using Computer Vision and Deep Learning (YOLOv5 and SORT, DeepSORT) approaches to identify trajectories and understand social behaviour of Lake Malawi Cichlids
- Leading the Journal Club for the lab focused on Genetics, Neuroscience and Machine Learning.

Synapsica Healthcare

June 2019 - July 2021

AI Scientist | Tech Stack: Python, PyTorch, MongoDB

Bangalore, India

- Developed, trained and deployed **Deep Learning** models for **diagnostic imaging** (<u>MRI</u> and <u>X-ray</u>) and reporting across multiple product suite which are deployed in radiology centers across the world.
- Implemented customised Convolution Neural Network (CNN) based architectures, student-teacher knowledge distillation models for effective image classification, regression and segmentation tasks.
- Applied YOLOv3 **object detection** algorithm and GRAD-CAM for explainability of the Deep Learning models for vertebrae and disc detections, chest xray abnormalities
- Created a Mask-No Mask classifier to check if people are wearing masks during Coronavirus in live video feeds

Decimal Point Analytics

April 2018 - June 2019

Full Stack Developer - Machine Learning | Tech Stack: Python, Tensorflow, Selenium, MySQL

Mumbai, India

- Developed, designed, automated and maintained a **sentiment analysis** model (CNN+RNN) to recommend news articles affecting business operations across several domains, saving a minimum **60 person-hours/month**
- Designed and built a Deep Learning CNN regression model by leveraging household images and predicting income of the families.
- Implemented machine learning as well as ensemble models for Credit Risk Default prediction
- Contributed to various in-house projects involving management tools (CRM), monitoring using AWS Lambda and automation tools for data-mining of newspapers text using selenium

PROJECTS

Automatic tumor infiltrating lymphocytes scoring for breast cancer. | Georgia Institute of Technology Ongoing

• Performing multi-class segmentation of whole slide images to identify the lymphocytes and providing a score to indicate prevalence of the tumor infiltrating lymphocytes using image processing and deep learning.

Effects of LPS on Macrophages - RNA Sequence Analysis | Georgia Institute of Technology

Oct 2021

• Transcriptomic Analysis to study the anti-inflammatory activity of Petiveria alliacea ethanol extract (PW) on macrophages in the presence and absence of Lipopolysaccharide (LPS) by creating a **RNA-seq pipeline** for analysis

Protein - Protein Network Analysis | Functional Analysis Lab insilico, University of Tokyo

May 2016

- Constructed a **protein-protein interaction network** from public databases (in XML) in Python and identified harmful nodes from this network using **Controllability Analysis** and Hopcroft Karp Algorithm for Maximal Matching.
- Implemented **Perl and R scripts** for alternative processing of **RNA-seq clinical data** and analyzing the results thus obtained for statistical significance.

TECHNICAL SKILLS

Languages: Python, R, Bash, C++, perl

Frameworks and Libraries: Pytorch, Tensorflow (Keras), OpenCV, Numpy, Pandas, Matplotlib, NLTK, Biopython, Flask Technologies: Linux, git, Gitlab CI/CD, Apache Spark, AWS EC2, MySQL, MongoDB

HONORS AND AWARDS

- Computational Biology Graduate Research Assistantship Spring 2022, Georgia Tech
- JICA Innovative Asia Scholarship awarded for Research Internship in the University of Tokyo
- Best Poster presentation in Research Conclave IIT Guwahati for 'Controllability Analysis of Human Protein-Protein Interaction network using a Disease Dataset'