

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: 8.18/10 , Batch Rank: 4th/75 Vidya Sanskar School , Patna, India (June '19 - Mar '21) Higher secondary (12th grade), CBSE Board Percentage: 92.2% , School Rank: 2nd/200 Delhi Public School Patna , Patna, India (June '18 - Mar '19) Secondary school (10th grade), CBSE Board Percentage: 95.2% , School Rank: 7th/420	
PUBLICATIONS	Pushkar Ambastha , <i>From AlphaFold 2 to AlphaFold 3: A Review on Advancements in Protein Structure Prediction</i> (Submitted to ACM Computing Surveys (IF: 23.8). Currently under review) <ul style="list-style-type: none">Investigated recent advances in protein structure prediction, like AlphaFold 3, which depicted a pattern toward the generalization ability of the models leading toward Large Language Models.Reviewed the developments related to current approaches to protein structure prediction and protein design and highlighted a selection of successful applications they have enabled.	
INTERNATIONAL RESEARCH INTERNSHIPS	Study of Synthetic Human Memories: AI-Edited Images and Videos which Implant False Memories and Distort Recollection (Aug. '24 - Present) Advisor: Prof. Pattie Maes (<i>Fluid Interfaces Group, MIT Media Labs, MIT</i>) Massachusetts Institute of Technology (MIT) Media Labs Report <ul style="list-style-type: none">Developed multi-modal pipeline using original image, AI-enhanced images, image to video, and AI-edited images to video in a successive survey used on old images showing a positive sentiment for potential therapeutic memory reframing. The false recollection is 2.05x compared to control.Created the architecture of the study that examines the impact of AI-altered visuals on false memories, which are recollections of events that didn't occur or deviate from reality. Automating Detection of APP Abnormalities in Porcine Brain Histology for Post-Traumatic Epilepsy Analysis (Aug. '24 - Present) Advisor: Prof. Ragini Verma (<i>Center for Biomedical Image Computing & Analytics</i>) University of Pennsylvania Report <ul style="list-style-type: none">Implemented an automated image annotation pipeline for analyzing Amyloid Precursor Protein (APP) in pig brain histology, significantly reducing manual annotation time and computational resources through efficient tiling and preprocessing techniques.Developed a fine-tuned Segformer model for detecting injury patterns in fornix and fimbria regions, incorporating histogram normalization and handling high-resolution histology images (78064 x 65075) with memory optimization (12GB RAM). Calibrating Agent-Based Models for Tumor-Immune Interactions using Spatial Biopsy Data and Multi-Modal Pipelines with AgentTorch (June '23 - Present) Guide: Ayush Chopra (<i>Camera Culture Group, MIT Media Labs, MIT</i>) Massachusetts Institute of Technology (MIT) Media Labs Report <ul style="list-style-type: none">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. (<i>for Cytotoxic CD8+ T Cells in multiple carcinoma cases</i>)Extended a novel pip library <i>AgentTorch</i> (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 - Aug '23) Guide: Katie Link (<i>Hugging Face X Healthcare</i>), Hugging Face, NY Report <ul style="list-style-type: none">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 (85th/1100)**: Open Problems – Single-Cell Perturbations, Kaggle, 2023
- **Bronze Medal (99th/1025)**: HuBMAP – Hacking the Human Vasculature, Kaggle, 2023
- **IITG.ai Hackathon**: Secured **6th/25** rank in hackathon conducted by IITG.ai club, 2022
- **Convolve Hackathon**: Secured **28th/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 : Python, C, C++, R; MATLAB

Frameworks : PyTorch, Tensorflow, Keras

Machine Learning/Data Analysis : Deep Learning, including CNNs, Transformers

KEY PROJECTS

Classifying SARS-CoV-2 genomes using advanced 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.
- Presented a poster at Conference Hall, IITG and achieved **1st/23** presenting groups

ProteoSynth & GrooveSynth: Advanced Protein Structure Analysis (Jan '24 - May '24)

Course: Computational Biology

[GitHub](#)

- Developed integrated [Flask-based platform](#) combining protein sequence generation and active site analysis: generated 10,000+ custom proteins with configurable amino acid sequences.
- Analyzed protein active binding sites, improving ligand-binding prediction accuracy by **20%**.
- Enhanced functionality via custom sequence length, amino acid exclusion, bulk generation (up to 100 sequences/request), and an automated .pdb file generation with downloadable .zip option.
- Secured **1st/75** 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 net 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](#).

RELEVANT COURSE WORK

Bioengineering (Computational):- Bioinformatics • Biological Data Analysis • Biophysics • Computational Biology • Systems Biology¹ • Research Methodology¹ • Analytical Biotechnology

Computer Science:- Intro to Computing • Computing Lab • Pattern Recognition and ML

Mathematics:- Linear Algebra • Basic Calculus • Complex Analysis

Bioengineering (Wet lab):- Genetic Engineering • Biochemistry • Microbiology • Immunology

MOOCs:- Machine Learning (ML)² • Deep Learning² • Computer Vision² • Natural Language Processing (NLP)² • Reinforcement Learning³

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