

CURRICULUM VITAE

MUHAMMAD KABIR

Postdoctoral Researcher

LAST UPDATED ON: June 18, 2023



Basic Information	
Degree	Ph.D. Computer Science and Technology.
Current Institute	Lund University, Sweden
Current Position	Postdoctoral Researcher
Department/School	Department of Experimental Medical Science - Biomedical Center (BMC).
Citizenship	Pakistan
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Email ID	kabiricp@gmail.com or muhammad.kabir@med.lu.se or mdkabircs@gmail.com
Google Scholar	http://scholar.google.com/citations?user=YCjWxh4AAAAJ&hl=en
Research gate	http://www.researchgate.net/profile/Muhammad-Kabir-3
Personal Webpage	https://mdkabir1.github.io/webpage/
ORCID	https://orcid.org/0000-0002-2488-1653
Looking for	Researcher (Permanent or long-term contract)

Research Objectives
<p>My research lies in the interface of statistical machine learning, pattern recognition, Evolutionary computing and some emerging data-rich areas such as computational biology and bioinformatics. I am interested in studying theoretically sound and empirically efficient evolutionary and machine learning algorithms to analyze, interpret, and integrate high volumes of multidimensional and heterogeneous data and based upon which building effective computational models. On one hand, I would like to develop computational methods for addressing a specific challenging problem by taking full advantage of domain- specific knowledge and data. On the other hand, I would like to study novel and scalable optimization/machine learning algorithms that are widely applicable. I have been focusing on analyzing the massive sets of biological sequence, structure and developed several web-predictors.</p> <p>Currently, during my postdoctoral research, I am working on development of advanced machine learning (artificial intelligence) methods for identification and classification of disease-causing genetic variations for research and clinical purposes.</p>

Educational Information			
Year	Degree	Major	Institute
2016-09 – 2020-06	Doctor of Philosophy	Computer Science and Technology	Nanjing University of Science & Technology, P.R. China
2013-03 – 2016-07	Master of Science	Computer Science	Abdul Wali Khan University, Mardan, Pakistan
2008-10 – 2012-09	Bachelor of Science	Computer Science	Islamia College University, Peshawar, Pakistan
2006-09 – 2008-08	Intermediate	Pre-Engineering	Board of Intermediate & Secondary Education, Mardan
2004-04 – 2006-06	Matriculation	Science	Board of Intermediate & Secondary Education, Mardan

Research Interests
<input checked="" type="checkbox"/> Bioinformatics
<input checked="" type="checkbox"/> Machine Learning
<input checked="" type="checkbox"/> Deep Learning
<input checked="" type="checkbox"/> Bioimaging
<input checked="" type="checkbox"/> Medical Image Processing

Thesis/Dissertations
<div> <input checked="" type="checkbox"/> Ph.D. Dissertation <i>Research on Prediction of Protein Attributes Based on Intelligent Computation.</i> Submitted to Nanjing University of Science and Technology, Nanjing, China. </div> <div> <input checked="" type="checkbox"/> MS Thesis <i>Identification of DNA Recombination Spots using Ensemble Classification.</i> Submitted to Abdul Wali Khan University Mardan, Khyber Pakhtunkhwa Pakistan. Read Thesis. </div>

Work Experience				
From	To	Institution	Designation	Duraton
2023-03-01	Till date	Biomedical Center, Lund University, Sweden	Postdoctoral Researcher	<i>continue</i>
2020-11-08	2023-03-05	University of Management and Technology, Lahore	Assistant Professor	2Y-3M-27D
2014-02-26	2016-12-31	Office of the Deputy Commissioner Mardan	Service Delivery Official	2Y-10M-7D

MS Students Under Supervision		
	Mehwish Gill	Completed
1	<i>Prediction and analysis of computational methods for the identification of enhancers and their strength.</i> Thesis submitted to <i>University of Management and Technology, Pakistan</i>	Supervisor 2022
	Muhammad Rashid Rasheed	Completed
2	<i>Prediction of protein phosphorylation sites based on multi-KELM.</i> Thesis submitted to <i>Tiangong University, Tianjin, China</i>	Co-Supervisor 2022
	Roha Arif (S2021393003)	Completed
3	<i>Identification of Tumor-Homing Peptides Using Deep features combined Support vector machine.</i> Thesis submitted to <i>University of Management and Technology, Pakistan</i>	Supervisor 2023
	Sameera Kanwal (S2021393004)	Completed
4	<i>Prediction of Antimicrobial peptides using feature representation learning.</i> Thesis submitted to <i>University of Management and Technology, Pakistan</i>	Co-Supervisor 2023
	Aqsa Amjad (F2021313012)	Completed
5	<i>Analysis and identification of promoters and their strength based on deep neural network with sequential features.</i> Thesis submitted to <i>University of Management and Technology, Pakistan</i>	Supervisor 2023
	Farwa Arshad (F2021313008)	Completed
6	<i>Identification of anti-diabetic peptides using stacked based ensemble learning.</i> Thesis submitted to <i>University of Management and Technology, Pakistan</i>	Co-Supervisor 2023

Honors and Awards
<div> <input checked="" type="checkbox"/> Postgraduate Full Scholarship awarded by the Chinese Government via Chinese Scholarship Council (CSC) consisting of free tuition fee, medical insurance, and 3500¥ stipend per month for studying PhD in Computer Science and Technology at Nanjing University of Science & Technology, China (September 2016 to June 2020). </div> <div> <input checked="" type="checkbox"/> Achieved research award +13000¥ for three papers published in high indexed journals, as the first author in 2016-20. </div>

Accepted Articles - Inpress

2022

1. M Arif, **M Kabir***, S Ahmad, A Khan, G Feng, A Khelifi, DJ 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*, 2022, 19(5), 2749-2759. [Read Paper](#).
2. S Ahmad, M. Arif, **M. Kabir***, Khaistah Khan, YD Khan; PredAoDP: Accurate Identification of Antioxidant Proteins by Fusing Different Descriptors Based on Evolutionary Information with Support vector machine. [J] *Chemometrics and Intelligent Laboratory Systems*, 2022, 228,104623. [Read Paper](#).
3. **M Kabir**, C Nantasenamat, S Kanthawong, P Charoenkwan, and W Shoombuatong*: Large-scale comparative review and assessment of computational methods for phage virion proteins identification. [J] *EXCLI Journal* 2022; 21:11-19. [Read Paper](#).
4. M Arif, S Ahmed, G Feng, **M Kabir***, YD Khan, DJ Yu*, Maha A. Thafar*; StackACPred: prediction of anticancer peptides by integrating optimized multiple feature descriptors with stacked ensemble approach. [J] *Chemometrics and Intelligent Laboratory Systems*, 2022, 220, 104458. [Read Paper](#).

2021

5. S Ahmad, **M Kabir**, M Arif, ZU Khan, and DJ Yu; DeepPPSite: A deep learning based model for analysis and prediction of phosphorylation sites using efficient sequence information. [J] *Analytical Biochemistry*, 2021, 612, 113955. [Read Paper](#).
6. M Rashid Rasheed, Mehwish Gill, M A Subhani, M Arif, S Ahmed, **M Kabir***; Comprehensive analysis of machine learning based predictors for identifying DNase I hypersensitive sites. [C] *4th International Conference on Innovative Computing (IC²-2021)*. [Read Paper](#).
7. A Yousaf, M Rashid Rasheed, M Arif, A Yousafzai, **M Kabir**, S Ahmed*; A Recent advancements in predicting protein phosphorylation sites using machine learning methods. [C] *4th International Conference on Innovative Computing (IC²-2021)*. [Read Paper](#).

2020

8. S Ahmad, **M Kabir***, M Arif, Z Ali and ZNK Swati; 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, 203, 104066. [Read Paper](#).
9. M. Arif, F Ali, S Ahmad, **M Kabir**, Z Ali and M Hayat*; Pred-BVP-Unb: Fast Prediction of Bacteriophage Virion Proteins Using Un-Biased Multi-Perspective Properties with Recursive Feature Elimination. [J] *Genomics*, 2020, 112(2):1565-1574. [Read Paper](#).
10. **M Kabir**, M Iqbal, S Ahmad, 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, 112(1):276-285. [Read Paper](#).
11. F Ali, S Ahmad, **M Kabir**, M Arif, ZU Khan, and DJ Yu*; 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, 589: 113494. [Read Paper](#).

2019

12. ZNK Swati, QH Zhao, **M Kabir**, Z Ali, F Ali, S Ahmad, and JF Lu: Content-Based Brain Tumors Retrieval for MR Images Using Transfer Learning. [J] *IEEE Access*, 2019, 7(1):17809-17822. [Read Paper](#).
13. ZNK Swati, QH Zhao, **M Kabir**, S Ahmad, Z Ali, and JF Lu: Brain Tumor Classification for MR Images using Transfer Learning and Fine-Tuning. [J] *Computerized Medical Imaging and Graphics*, 2019, 75: 34-46. [Read Paper](#).
14. S Akbar, M Hayat, **M Kabir**, and M Iqbal; iAFP-gap-SMOTE: An efficient feature extraction scheme gapped dipeptide composition is coupled with oversampling technique for Identification of Antifreeze proteins. [J] *Letters in Organic Chemistry*, 2019, 16(4):294-302. [Read Paper](#).
15. **M Kabir**, M Arif, S Ahmad, F Ali, ZNK Swati, and DJ Yu; Prediction of membrane protein types by exploring local discriminative information from evolutionary profiles. [J] *Analytical Biochemistry*, 2019, 564-565:123-132. [Read Paper](#).

2018	<p>16. S Ahmad, M Kabir, Z Ali, M Arif, DJ Yu: An Integrated Feature Selection algorithm for Cancer Classification using Gene Expression Data. [J] <i>Combinatorial Chemistry & High Throughput Screening</i>, 2018, 21(9):631-645. Read Paper.</p> <p>17. S Ahmad, M Kabir, M Arif, Z Ali, F Ali, and ZNK Swati: Improving secretory proteins prediction in Mycobacterium tuberculosis using oversampling technique with combination of support vector machine. [J] <i>International Journal of Data Mining and Bioinformatics</i>, 2018, 21(3):212-229. Read Paper.</p> <p>18. M Kabir, M Arif, S Ahmad, Z Ali, ZNK Swati, and DJ Yu: Intelligent computational method for discrimination of anticancer peptides by incorporating sequential and evolutionary profiles information. [J] <i>Chemometrics and Intelligent Laboratory Systems</i>, 2018, 182:158-165. Read Paper.</p> <p>19. F Ali, M Kabir, M Arif, ZNK Swati, ZU Khan, M Ullah, and DJ Yu: DBPPred-PDSD: Machine Learning Approach for Prediction of DNA-binding Proteins using Discrete Wavelet Transform and Optimized Integrated Features Space. [J] <i>Chemometrics and Intelligent Laboratory Systems</i>, 2018, 182:21-30. Read Paper.</p> <p>20. M Kabir, M Iqbal, S Ahmad, ZNK Swati, Z Liu, and DJ Yu: Improving prediction of extracellular matrix proteins using evolutionary information via a grey system model and asymmetric under-sampling technique. [J] <i>Chemometrics and Intelligent Laboratory Systems</i>, 2018, 174:22-32. Read Paper.</p>
2017	<p>21. M Tahir, M Hayat, and M Kabir; Sequence based predictor for discrimination of Enhancer and their types by applying general form of Chou's Trinucleotide Composition. [J] <i>Computer Methods and Programs in Biomedicine</i>, 2017, 146:69-75: Read Paper.</p> <p>22. M Kabir and DJ Yu; Predicting DNase I Hypersensitive sites via un-biased Pseudo Trinucleotide Composition. [J] <i>Chemometrics and Intelligent Laboratory Systems</i>, 2017, 167:78-84. Read Paper.</p>
2016	<p>23. M Waris, K Ahmad, M Kabir, and M Hayat; Identification of DNA Binding Proteins Using Evolutionary profile position specific scoring matrix. [J] <i>Neurocomputing</i>, 2016, 199:154-162. Read Paper.</p> <p>24. M Kabir and M Hayat; iRSpot-GAEnsC: identifying recombination spots via ensemble classifier and extending the concept of Chou's PseAAC to formulate DNA samples. [J] <i>Molecular Genetic and Genomics</i>, 2016, 291(1):285-296. Read Paper.</p>
2015	<p>25. S Ahmad, M Kabir, and M Hayat; Identification of heat shock protein families and J-protein types by incorporating Dipeptide composition into Chou's general PseAAC. [J] <i>Computer Methods and Programs in Biomedicine</i>, 2015, 122:165-174. Read Paper.</p> <p>26. M Kabir, M Iqbal, S Ahmad, and M Hayat; iTIS-PseKNC: Identification of Translation Initiation site in human genes using pseudo k-tuple Nucleotides Composition. [J] <i>Computers in Biology and Medicine</i>, 2015, 66:252-257. Read Paper.</p>
Under review/ Submitted/In progress	
	<ol style="list-style-type: none"> MR Rasheed, M Arif, SAhmed, M Kabir*, YD Khan, J Wang*; <i>PredPSite</i>: Boosting multiple kernel extreme learning machines for accurate prediction of protein phosphorylation sites. (Minor Revision Analytical Biochemistry – IF: 3.191) Accurate prediction of Pseudouridine sites via effective feature representation. (In progress) M Gill, M Kabir*, S Ahmed, MA Subhani, and M Thafar; Large-scale analysis and comparative review of computational predictors for identification of enhancer and their strength. (Submitted) M Gill, S Ahmed, M Kabir, and M Hayat*; NEPERS: A Novel approach for the analysis and prediction of enhancer and their strength via multi-view features and deep forest. (Submitted)
Taught Courses (Undergraduate Level)	
	<ul style="list-style-type: none"> ▶ Introduction to Information and Communication Technologies ▶ Introduction to Computing ▶ Discrete Structures ▶ Digital Image Processing ▶ Artificial Intelligence ▶ Programming Fundamentals with python ▶ Machine Learning

Administrative Responsibilities

- ▶ *Member* of **Editorial Board** for the *Innovative Computing Review Journal* under UMT.
- ▶ *Member* of the *organizing committee* for the *4th ICIC Conference* virtually held at UMT in 2021.
- ▶ *Batch Advisor* for the student of MS-Computer Science and MS-Computing and Data Science.
- ▶ Nominated representative from CS-Department for the *Cooperative Education (COOP) Program*.
- ▶ *Member* of Accreditation Committee and Outcome Base Education (OBE) Committee for BS Programs at SST.
- ▶ *Member* of Research Steering Committee at CS-Department.
- ▶ *Member* of Exam Monitoring Team at SST.

Editorial Services

- ▶ *Guest Editoror* for Special Issue "Applications of Deep Learning in Bioinformatics and Image Processing" *Information Journal in MDPI* – On going issue.

Referee services

The review services have been provided for the following journals.

- *Briefings in Bioinformatics*
- *Knowledge-Based Systems*
- *Information Science*
- *Current Opinion in Biomedical Engineering*
- *Artificial Intelligence In Medicine*
- *Genomics*
- *Journal of Computational Biology*
- *Computers in Biology and Medicine*
- *Current Opinion in Biomedical Engineering*
- *SAR and QSAR in Environmental Research*
- *IEEE Journal of Biomedical and Health Informatics*
- *Visual Computing for Industry, Biomedicine, and Art*
- *Journal of King Saud University - Computer and Information Sciences.*
- *IEEE Access*
- *AI Open*
- *Genes (MDPI)*
- *International Conference on Innovative Computing – UMT*
- *International Conference on Frontiers of Information Technology - COMSATS*