



SAEED AHMED

📍 **Home** : Village and post office nawagai tehsil mandnr district buner, 19300, Buner, Pakistan

📍 **Work** : Blidvädersvägen 4H, lgh 1703,, 22275, Lund, Sweden

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🌐 **LinkedIn**: <https://www.linkedin.com/mynetwork/>

👤 **sciprofiles**: <https://sciprofiles.com/profile/390359>

Gender: Male **Date of birth**: 02/02/1987 **Nationality**: Pakistani

ABOUT ME

I will always use my skills like honesty, and devotion to my job, to achieve high carrier growth through continuous learning, keep myself a dynamic visionary, and be competitive with the changing world scenario. A motivated learner, researcher, and entrepreneur with extensive professional experience with diverse and prestigious organizations and institutes in the field of Computer Science, Machine learning, and its application especially in bioinformatics. A creative and critical manager enriched with leadership, management, and communication skills, proficient in completing tasks on time, and adaptable to any work environment. A dedicated worker with a sense of responsibility and professionalism with a vision to learn and excel to serve.

RESEARCH INTEREST

Research Interest

My research interests are large-scale data mining, machine learning, bioinformatics, and computational systems biology. More specifically, my research focuses on machine learning, sequence analysis, structural analysis, DNA/RNA, Proteins, post-transcriptional and protein post-translational modification prediction, and peptides prediction of human bacterial pathogens using whole-genome sequence data. I am highly motivated to design and develop cutting-edge computational algorithms, models, and pipelines to address a range of challenging problems in drug discovery and development.

WORK EXPERIENCE

[10/09/2023 – Current]

Postdoctoral Researcher

Department of Experimental Medical Science Lund University BMC B13 SE-22184 Lund Sweden

City: Lund

Country: Sweden

- Develops methods and performs analyses to understand biological and medical phenomena at genetic, functional, mechanical, and system levels.
- Identification and development of prediction tools for pathogenic variations
- Phenotype-genotype-correlations in diseases relations with suppliers

[02/09/2021 – Current]

Assistant Professor in Computer Science

University Management and Technology Lahore

[01/06/2021 – 28/02/2022] **Postdoctoral Research Fellowship**
Center of data mining and biomedical informatics, Mahidol University, Bangkok Thailand,

[05/10/2020 – 31/08/2021] **Lecturer in Computer Science**
Higher Education Department KPK, Govt: Degree Collage Daggar Buner, KPK

EDUCATION AND TRAINING

[08/10/2016 – 25/03/2021] **PhD in Computer Science and Technology (Bioinformatics)**
Nanjing University of science and technology Nanjing China <https://english.njust.edu.cn/>
Address: 200 xiaolingwei, Xuanwu district, jiangsu province, 210094, Nanjing, China

[03/03/2013 – 28/09/2016] **MS in Computer Science**
Abdul Wali Khan University Mardan, KPK, Pakistan <https://awkum.edu.pk/>
Address: Bacha Khan Monument, Nowshera Mardan Rd, Muslimabad, Mardan, Khyber Pakhtunkhwa, 23200, Mardan, Pakistan

[08/10/2007 – 28/12/2011] **BS in Telecommunication**
Institute of Engineering and Technology, University of Science and Technology Bannu KPK, Pakistan <https://www.ustb.edu.pk>
Address: Bannu, Khyber Pakhtunkhwa, 28210, Bannu, Pakistan

[01/08/2004 – 13/07/2006] **Fsc Pre-Engineering**
Board of Intermediate and Secondary Education Swat, KPK Pakistan <https://bisess.result.pk>
Address: Kukrai, Saidu Sharif, Swat, Khyber Pakhtunkhwa , 19200, Swat, Pakistan

[04/10/2000 – 18/07/2004] **Matriculation**
Board of Intermediate and Secondary Education Swat, KPK Pakistan <https://www.bisess.edu.pk>
Address: Kukrai, Saidu Sharif, Swat, Khyber Pakhtunkhwa , 19200, Swat, Pakistan

THESIS/DISSERTATIONS

Research on Prediction of Protein Phosphorylation and Cancer Subtypes via Intelligent Computation.

Ph.D. Dissertation:

Submitted to Nanjing University of Science and Technology, Nanjing, China.

Identification of Heat Shock Protein Families and J-Protein Types using Dipeptide Composition and Support Vector Machine.

MS Thesis: Submitted to Abdul Wali Khan University, Mardan, Khyber Pakhtunkhwa, Pakistan.

LANGUAGE SKILLS

Mother tongue(s): Pashto

Other language(s):

Urdu

LISTENING C2 READING C2 WRITING C2

SPOKEN PRODUCTION C2 SPOKEN INTERACTION C2

English

LISTENING C2 READING C2 WRITING C2

SPOKEN PRODUCTION C2 SPOKEN INTERACTION C2


Chinese

LISTENING A1 READING A1 WRITING A1

SPOKEN PRODUCTION A1 SPOKEN INTERACTION A1

Levels: A1 and A2: Basic user; B1 and B2: Independent user; C1 and C2: Proficient user

DIGITAL SKILLS

Python libraries (Numpy Pandas Matplotlib Tensorflow networkx) | Basics of Tensorflow | Python/PyTorch | -PyCharm -Matlab -Atmel -MS Office | Knowledge of C, Python, Java, Matlab | Microsoft Office (word, excel, Visio, access, power point) | Python (matplotlib numpy scipy pandas scikit-learn tensorflow) | Deep Learning |  Machine Learning | pattern recognition | C, C#, C++ | Artificial Intelligence | Computational biology | Bioinformatics and Computational Biology | Gene Expression

PUBLICATIONS

[2024]

[A 16 × 16 Patch-Based Deep Learning Model for the Early Prognosis of Monkeypox from Skin Color Images](#)

Reference: M A Arshed, H A, Rehman, S Ahmed, C Dewi, and H J Christanto; Computation 2024, 12(2), 33

[2024]

[Multiclass AI-Generated Deepfake Face Detection Using Patch-Wise Deep Learning Model](#)

Reference: M. A. Arshed, S. Mumtaz, M. Ibrahim, C. Dewi, M. Tanveer and S. Ahmed

[2023]

[A Novel Predictor for the Analysis and Prediction of Enhancers and Their Strength via Multi-View Features and Deep Forest](#)

Reference: M Gill, S Ahmed, M Kabir, and M Hayat; Information 14.12 (2023): 636.

[2023]

[Chem2Side: A Deep Learning Model with Ensemble Augmentation \(Conventional+ Pix2Pix\) for COVID-19 Drug Side-Effects Prediction from Chemical Images](#)

Reference: M A Arshed, M Ibrahim, S Mumtaz, M Tanveer and S Ahmed, Information 14.12 (2023): 663.

[2023]

[Multi-class skin cancer classification using vision transformer networks and convolutional neural network-based pre-trained models](#)

Reference: Arshed, M. A., Mumtaz, S., Ibrahim, M., Ahmed, S., Tahir, M., & Shafi, M.. Information, 14(7), 415.

[2023]

[IoT Based Smart Baby Monitoring System with Emotion Recognition Using Machine Learning](#)

[2022]

[**PredAoDP: Accurate Identification of Antioxidant Proteins by Fusing Different Descriptors Based on Evolutionary Information with Support vector machine. Accepted, \[J\] Chemometrics and Intelligent Laboratory Systems.**](#)

S Ahmed, M. Kabir*, M. Arif, K. Khan, Y. D Khan;

[2022]

[**AMY-FRL: a novel sequence-based approach for accurate prediction of amyloid proteins by using feature representation learning. \[J\] Scientific Report.**](#)

P Charoenkwan, **S Ahmed**, C Nantasenamat, W Shoombuatong,*;

[2022]

[**SCORPION is a stacking-based ensemble-learning framework for accurate prediction of phage Virion proteins. \[J\] Scientific Report**](#)

S Ahmed, P Charoenkwan, J M.W. Quinn, M A Moni, Md Mehedi Hasan, Pietro Lio' and W Shoombuatong;

[2022]

[**StackACPred: prediction of anticancer peptides by integrating optimized multiple feature descriptors with stacked ensemble approach. \[J\] Chemometrics and Intelligent Laboratory Systems**](#)

M Arif, **S Ahmed**, M Kabir, and D-J Yu*

[2021]

[**DeepCPPred: a deep learning framework for discrimination of cell-penetrating peptides and their uptake efficiencies. \[J\] IEEE/ACM Transactions on Computational Biology and Bioinformatics.**](#)

M Arif, M Kabir*, **S Ahmed**, A Khan, G Feng, A Khelifi, DJ Yu;

[2021]

[**DeepPPSite: A deep learning-based model for analysis and prediction of phosphorylation sites using efficient sequence information. \[J\] Analytical Biochemistry.**](#)

S Ahmed, M Kabir, M Arif, Z U Khan and D.J Yu*;

[2020]

[**TargetCPP: accurate prediction of cell-penetrating peptides from optimized multi-scale features using gradient boost decision tree.\[J\] Journal of Computer-Aided Molecular Design.**](#)

M Arif, **S Ahmad**, F Ali, G Fang, M Li, DJ Yu;

[2020]

[**HPhosPPred: Prediction of human phosphorylated proteins by extracting discriminative features from the evolutionary profile and physicochemical properties through LFDA. \[J\] Chemometrics and Intelligent Laboratory Systems**](#)

S Ahmad*, M Kabir*, M Arif, Z Ali and ZNK Swati;

[2020]

[**Pred-BVP-Unb: Fast Prediction of Bacteriophage Virion Proteins Using Un-Biased Multi-Perspective Properties with Recursive Feature Elimination. \[J\] Genomics**](#)

M. Arif, F Ali, **S Ahmad**, M Kabir, Z Ali and M Hayat;

[2020]

[**iNR-2L: a two-level sequence-based predictor developed via Chou's 5-steps rule and general PseAAC for identifying nuclear receptors and their families. \[J\] Genomics.**](#)

M Kabir, **S Ahmad**, M Iqbal, and M Hayat;

[2020]

[**SDBP-Pred: Prediction of single-stranded and double- stranded DNA-binding proteins by extending consensus sequence and K-segmentation strategies into PSSM. Analytical Biochemistry.**](#)

F Ali, **S Ahmad**, M Kabir, M Arif, ZU Khan, and DJ Yu;

[2019]

[**DP-BINDER: machine learning model for prediction of DNA-binding proteins by fusing evolutionary and physicochemical information. \[J\] Journal of Computer-Aided Molecular Design.**](#)

F Ali, **S Ahmed**, ZNK Swati, S Akbar,

[2019]

[**Content-Based Brain Tumors Retrieval for MR Images Using Transfer Learning. \[J\] IEEE Access.**](#)

ZNK Swati, QH Zhao, M Kabir, Z Ali, F Ali, **S Ahmad**, and JF Lu:

[2019]

[**Brain Tumor Classification for MR Images using Transfer Learning and Fine-Tuning. \[J\] Computerized Medical Imaging and Graphics**](#)

ZNK Swati, QH Zhao, M Kabir, **S Ahmad**, Z Ali, and JF Lu:

[2019]

[**Prediction of membrane protein types by exploring local discriminative information from evolutionary profiles. \[J\] Analytical Biochemistry.**](#)

M Kabir, M Arif, **S Ahmad**, F Ali, ZNK Swati, and DJ Yu;

[2019]

[**iDTi-CSsmoteB: identification of drug-target interaction based on drug chemical structure and protein sequence using XGBoost with over-sampling technique SMOTE**](#)

SMH Mahmud, W Chen, H Jahan, Y Liu, NI Sujan, **S Ahmed**;

[2018]

[**An Integrated Feature Selection algorithm for Cancer Classification using Gene Expression Data. \[J\] Combinatorial Chemistry & High Throughput Screening**](#)

S Ahmad, M Kabir, Z Ali, M Arif, DJ Yu;

[2018]

[Improving secretary proteins prediction in Mycobacterium tuberculosis using oversampling technique with combination of support vector machine. \[J\] International Journal of Data Mining and Bioinformatics](#)

S Ahmad, M Kabir, M Arif, Z Ali, F Ali, and ZNK Swati;

[2018]

[Intelligent computational method for discrimination of anticancer peptides by incorporating sequential and evolutionary profiles information. \[J\] Chemometrics and Intelligent Laboratory Systems](#)

M Kabir, M Arif, S Ahmad, Z Ali, ZNK Swati, and DJ Yu;

[2018]

[Improving prediction of extracellular matrix proteins using evolutionary information via a grey system model and asymmetric under-sampling technique. \[J\] Chemometrics and Intelligent Laboratory Systems](#)

M Kabir, M Iqbal, S Ahmad, ZNK Swati, Z Liu, and DJ Yu;

[2017]

[Bi-PSSM: Position specific scoring matrix based intelligent computational model for identification of mycobacterial membrane proteins. \[J\] Journal of theoretical biology](#)

M Khan, M Hayat, SA Khan, S Ahmad, N Iqbal;

[2015]

[Identification of heat shock protein families and J-protein types by incorporating Dipeptide composition into Chou's general PseAAC. \[J\] Computer Methods and Programs in Biomedicine](#)

S Ahmad, M Kabir, and M Hayat;

[2015]

[iTIS-PseKNC: Identification of Translation Initiation site in human genes using pseudo k-tuple Nucleotides Composition. \[J\] Computers in Biology and Medicine](#)

M Kabir, M Iqbal, S Ahmad, and M Hayat;

CONFERENCES AND SEMINARS

Comprehensive analysis of machine learning based predictors for identifying DNase I hypersensitive sites

4th International Conference on Innovative Computing (IC2-2021), UMT, Lahore

M Rashid Rasheed, Mehwish Gill, M A Subhani, M Arif, S Ahmed, M Kabir*;

A Recent advancements in predicting protein phosphorylation sites using machine learning methods.

4th International Conference on Innovative Computing (IC2-2021), UMT, Lahore

A Yousaf, M Rashid Rasheed, M Arif, A Yousafzai, M Kabir, S Ahmed*;

NETWORKS AND MEMBERSHIPS

[08/12/2023 – Current] **Editorial Board Member, BMC Bioinformatics**

Write here the description...

**IDENTIFICATION OF TUMOR HOMING PEPTIDES USING DEEP FEATURES
COMBINED WITH SUPPORT VECTOR MACHINE**

Write here the description...

**PREDICTION OF ANTIMICROBIAL PEPTIDES USING FEATURE REPRESENTATION
LEARNING**

**PREDICTION OF ANTIMICROBIAL PEPTIDES USING FEATURE REPRESENTATION
LEARNING**

**RESEARCH ON ANALYSIS AND IDENTIFICATION OF ANTI DIABETIC PEPTIDES
USING FEATURE REPRESENTATION LEARNING**

**LARGE-SCALE COMPARATIVE REVIEW AND ASSESSMENT OF COMPUTATIONAL
METHODS FOR IDENTIFICATION OF NUCLEOSOME POSITIONING**

**A NOVEL APPROACH FOR ACCURATE PREDICTION OF CYCLIN PROTEINS BY
USING STACKING ENSEMBLE LEARNING**

**PREDICTION OF AMPYLATION SITES USING MULTIVIEWE FEATURES WITH
DEEP CASCADE RANDOM FOREST**

**PREDICTION OF ANTIVIRAL PEPTIDES USING LONG-SHORT-TERM-MEMORY
(LSTM) BASED CONVOLUTION NEURAL NETWORK**

**ANALYSIS ON PREDICTION OF LYSINE MALONYLATION SITES BY EXPLOITING
INFORMATIVE FEATURES IN MACHINE LEARNING FRAMEWORK USING
PRINCIPAL COMPONENT ANALYSIS**

**Title – Cell-Specific Long Non-Coding RNA Prediction Using Deep Learning
Techniques Student Name – Zoha Kashaf**

**HONOURS AND
AWARDS**

Honors and Awards

- **Postgraduate Full Scholarship** awarded by the Chinese Government via the Chinese Scholarship Council (CSC) consisting of free tuition fee, medical insurance, and 3500¥ stipend per month for studying Ph.D. in Computer Science and Technology at Nanjing University of Science & Technology, China (September 2016 to June 2020).
- **International Postdoctoral fellowship** fund 2021 was received from the Faculty of Medical Technology, University of Mahidol Bangkok, Thailand to support the research work from June 1, 2021, to February 28, 2022.
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HOBBIES AND INTERESTS

Hobbies and interests

Have a motivational and goal-oriented problem-solving attitude with time management skills. Effective communication to varied audiences including formal public speaking. Experience in working in teams can lead also to required situations. I like and promote cultures, and do sports and other activities, such as cricket, hiking, and fitness exercise.

DRIVING LICENCE

Cars: B1

24/11/2020 – 23/11/2025

REFEREE SERVICES

Referee services

- Briefings in Bioinformatics
- IEEE Access.
- Genomics.
- Artificial Intelligence in Medicine.
- Computers in Biology and Medicine.
- Visual Computing for Industry, Biomedicine, and Art
- Genes (MDPI)
- Electronic (MDPI)
- International Journal of Molecular Science (MDPI)
- International Conference on Innovative Computing – UMT
- International Conference on Frontiers of Information Technology – COMSATS
- Journal of Soft Computing
- Applied Soft computing
- Advance Bioinformatics (Oxford press)
- PLOS One

UNDER REVIEW/UNDER PROCESS PAPERS

Under Review/Under process PAPERS

1. **Saeed Ahmed**, Muhammad Kabir, and Muhammad Arif; CyclinPred-FRL is a novel approach for the accurate prediction of cyclin proteins by using feature representation learning.
2. Mehwish Gill, Muhammad Kabir*, **Saeed Ahmed**, Muhammad Asif Subhani; Large-Scale Analysis and Comparative Review of Computational Predictors for Identification of Enhancer and their Strength.
3. **Saeed Ahmed**, Muhammad Kabir, Muhammad Arif; BBPPred-FRL: Sequence-Based Prediction of Blood-Brain Barrier Peptides with Feature Representation Learning and Logistic Regression
- 4.

REFERENCES

[10/09/2023 – Current]

Reference-1

Name: Prof. Dr. Mauno Vihinen

Position: Full Professor

Contact: +46725260022

Email: mauno.vihinen@med.lu.se

Institute: Faculty of Medicine, Department of Experimental Medical Science

Webpage: <https://portal.research.lu.se/en/persons/mauno-vihinen>

References-2

Name: Dr. Watshara Shoombuatong

Position: Associate Professor

Contact: +66 939384256

Email: watshara.sho@mahidol.ac.th

Institute: Center of Data Mining and Biomedical Informatics, University of Mahidol
Thailand, Bangkok.

Reference-3

Name: Prof. Dong-Jun Yu

Position: Professor

Contact:

Email: njyudj@njust.edu.cn

Mobile No. +86-136-01456676

Office No. +86-25-84315751

Institute: School of Computer Science and Engineering, Nanjing University of Science &
Technology, P.R. China.

Webpage: <http://csbio.njust.edu.cn/djyu/>

Reference-4

Name: Dr. Maqsood Hayat

Position: Associate Professor

Contact: +92-308-5598123

Email: m.hayat@awkum.edu.pk or Maqsood.hayat@gmail.com

Institute: Department of Computer Science, Abdul Wali Khan University Mardan, Khyber
Pakhtunkhwa, Pakistan.

Webpage: [https://www.awkum.edu.pk/Departments/Computer_Science/
CS_Faculty_Maqsood_Hayat.html](https://www.awkum.edu.pk/Departments/Computer_Science/CS_Faculty_Maqsood_Hayat.html)
