BIOGRAPHICAL SKETCH

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NAME: Sadia Akter, PhD, MS, FAMIA

eRA COMMONS USER NAME (credential, e.g., agency login): AKTERSADIA

POSITION TITLE: Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Dhaka, Bangladesh	B.S.	11/2007	Applied Statistics
University of Dhaka, Bangladesh	M.S.	03/2009	Applied Statistics
University of Missouri, Columbia	Ph.D.	05/2019	Bioinformatics
University of Missouri, Columbia	Postdoctoral Fellow	12/2020	Bioinformatics and Computational Biology

A. Personal Statement

I am an Assistant Professor of Biomedical Sciences at Marshall University School of Medicine, with a decade of research experience in bioinformatics, multi-omics data integration, and the application of AI/Machine Learning (AI\ML) in biomedical science. My interdisciplinary training spans applied statistics, bioinformatics and computational biology, and AI/ML, positioning me to lead innovative computational efforts in diverse biomedical domains. I have led bioinformatics components on multiple NIH- and NSF-funded projects, including studies focused on tuberculosis, asthma, COVID-19, addiction, and neuroinflammatory diseases. My research integrates high-dimensional omics data such as single-cell RNA sequencing (scRNA-seq), spatial transcriptomics, and methylomics with AI/ML methods to uncover molecular mechanisms of complex diseases. I have developed and published machine learning frameworks for biomarker discovery and am expanding this work into AI-based multi-modal disease modeling. My recent ongoing work includes AI-Based approach to identify potential biomarkers for asthma mechanism and build prediction model using transcriptomics data from Latino American pediatric cohorts. In addition, my other works include integrating scRNA-seq data with functional annotation pipelines to understand immune responses to infection and intervention at single-cell level of Tuberculosis and addiction studies. My lab is experienced with the Biostatistics, Bioinformatics and Computational Biology, and AI\ML. As a recipient of NIH AIM-AHEAD fellowship program and a Fellow of the American Medical Informatics Association (FAMIA), I am committed to translating computational insights into meaningful biomedical impact while advancing inclusive, collaborative, and team-based science.

Recent articles relevant to this application:

1. **Akter, S.**, Ahmed M, Singh D. K., Chauhan K. S., Kaushal D., Khader S. A. (2025). Single-cell transcriptome analysis of bronchoalveolar lavage during early SARS-CoV-2 infection. Microbiol Spectr. 2025 Jul 31:e0271524. doi: 10.1128/spectrum.02715-24. Epub ahead of print. PMID: 40742121.
2. Singh, D. K., Ahmed, M., **Akter, S.**, Shivanna, V., Bucşan, A. N., Mishra, A., Golden, N. A., Didier, P. J., Doyle, L. A., Hall-Ursone, S., Roy, C. J., Arora, G., Dick, E. J., Jagannath, C., Mehra, S., Khader, S. A., & Kaushal, D. (2025). Prevention of tuberculosis in cynomolgus macaques by an attenuated Mycobacterium tuberculosis vaccine candidate. Nat Comm., 16(1), 1957. https://doi.org/10.1038/s41467-025-57090-4

3. **Akter, S.**, Khader, S.A. (2023). A protocol to analyze single-cell RNA-seq data from Mycobacterium tuberculosis infected mice lung. STAR Protoc. 2023 Aug 31;4(3):102544. https://doi.org/10.1016/j.xpro.2023.102544
4. **Akter, S.**, Chauhan, K.S., Dunlap, M.D., Choreño-Parra, J.A., Lu, L., Esaulova, E., Zúñiga, J., Artyomov, M.N., Kaushal, D., Khader, S.A. (2022). Mycobacterium tuberculosis infection drives a type I IFN signature in lung lymphocytes. Cell Rep. 39. https://doi.org/10.1016/j.celrep.2022.110983

B. Ongoing Research

NIH OT2OD032581 Vishwanatha (Prime PI) 09/2024-09/2025
AIM-AHEAD Research Fellowship
I was awarded NIH's AIM-AHEAD Research Fellowship (2024) to expand my research into the application of cutting-edge bioinformatics and AI/ML approaches into complex disease such as asthma. By utilizing secondary single-cell transcriptomics, genetic and environmental data from dbGaP from Latino and African American cohorts, I aim to identify genetic, environmental risk factors, and immune response dynamics due to asthma at single-cell level specific to these cohort. This project not only addresses health disparities but also aligns with my long-term goal of advancing translational research through innovative AI/ML approaches.

NSF OIA-2242771 Serafin (PI) 06/01/23-05/31/28
West Virginia Network for Functional Neuroscience and Transcriptomics (WV-NFNT)
I am key bioinformatics personnel in the NSF's West Virginia Network for Functional Neuroscience and Transcriptomics (WV-NFNT) where I am responsible for building transcriptomic infrastructure and support faculties, postdoctoral researchers, activities to engage students, especially rural, first-generation college students, in neuroscience-bioinformatics research.

R01 HL105427 Khader (PI) 06/01/23-05/31/28
Role of IL-17 in Protective Vaccine-induced Immune Responses Against Tuberculosis
I am key bioinformatics personnel in this study that investigates conserved and diversified immune pathways across diversity Tuberculosis (TB) models. We aim to investigate infected animals to identify the molecular and cellular changes resulting from infection/treatment at single-cell level. These insights enhance our understanding of TB immunopathology and improve disease modeling for translational research.

C. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2024- present	Assistant Professor (Tenure track), Department of Biomedical Sciences, Joan C. Edwards School of Medicine, Marshall University, Huntington, WV
2022 – 2024	Staff Scientist, Department of Microbiology, The University of Chicago School of Medicine, Chicago, IL
2021 – 2022	Staff Scientist, Department of Molecular Microbiology, School of Medicine, Washington University Medical School in St. Louis, MO, USA
2019 – 2020	Postdoctoral Fellow, Bioinformatics and Computational Biology, Department of Molecular Microbiology and Immunology, and Christopher S. Bond Life Sciences Center, University of Missouri, Columbia, MO, USA
2012 – 2019	Graduate Research Assistant, University of Missouri, Columbia, MO, USA
2010 – 2011	Visiting Researcher, Urban Modelling Group, School of Architecture, Landscape, and Civil Engineering (SALCE), University College Dublin, Ireland
2009 – 2010	Teaching Assistant, United International University, Dhaka, Bangladesh

Honors

2024	Fellow of American Medical Informatics Association (FAMIA)
2019	National Science Foundation Travel Award (NSF CCF-1917325) to attend ISCB Great Lakes 2019 Bioinformatics Conference (GLBIO), Madison, WI
2019	Poster Research Competition (1st Place, Bioinformatics and Computational Biology category), Life Sciences Week, University of Missouri, Columbia, MO, USA

2018 Poster Research Competition (1st Place, Bioinformatics category), Life Sciences Week, University of Missouri, Columbia, MO, USA
2008 University Scholarship, University of Dhaka, Bangladesh
2002 – 2004 ISRT Scholarship, University of Dhaka, Bangladesh, 2002-2004

D. Contributions to Science

1. **Early Career:** Early in my career, I co-authored a paper investigating NSF funding trends for America's research-active civil engineering faculty. The study analyzed funding patterns by rank and sub-discipline, focusing on geotechnical engineering. It highlighted critical tenure-related parameters and revealed a higher reliance on traditional NSF funding programs among senior geotechnical engineers.
    a. Laefer, D. F., **Akter, S.**, & McHale, C. (2011). America's Research-Active, Geotechnical Faculty Members-An Investigation of National Science Foundation Funding Trends. In 2011 ASCE Geo-Frontiers (pp. 2887–2896). Geo-Frontiers. https://doi.org/10.1061/41165(397)296
2. **Graduate Career (Endometriosis):** In the area of endometriosis, my research projects focused on developing novel diagnostic methods by employing machine learning and data mining techniques on transcriptomics and methylomics data. These studies experimented how well various supervised machine learning methods perform in classifying endometriosis from the control samples, trained on both transcriptomics and methylomics data. Moreover, identify potential biomarkers and molecular mechanisms related to the disease to reduce diagnostic latency and improve patients' quality of life.
    a. **Akter, S.**, Xu, D., Nagel, S. C., Bromfield, J., Pelch, K., Wilshire, G. B., Joshi, T. (2019). Machine Learning Classifiers for Endometriosis Using Transcriptomics and Methylomics Data. Frontiers in Genetics, Section Bioinformatics and Computational Biology. https://doi.org/10.3389/fgene.2019.00766
    b. **Akter, S.**, Xu, D., Nagel, S. C., Bromfield, J., Pelch, K., Wilshire, G. B., Joshi, T. (2020). GenomeForest: An ensemble Machine Learning Classifier for Endometriosis. AMIA Joint Summits on Translational Science Proceeding. http://www.ncbi.nlm.nih.gov/pubmed/32477621.
    c. **Akter, S.**, Xu, D., Nagel, S. C., & Joshi, T. (2018). A Data Mining Approach for Biomarker Discovery Using Transcriptomics in Endometriosis. In Proceedings - 2018 IEEE International Conference on Bioinformatics and Biomedicine, BIBM 2018 (pp. 969–972). IEEE. https://doi.org/10.1109/BIBM.2018.8621150
    d. **Akter, S.**, Wilshire, G., Davis, J. W., Bromfield, J., Crowder, S., Joshi, T., Nagel, S. C. (2017). A multi-omics informatics approach for identifying molecular mechanisms and biomarkers in clinical patients with endometriosis. In Proceedings - 2017 IEEE International Conference on Bioinformatics and Biomedicine, BIBM 2017 (Vol. 2017-January, pp. 2221–2223). IEEE. https://doi.org/10.1109/BIBM.2017.8218003
3. **Graduate Career (Obesity):** My research on obesity and metabolism examined the effects of metformin, a commonly used antidiabetic drug, treatment, and exercise on gene expression in arteries and arterioles of skeletal muscles in obese rats. This study provides evidence that metformin treatment produces distinct gene expression effects throughout the arterial tree, and training-induced changes in arteriolar gene expression patterns differ by muscle fiber type composition and along the arteriolar tree in a rat model of obesity and insulin resistance.
    a. Padilla, J., Thorne, P. K., Martin, J. S., Rector, R. S., **Akter, S.**, Davis, J. W., Laughlin, M. H., Jenkins, N. T. (2017). Transcriptomic effects of metformin in skeletal muscle arteries of obese insulin-resistant rats. Experimental Biology and Medicine, 242(6), 617–624. https://doi.org/10.1177/1535370216689825
    b. Laughlin, M. H., Padilla, J., Jenkins, N. T., Thorne, P. K., Martin, J. S., Rector, R. S., **Akter, S.**, Davis, J. W. (2015). Exercise-induced differential changes in gene expression among arterioles of skeletal muscles of obese rats. Journal of Applied Physiology, 119(6), 583–603. https://doi.org/10.1152/japplphysiol.00316.2015
    c. Laughlin, M. H., Padilla, J., Jenkins, N. T., Thorne, P. K., Martin, J. S., Rector, R. S.**, Akter, S.**, Davis, J. W. (2015). Exercise training causes differential changes in gene expression in diaphragm arteries and 2A arterioles of obese rats. Journal of Applied Physiology, 119(6), 604–616. https://doi.org/10.1152/japplphysiol.00317.2015

4. **Graduate Career (Microbiome and Colorectal Cancer):** My work on the relationship between gut microbiota and colorectal cancer development revealed that gut microbiota composition varies between rat strains and is associated with significant differences in colorectal cancer severity. These findings underscore the importance of understanding the role of gut microbiota in colorectal cancer susceptibility and progression, potentially leading to novel therapeutic strategies.
    a. Ericsson, A. C., **Akter, S.**, Hanson, M. M., Busi, S. B., Parker, T. W., Schehr, R. J., Bryda, E. C. (2015). Differential susceptibility to colorectal cancer due to naturally occurring gut microbiota. Oncotarget, 6(32). https://doi.org/10.18632/oncotarget.5604
5. **Postdoctoral Career (Infectious Disease):** I have explored the genomic diversity, pathogenicity, and antimicrobial resistance of Escherichia coli (E. coli) isolates from poultry. This study identifies a large extent of genomic and serological diversity among E. coli isolates in southern United States poultry and the genetic markers associated with virulence and the presence of AMR associated genes. Such a study is important to the development of an effective E. coli vaccine. Moreover, my research on Influenza A viruses (IAV) has investigated the role of wild bird migration in the global dissemination of IAV through arctic and subarctic zones, providing valuable insights into virus movement and informing future surveillance strategies.
    a. Feng, Aijing*; **Akter, S*.**; Leigh, Spencer A; Wang, Hui; Pharr, G. Todd; Evans, Jeff; Branton, Scott L.; Landinez, Martha Pulido; Pace, Lanny; Wan, X.-F., 2023. Genomic Diversity, Pathogenicity and Antimicrobial Resistance of Escherichia coli Isolated from Poultry in the Southern United States. BMC Microbiol. https://doi.org/10.1186/s12866-022-02721-9
    b. Gass, J.D., Dusek, R.J., Hall, J.S., Hallgrimsson, G.T., Halldórsson, H.P., Vignisson, S.R., Ragnarsdottir, S.B., Jónsson, J.E., Krauss, S., Wong, S., Wan, X., **Akter, S.**, Sreevatsan, S., Trovão, N.S., Nutter, F.B., Runstadler, J.A., Hill, N.J., 2022. Global dissemination of Influenza A virus is driven by wild bird migration through arctic and subarctic zones. Mol. Ecol. https://doi.org/10.1111/mec.16738
6. **Staff Scientist (Mycobacterium tuberculosis):** I have conducted multiple single-cell RNA-seq projects investigating immune response and factors contributing to Mycobacterium tuberculosis. These studies contribute toward understanding and characterizing the transcriptional parameters at a single-cell depth in mouse and non-human primate models due to the infection. The findings of these studies can improve the fundamental understanding of the TB immunology relevant for testing of TB vaccines and therapeutics.
    a. Das S, Chauhan KS, Ahmed M, **Akter S**, Lu L, Colonna M, Khader SA. Lung type 3 innate lymphoid cells respond early following Mycobacterium tuberculosis infection. mBio. 2024 Apr 10;15(4):e0329923. doi: 10.1128/mbio.03299-23. Epub 2024 Feb 26. https://doi.org/10.1128/mbio.03299-23
    b. Chauhan KS, Dunlap MD, **Akter S.**, Gupta A, Ahmed M, Rosa BA, Dela Peña NB, Mitreva M, Khader SA. NF-κB signaling deficiency in CD11c-expressing phagocytes mediates early inflammatory responses and enhances Mycobacterium tuberculosis control. J Infect Dis. 2024 Aug 16:jiae060. https://doi.org/10.1093/infdis/jiae060
    c. Swanson, R. V., Gupta, A., Foreman, T.W., Lu, L., Choreno-Parra, J.A., Mbandi, S.K., Rosa, B.A., **Akter, S.**, Das, S., Ahmed, M., Garcia-Hernandez, M. de la L., Singh, D.K., Esaulova, E., Artyomov, M.N., Gommerman, J., Mehra, S., Zuniga, J., Mitreva, M., Scriba, T.J., Rangel-Moreno, J., Kaushal, D., Khader, S.A., 2023. Antigen-specific B cells direct T follicular- like helper cells into lymphoid follicles to mediate Mycobacterium tuberculosis control. Nat. Immunol. https://doi.org/10.1038/s41590-023-01476-3
    d. Bucşan, A.N., Veatch, A., Singh, D.K., **Akter, S.**, Golden, N.A., Kirkpatrick, M., Threeton, B., Moodley, C., Ahmed, M., Doyle, L.A., Russell-Lodrigue, K., Norton, E.B., Didier, P.J., Roy, C.J., Abramovitch, R.B., Mehra, S., Khader, S.A., Kaushal, D., 2022. Response to Hypoxia and the Ensuing Dysregulation of Inflammation Impacts Mycobacterium Tuberculosis Pathogenicity. Am. J. Respir. Crit. Care Med. https://doi.org/10.1164/rccm.202112-2747OC

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