Nallapareddy Mohan Vamsi

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EDUCATION

Birla Institute of Technology and Science, Pilani

Hyderabad, India Bachelor of Engineering in Computer Science; GPA: 8.73/10 Aug 2017 - May 2021

o Relevant Courses: Deep Learning, Artificial Intelligence, Information Retrieval, and Data Mining

Research Experience

University College London

London, UK

Bachelor's Thesis Student (Supervisor: Prof. Christine Orengo)

Jan 2021 - Present

Application: Research Assistant at UCL

- Classification of Structurally Similar Groups
 - * Classified protein sequences present in CATH v4.3 into structurally similar groups using DL techniques
 - * Performances using BioVec, One-Hot Encoding, and ProtBert embeddings were compared [code]
- PETase Melting Point Prediction
 - * A DL model was designed to predict the melting point from protein sequence using the BRENDA database
 - * This model made binary predictions to judge whether a sequence could be used for PETase experiments [code]

SciLifeLab Stockholm, Sweden

Research Assistant (Supervisor: Prof. Arne Elofsson)

Jun 2020 - Dec 2020

- Constructed a dataset by extracting pairwise features such as gaussian DCA, mutual information, and cross-entropy from the multiple sequence alignment of 25,000+ protein chains, for studying inter-residue distance prediction
- o Designed a U-Net model which attained a PPV of 59.74%, comparable to the state-of-the-art trRosetta [code]

University of Ljubljana

Ljubljana, Slovenia

Research Assistant (Supervisor: Prof. Peter Peer)

Jun 2020 - Dec 2020

- o Curated the largest, most comprehensive dataset of COVID-19 chest x-ray images by far, to diagnose COVID-19
- Proposed an ensemble CNN model of MobileNetv2 & VGG 19, and attained 99.84% accuracy [code]

Carnegie Mellon University

Pittsburgh, USA

Research Intern (Supervisor: Prof. Min Xu)

Jul 2020 - Sep 2020

- Applied CV algorithms to classify bio-molecules simulated in cryo-ET tomograms at three different SNR values
- o Devised an end-to-end model with a denoising Convolutional Auto-Encoder and a 3D SqueezeNet [code]

International Institute of Information Technology Hyderabad

Hyderabad, India

Research Intern (Supervisor: Prof. Vinod P.K.)

May 2020 - Jun 2020

- o Studied drug repurposing by preprocessing the LINCS (GSE92742) gene expression dataset into a graph with each node as an individual perturbagen, and edges between perturbagens with the same mechanism of action
- Modeled a Graph Convolutional Network with GraphSAGE to predict links between perturbagens [code]

BITS Pilani, Hyderabad Campus

Hyderabad, India

Undergraduate Researcher

Aug 2018 - Dec 2020

- Cysteine Modification Prediction (Supervisor: Prof. Debashree Bandyopadhyay)
 - * Scraped the Protein Data Bank to develop a dataset for the detection of four different cysteine modifications, and extracted features such as buried fraction, rHpv, secondary structure, motifs, enzyme class, and pKa
 - * Designed a deep neural network with residual blocks and tested it on domains of unknown functions
 - * Built a web server for the model using Django and deployed it to the internet using Heroku [web-server] [code]
- Prediction of N6-Methyladenosine (m6A) Sites (Supervisor: Prof. Piyush Khandelia)
 - * Constructed a Convolutional LSTM with Attention to detect m6A sites at a single-base resolution in RNA using sequence motifs and secondary structure features, for studying the infectivity of SARS-CoV-2
 - * Achieved a precision of 94%, outperforming the state-of-the-art DeepM6ASeq model by 6% [code]
- Serine Repeat Antigen and Egress (Supervisor: Prof. Vidya Rajesh)
 - * Devised multiple hypotheses to understand the negative kinetic regulator action of Serine Repeat Antigen 5 (SERA5) in the egress mechanism of red blood cells, pertinent to the malaria parasite Plasmodium falciparum
 - * Conducted molecular docking simulations using Schrödinger for in-silico validation of these hypotheses
- Adaptive Bit Rate (ABR) Estimation in Video Streaming (Supervisor: Prof. Paresh Saxena)
 - * Advanced the state-of-the-art Pensieve framework by implementing the Follow then Forage method to increase exploration in the Asynchronous Advantage Actor-Critic (A3C) deep reinforcement learning network
 - * Attained a 6% increase in the Quality of Experience (QoE) and a 3% decrease in the training time [code]

Personal & Course Projects

- ABLE: Created a dataset and developed a Bidirectional LSTM network with Attention to classify protein sequences into the six enzyme classes and a negative class, using labels from their Enzyme Commission (EC) numbers [code]
- Player Detection and Tracking: An OpenCV and MobileNetv2 ensemble network to detect, categorize, and track the players along with the ball in a football match video. Used for generating training statistics for football teams [code]
- RL Game Agents: Implemented various reinforcement learning algorithms such as Q-Learning, Deep Q-Network, Temporal Difference (TD) Learning, SARSA, and Expected SARSA to solve game environments in OpenAI Gym [code]
- Recommender System: Built a movie recommender system using collaborative filtering (with and without baselines), Singular Value Decomposition, CUR and the Latent Factor model for the course Information Retrieval [code]
- Other Projects: Route Planning System using A* search, Course Recommender Chatbot using AIML, Predictive Machine Maintenance System, Phylogenetic Tree building using Hierarchical Clustering, Fake News Detection, Medical Expert System, Fraud Detection using Local Outlier Factor, Sales Analysis using Apriori and Frequent-Pattern Growth

Publications and Presentations

- Nallapareddy, Vamsi et al. "DeepCys: Structure-based multiple cysteine function prediction method trained on deep neural network: Case study on domains of unknown functions belonging to COX2 domains." Proteins, 10.1002/prot.26056. 12 Feb. 2021, doi: 10.1002/prot.26056
- Liu, S., Ma, Y., Ban, X., Zeng, X., Nallapareddy, M. V., Chaudhari, A. and Xu, M. (2020). "Efficient Cryo-ET Simulation of Macromolecules with Neighbors and SARS-CoV-2" in 2020 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Seoul, Korea (South), pp. 80-87. doi: 10.1109/BIBM49941.2020.9313185
- Nallapareddy, M. V., Bhat, S., and Rajesh, V. (January 15, 2020). "Evaluating SERA 5 Competition for Sub-1 Mediated Cleavage of SERA 6 in *Plasmodium Falciparum* and Its Role in the Kinetics of Egress Using In-Silico Tools". Proceedings of International Conference on Drug Discovery (ICDD) 2020. [abstract] [poster]
- Nallapareddy, M. V. and Dwivedula, R. (2020) "ABLE: Attention Based Learning for Enzyme classification". Under review at The Journal of Computational Biology and Chemistry [preprint]

AWARDS & HONORS

- Max Planck Institute for Informatics 2020 Research Scholar Fellowship
- National Talent Search Examination (NTSE) Scholar (Merit Scholarship by the Government of India)
- BITS Pilani Merit Scholarship (Awarded for being in the top 1% of my class)
- Google India AI Summer School Attendee
- First Runner Up at InnoHack 7.0 Pan-India Hackathon

SKILLS

- Languages: Python, C/C++, Java, SQL, R, MATLAB/Octave, Fortran
- Python Libraries: PyTorch, TensorFlow/Keras, Scikit-Learn, OpenCV, Numpy, Pandas, Matplotlib/Seaborn, Gensim, NLTK, Biopython, and OpenAI Gym
- Bioinformatics Tools: Schrödinger Suite, PyMOL, AutoDock, ClusPro 2.0, SwissDock, SwissModel, DSSP, GEPOL93, PROPKA, I-TASSER, Robetta, VMD, ClustalW, BLAST, ViennaRNA, and ORF FINDER

ACTIVITIES & INTERESTS

- Co-Founder, Humble Servants. Lead a team of 20+ individuals and spearheaded missions for COVID-19 relief, Sanitation and Hygiene, Digital Literacy and Aid for the Differently-Abled [facebook-page]
- Member, Rotary Club of BITS Pilani, Hyderabad Campus
- Co-Founder, ML/AI Research Society
- Head for Machine Learning, IEEE Student Chapter
- Teaching Assistant for the courses Mechanics, Oscillations, and Waves and Discrete Structures for Computer Science
- Student Representative, Academic Counselling Cell
- Head for Writing & Debate Adjudicator, English Languages and Activities Society