Pushkar Ambastha

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EDUCATIONAL QUALIFICATIONS

Indian Institute of Technology (IIT) Guwahati, Guwahati, India *(Nov '21 - Present)*
B.Tech - Bio Science and BioEngineering
CGPA: **8.08/10**, Batch Rank: **4$^{\text{th}}$**/85

Vidya Sanskar School, Patna, India *(June '19 - Mar '21)*
Higher secondary(12th grade), CBSE Board
Percentage: **92.2%**, School Rank: **2$^{\text{nd}}$**/200

Delhi Public School Patna, Patna, India *(June '18 - Mar '19)*
Secondary school(10th grade), CBSE Board
Percentage: **95.2%** , School Rank: **7$^{\text{th}}$**/420

INTERNATIONAL RESEARCH INTERNSHIPS

Calibrating Agent-Based Models for Tumor-Immune Interactions using Spatial Biopsy Data and Multi-Modal Pipelines with AgentTorch *(June '23 - Present)*
 Guide: Ayush Chopra *(Camera Culture Group, MIT Media Labs, MIT)*

Massachusetts Institute of Technology (MIT) Media Labs
- Developed methods to calibrate clinical Agent-Based Models (ABM) directly from biopsies to have a mean accuracy of **77%** under the Spatial Agreement Measure *(SAM)* Metric, minimizing the number of biopsy samples taken.
- Designed a novel multi-modal calibrated ABM pipeline to apply gradient-based ABMs to simulate tumor-immune cell interactions. *(for Cytotoxic CD8+ T Cells in multiple carcinoma cases)*
- Extended a novel pip library *AgentTorch* (Pytorch framework to design, simulate, and optimize agent-based models) for the cancer immunotherapy domain. Extracting the parameters from the classification model with an accuracy of **90%**.

Optimizing Medical Segmentation with Integrated Med-SAM and Fast-SAM Models for Enhanced Accuracy in Multi-Modal Imaging *(May '23 - Dec '23)*
Guide: Katie Link *(Hugging Face X Healthcare)* **Hugging Face, NY** [Report](#)
- Developed novel models derived from the cumulative performance and extrapolation of Segment Anything Model *(SAM)*, Medical SAM *(Med-SAM)*, and Fast-SAM.
- Created a streamlined process that reduced the time it takes to analyze images by **68%** and decreased the model size by **82%** compared to the Vanilla SAM model.
- The results observed in Pathology and CT modalities gave an average improvement of **0.48** in mean Intersection of Union *(mIOU)* and **0.42** in Dice Score Coefficient *(DSC)*.

Adaptive Biomedical Segmentation: Enhancing model Explainability through Domain Shift Analysis *(Nov. '22 - Feb. '23)*
Guide: Tushar Kataria *(Computer Vision Group)* **University of Utah** [Report](#)
- Analysed Domain Shift in biomedical image segmentation models as a critical insight into Model Explainability. (for both binary and multiclass semantic segmentation instances)
- Fine-tuned U-Net, DeepLabV3 model on Dataset like GlaS from MICCAI *(2015)*, CRAG, CPM15 to observe domain dependency of models on the dataset, created a pipeline to improve Image masks mIOU and Dice Score.
- The results achieved for metrics like mIOU Loss, Pixel Accuracy, Jaccard Loss, and Dice Score met the standards of prior field experiments, like **0.96** for CRAG and **0.89** for GLAS *(mIOU)*.

SCHOLASTIC ACHIEVEMENTS
- **Inter IIT Tech Meet 11.0 :** Secured **Gold** Medal in building QA Chatbot by *DevRev.ai*, 2023
- **Kaggle 4X Expert:** Reached the Expert tier in all the categories of Kaggle, 2023
- **Bronze Medal (85$^{\text{th}}$/1100):** Open Problems – Single-Cell Perturbations, Kaggle, 2023
- **Bronze Medal (99$^{\text{th}}$/1025):** HuBMAP – Hacking the Human Vasculature, Kaggle, 2023
- **IITG.ai Hackathon:** Secured **6$^{\text{th}}$**/25 rank in hackathon conducted by IITG.ai club, 2022
- **Convolve Hackathon:** Secured **28$^{\text{th}}$**/231 rank in hackathon among 6 IITs by *Cisco*, 2022
- All India Rank **140** out of 100,000 candidates in National Entrance Screening Test (NEST), 2021
- Qualified for the Pre-Regional Mathematics Olympiad in **PRMO**, 2019

COMPUTATIONAL SKILLS

Programming languages	: C, C++, Python, R; MATLAB
Frameworks	: PyTorch, Tensorflow, Keras
Machine Learning/Data Analysis:	: Deep Learning, including CNNs, RNNs, VAEs, GANs, Bayesian NNs, Transformers

KEY PROJECTS	**Classifying SARS-CoV-2 genomes using advanced Natural Language Processing (NLP)** *(July '23 - Nov '23)*

Classifying SARS-CoV-2 genomes using advanced Natural Language Processing (NLP) *(July '23 - Nov '23)*
Course: Bio-informatics [Poster]

- Developed DNABERT, a pre-trained bidirectional encoder that achieved state-of-the-art performance in predicting promoters, splice sites, and transcription factor binding sites with a **5%** increase in F1-score over traditional models, using minimal fine-tuning on small datasets.
- Implemented a transformer-based pipeline with **99%** accuracy for SARS-CoV-2 genome classification, outperforming traditional random forest and SVC models by **40%** in precision.
- Enhanced viral genome classification by integrating model probabilities, resulting in a **12%** improvement in the correct assignment of cDNA sequences to distinct viral classifications.
- Presented as poster presentation at Conference Hall, IITG and achieved 1st/23 presenting groups

ProteoSynth - Automated Custom Protein Sequence Generator *(Jan '24 - May '24)*
Course: Computational Biology [Github]

- Developed Flask-based app generating 10,000 custom proteins with random amino acid sequences.
- Implemented custom options for sequence length, amino acid exclusion, and protein quantity, allowing users to generate up to 100 different protein sequences in a single request.
- Created functionality to output multiple .pdb files with sequences with downloadable .zip files.

GrooveSynth - Protein Active Site Structure Generator *(Jan '24 - May '24)*
Course: Computational Biology [Github]

- Developed a Flask-based app to analyze and visualize protein active binding sites, achieving a **20%** increase in the accuracy of ligand-binding predictions as a continuation of **ProteoSynth**.
- Developed an algorithm to identify and connect key amino acids in protein structures, enhancing understanding of ligand-binding mechanisms.
- Created a novel system to generate simplified Protein Data Bank (PDB) structures, reducing analysis time by **30%** and aiding drug design efforts.
- Secured 1st/80 position in the course with **AS** (Outstanding) grade for the project presentation.

PRODUCT DEVELOPMENT PROJECTS

Domain-specific Question Answering chatbot *(Dec. '22 - Feb. '23)*
11th Inter IIT TechMeet, IIT Kanpur [Github]

- Developed a question-answering system by retrieving the top candidate sentences from the corpus, used up to free collab resources, and *quantized* models to keep *latency* less than *1000 ms*.
- Developed question-answering pipeline using techniques like model distillation, sparsification, pruning, and fine-tuning the *DebertaV3-Base* model to decrease inference time and have a minimum loss in accuracy.

Cover Generation using all the OpenAI tools *(Jan. '23 - March '23)*
IITG.ai Club, IIT Guwahati [Github]

- Developed a multi-modal pipeline that converts audio/text input into images. Generated optimal transcripts for the podcasts and songs with *OpenAI Whisper* to create prompts.
- Designed pipeline with Latent Diffusion Models (*DALL-E*) to generate aesthetic cover images from created prompts using *ChatGPT/GPT-2* models, and deployed this on Hugging Face Spaces.

Super Resolution Photographic Mosaic *(March '23 - April '23)*
Coding Club, IIT Guwahati [Github]

- Developed a Computer Vision pipeline that enhances images by super-resolution and stitching.
- Designed multi-model pipeline consisting mainly of Latent Diffusion Upscaler model for super-resolution and Image Stitcher for creating a panorama.

Re-colorisation of monochrome images using conditional GANs *(Aug. '22 - Sep. '22)*
Coding Club, IIT Guwahati [Github]

- Trained a conditional GAN model based on *U-Net* block with *Resnet18* backbone and devised Image Processing strategies for colorization of monochrome images.
- Deployed a web app using Streamlit library on HuggingFace for COCO dataset fine-tuned model.

COURSE WORK

Bioengineering (Computational):- Bioinformatics ● Biological Data Analysis ● Biophysics ● Computational Biology ● Systems Biology[1] ● Research Methodology[1]

Computer Science:- Data Structures and Algorithms ● Computing Lab ● Pattern Recognition and Machine Learning

Mathematics:- Linear Algebra ● Basic Calculus ● Complex Analysis

Bioengineering (Wet laboratory):- Genetic Engineering ● Biochemistry ● Microbiology ● Cell and Molecular Biology ● Analytical Biotechnology ● Bioseparation Engineering ● Immunology

MOOCs:- Machine Learning[2] ● Deep Learning[2] ● Computer Vision[2] ● Natural Language Processing (NLP)[2] ● Reinforcement Learning[3]

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[1] Ongoing course [2] Course undertaken from Coursera DL Spec. [3] Course undertaken from Kaggle