



SAEED AHMED

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

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

<https://sciprofiles.com/profile/390359> | **WeChat:** saeedbuner | **Skype:** saeed86 |

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Address: Village and post office nawagai tehsil mandnr district buner, 19300, Buner, Pakistan (Home) |

Address: Blidvädersvägen 4H, lgh 1703,, 22275, Lund, Sweden (Work)

● 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.

● WORK EXPERIENCE

10/09/2023 – CURRENT Lund, Sweden

POSTDOCTORAL RESEARCHER DEPARTMENT OF EXPERIMENTAL MEDICAL SCIENCE LUND UNIVERSITY BMC B13 SE-22184 LUND 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 Nanjing, China

PHD IN COMPUTER SCIENCE AND TECHNOLOGY (BIOINFORMATICS) Nanjing University of science and technology Nanjing China

Address 200 xiaolingwei, Xuanwu district, jiangsu province, 210094, Nanjing, China |

Website <https://english.njust.edu.cn/>

03/03/2013 – 28/09/2016 Mardan, Pakistan

MS IN COMPUTER SCIENCE Abdul Wali Khan University Mardan, KPK, Pakistan

Address Bacha Khan Monument, Nowshera Mardan Rd, Muslimabad, Mardan, Khyber Pakhtunkhwa, 23200, Mardan, Pakistan |

Website <https://awkum.edu.pk/>

08/10/2007 – 28/12/2011 Bannu, Pakistan

BS IN TELECOMMUNICATION Institute of Engineering and Technology, University of Science and Technology Bannu KPK, Pakistan

Address Bannu, Khyber Pakhtunkhwa, 28210, Bannu, Pakistan | **Website** <https://www.ustb.edu.pk>

01/08/2004 – 13/07/2006 Swat, Pakistan

FSC PRE-ENGINEERING Board of Intermediate and Secondary Education Swat, KPK Pakistan

Address Kukrai, Saidu Sharif, Swat, Khyber Pakhtunkhwa , 19200, Swat, Pakistan | **Website** <https://bisess.result.pk>

04/10/2000 – 18/07/2004 Swat, Pakistan

MATRICULATION Board of Intermediate and Secondary Education Swat, KPK Pakistan

Address Kukrai, Saidu Sharif, Swat, Khyber Pakhtunkhwa , 19200, Swat, Pakistan |

Website <https://www.bisess.edu.pk>

● LANGUAGE SKILLS

Mother tongue(s): **PASHTO**

Other language(s):

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken production	Spoken interaction	
URDU	C2	C2	C2	C2	C2
ENGLISH	C2	C2	C2	C2	C2
CHINESE	A1	A1	A1	A1	A1

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

● DIGITAL SKILLS

Artificial Intelligence | 📖 Machine Learning | Deep Learnig | pattern recognition | Bioinformatics and Computational Biology | Computational biology | Gene Expression | Python libraries (Numpy Pandas Matplotlib Tensorflow networkx) | Pyhton/PyTorch | -PyCharm -Matlab -Atmel -MS Office | Knowledge of C, Python, Java, Matlab | Python (matplotlib numpy scipy pandas scikit-learn tensorflow) | C , C# , C++ | SLURM HPC | HPC clusters (Slurm)

● ADDITIONAL INFORMATION

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.

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.

PUBLICATIONS

[A novel stacking-based predictor for accurate prediction of antimicrobial peptides](#) – 2024

S Kanwal, R Arif, S Ahmed and M Kabir; Journal of Biomolecular Structure and Dynamics [], 1-12

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

– 2024

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

[Multiclass AI-Generated Deepfake Face Detection Using Patch-Wise Deep Learning Model](#) – 2024

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

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

– 2023

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

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

– 2023

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

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

– 2023

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

[IoT Based Smart Baby Monitoring System with Emotion Recognition Using Machine Learning](#) – 2023

Hina Alam, Muhammad Burhan, Anusha Gillani, Ihtisham ul Haq, Muhammad Asad Arshed, Muhammad Shafi, and **Saeed Ahmad**

[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.](#)

– 2022

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

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

– 2022

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

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

– 2022

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

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

– 2022

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

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

– 2021

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

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

– 2021

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

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

– 2020

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

[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](#)

– 2020

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

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

– 2020

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

[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.](#)

– 2020

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

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

– 2020

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

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

– 2019

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

[Content-Based Brain Tumors Retrieval for MR Images Using Transfer Learning. \[J\] IEEE Access.](#) – 2019

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

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

– 2019

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

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

– 2019

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

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

– 2019

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

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

– 2018

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

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

– 2018

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

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

– 2018

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

[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](#)

– 2018

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

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

– 2017

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

[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](#)

– 2015

S Ahmad, M Kabir, and M Hayat;

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

– 2015

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

CONFERENCES AND SEMINARS

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

Comprehensive analysis of machine learning based predictors for identifying DNase I hypersensitive sites M Rashid Rasheed, Mehwish Gill, M A Subhani, M Arif, **S Ahmed**, M Kabir*;

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

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

DRIVING LICENCE

Driving Licence: B1 | 24/11/2020 – 23/11/2025

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.

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.

THESIS SUPERVISION/ CO-SUPERVISION

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

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

