Rana Sheraz Ahmad

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Education

Bachelor of Science in Bioinformatics
Government College University Faisalabad, Pakistan *Oct 2021 - July 2025*
CGPA till 6th semester: 3.12/4.0
Major Courses: Biological Data Analysis; Immuno-informatics; Proteomics; Genomics and Transcriptomics; Bioinformatics Software Development; Systems Biology; Bioinformatics Scripting; Artificial Intelligence; Modelling and Simulation.

Research Interests

Health-Informatics; Computational & Comparative genomics; Disease Diagnosis; ML Assisted Bioinformatics Resource development.

Experience

Research Intern at Integrative Omics and Molecular Modeling Lab *June 2024 - Present*
Department of Bioinformatics and Biotechnology, GCUF, Pakistan

Research Projects

Developing Machine Learning Predictive Model to Accelerate Diagnosis of Heart Disease Risk

- Developed a machine learning-based model to predict the risk of heart disease in patients, with a focus on practical implementation for early diagnosis.
- Integrated multiple machine learning algorithms, such as **decision trees, random forest** and **GradientBoosting**, to predict heart disease risk across various patient demographics
- Optimized model parameters to enhance prediction **accuracy up to 97.7%** and enabled clinicians to reliably monitor patient risk factors for informed decision-making

Multi-Class Brain Tumors Neurological Disorder Stratifying Algorithm

- Employed a deep ensemble model using transfer learning technique to classify brain tumor types, including **meningioma, pituitary, and glioma,** from MRI images.
- Built a deep convolutional architecture by concatenating two pre-trained models which are **VGG19** and **Xception**.
- The designed algorithm **outperforms existing methods**, providing reliable support for the early diagnosis of brain tumors type and offering valuable assistance to healthcare professionals in clinical decision-making.

Comprehensive Design and Evaluation of a Multi-Epitope Subunit Vaccine Targeting Respiratory Syncytial Virus (RSV)

- Identified **Fusion (F)** and **Nucleoprotein (N)** from the Respiratory Syncytial Virus (RSV) as optimal candidates for multi-epitope vaccine development based on their immunogenic potential.
- Engineered T-cell and B-cell epitopes with minimal homology to human proteins to minimize immunogenic cross-reactivity and potential adverse effects.
- Constructed a **253-residue peptide construct** incorporating a beta-defensin adjuvant to enhance immunogenicity, followed by structural validation through molecular docking and molecular dynamics simulations.
- The proposed epitope-based vaccine, designed using immunoinformatics approaches, shows promise as a therapeutic candidate to mitigate RSV infections and associated pathologies.

Deep Learning-Based Diagnostic System for Citrus Plant Diseases

- Automated identification of citrus diseases in orchards using a convolutional neural network (CNN) deep learning approach.
- Designed a 7-layer deep CNN architecture to diagnose diseases in citrus plants such as **greening** (HLB), **canker**, **sunscald**, and **leaf minor**.
- Deployed the algorithm on raw orchard images, achieving 98% accuracy in disease diagnosis.

Technical Skills

Bioinformatics databases: NCBI, EMBL, GenBank, UniProt, PDB, GEO-database, Cath, Scop, swiss-Prot, Ref-Seq, UCSC-Genome browser

Programming Languages: Python, C, C++, Java, Html/Css, MySql

ML & Python Libraries: TensorFlow, scikit learn, NumPy, OpenCV, Biopython, SciPy, Pandas, sys, Matplot, Plotly, Seaborn

Bioinformatics Tools:

- **Gene manipulation:** Blast, GenScan, Augustus, gProfile, PromH, GeneMark Interpro
- **Protein Manipulation:** PSI-Pred, InterProScan Blastp, Swiss-PdbViewer, I-Tasser, Prosite, Hmmer, Meme, Procheck, GrammX, Rosetta, Chimera
- **Alignment & Phylogenetic:** ClustalW, Mega, ClustalOmega, MUSCLE, MAFFT
- **Others:** Protparam, PSI-Blast, Emboss, Pssm, Plantcare, CpGProD, Vaxigen, AllerTop, IEDB, Rampage, PDB-Sum, FASTA, FASTAX, FASTAY, TBLASTx, TBLASTn, C-ImmmSim

Deep Learning Models: DNNs, RNNs, GANs, CNNs,Transformers

Global and Local Alignment-Tool on the basis of the Smith-Waterman and Needle-Wunsch Algorithm in Python.

Phylogenetic analysis of 20 organisms by using Mega and also their Bootstrap and footprinting analysis

HelixLink - A Startup website course project work by using HTML, CSS and Java-Script

Sentimental Analysis NLP task by using recurrent neural network.

Workshops & Extracurricular Activities

Workshop on Oxford-Nanopore Third Generation Sequencing
Department of Bioinformatics & Biotechnology, GCUF *04 October 2024*

One-Day Symposium on Soil Health
Government College University Faisalabad *05 December 2023*

Media Secretary - Head
Green Youth Movement, GCUF Chapter *05 August 2024 - Present*

Amal Fellowship - 3-month Fellowship funded by Stanford University and PepsiCo
University of Agriculture Faisalabad *December 2024 - Present*

Language

English: ●●●●◐
Urdu: ●●●●●
Punjabi: ●●●●●

REFERENCES Can be provided on Request