

Badri ADHIKARI

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🌐 <https://badriadhikari.com>

Employment

2023 – present Associate Professor of Computer Science, University of Missouri-St. Louis
2017 – 2023 Assistant Professor of Computer Science, University of Missouri-St. Louis
2012 – 2017 Graduate Research Assistant, University of Missouri-Columbia
2015 Visiting Instructor, Westminster College, Fulton, MO
2011 Adjunct Lecturer, Advanced College of Engineering, Nepal
2011 Adjunct Lecturer, Kathford College of Engineering, Nepal
2011 Senior Software Engineer, Yomari Information Services, Nepal
2009 – 2011 Software Engineer, VeriskHealth Analytics Inc., Nepal

Education

2017/07 PhD, Computer Science, University of Missouri-Columbia, MO
2009/05 B.E., Computer Engineering, Tribhuvan University, Nepal

Research interests

Explainable AI (XAI), AI in education, and health informatics.

Select grants

2024 \$100,000, CooperVision, “Using Deep Neural Networks to Predict Success in Orthokeratology Lens Fitting,” Role: Co-PI
2021 \$12,150, UMSL Research Award, “Explainable Deep Learning for Protein Structure Prediction”, Role: PI
2020 \$163,535, National Science Foundation (NSF) CISE, “CRII: III: Deep Learning Methods for Protein Inter-residue Distance Prediction”, Role: Principal Investigator (PI)
2020 \$256,496, SPEC SENSORS LLC (National Aeronautics and Space Administration (NASA) STTR), “STTR Phase 1: Autonomous Environmental Monitoring and Management Platform for Remote Habitats”, Role: Co-PI
2019 \$6,450, UMSL Research Award, “Protein Structure Scoring using Deep Learning”, Role: PI
2018 \$5,415, UMSL Research Award, “Open source deep learning Python framework for protein contact prediction”, Role: PI

Courses taught

1. Interpretable Machine Learning (2023S - present)
2. Data Visualization (2022F - present)
3. Artificial Intelligence (2018F - present)
4. Deep Learning (2019S - present)
5. Programming & Data Structures (2015S and 2018S)
6. Advanced Data Structures & Algorithms (2017F and 2020F)

Professional memberships & activities

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| 2022 | University Ambassador, NVIDIA Deep Learning Institute |
| 2022 | Treasurer, IEEE St. Louis Section |
| 2019 - present | Member at International Society for Computational Biology (ISCB) |
| 2019 - present | Senior Member, IEEE |
| 2020 – 2023 | Program Committee Member for International Conference on Deep Learning Theory and Applications (DeLTA) |
| 2019 – present | Reviewer for various NSF proposal review panels |
| 2018 – 2022 | Editorial board member for Computational Biology and Bioinformatics, Science Publishing Group |
| 2018 – 2022 | Reviewer for PeerJ and BioData Mining |
| 2015 – present | Reviewer for peer-reviewed journals: PloS One, Bioinformatics, Interdisciplinary Sciences: Computational Life Sciences, IEEE/ACM Transactions on Computational Biology and Bioinformatics, and Computational and Structural Biotechnology, Nature Scientific Reports |

Academic awards/honors

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| 2024 | Outstanding Teaching Award, Computer Science Department, University of Missouri-St. Louis. |
| 2022 | Outstanding Research Award, Computer Science Department, University of Missouri-St. Louis. |
| 2018 | Received scholarship for participating in “Faculty Success Program” in Summer 2018. Awarded by University of Missouri System. Award worth of \$3,950. |
| 2015 | First place in 12th annual MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference “Oral Presentation Student Award” (one of the three first place awards), Little Rock, AR. Received \$300 as award. |
| 2013 | First place in Annual Programming Contest organized by Computer Science Graduate Student Council at University of Missouri-Columbia. Received \$400 award. |
| 2009 | Second place in KUCC Inter-University Software Competition organized by Kathmandu University, Nepal. Received NRs. 15,000 (\$150) as award. |
| 2009 | College Batch Topper in the class of 35 students in Advanced College of Engineering and Management, Tribhuvan University. Awarded tuition waiver for 6 semesters during bachelor’s degree. |

Publications:

- [1] Kate Arendes, Shea Kerkhoff, and Badri Adhikari. “Engaging Students to Learn Coding in the AI Era with Emphasis on the Process”. In: *Edukasiana: Jurnal Inovasi Pendidikan* 3.2 (2024), pp. 257–268.
- [2] Badri Adhikari. “Thinking Beyond Chatbots’ Threat to Education: Visualizations to Elucidate the Writing or Coding Process”. In: *Education Sciences* 13.9 (2023).
- [3] Bishal Shrestha et al. “Adversarial sample generation and training using geometric masks for accurate and resilient license plate character recognition”. In: *arXiv preprint arXiv:2311.12857* (2023).
- [4] Bikash Shrestha and Badri Adhikari. “Scoring protein sequence alignments using deep Learning”. In: *Bioinformatics* (Apr. 2022). ISSN: 1367-4803.
- [5] Badri Adhikari et al. “DISTEVAL: A web server for evaluating predicted protein distances”. In: *BMC bioinformatics* 22.1 (2021), pp. 1–9.
- [6] Jacob Barger and Badri Adhikari. “New Labeling Methods for Deep Learning Real-valued Inter-residue Distance Prediction”. In: *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (2021).
- [7] Subash C Pakhrin et al. “Deep learning-based advances in protein structure prediction”. In: *International Journal of Molecular Sciences* 22.11 (2021), p. 5553.
- [8] Badri Adhikari. “A fully open-source framework for deep learning protein real-valued distances”. In: *Scientific reports* 10.1 (2020), pp. 1–10.
- [9] Badri Adhikari. “DEEPCON: protein contact prediction using dilated convolutional neural networks with dropout”. In: *Bioinformatics* 36.2 (2020), pp. 470–477.
- [10] Badri Adhikari. “REALDIST: Real-valued protein distance prediction”. In: *bioRxiv* (2020).
- [11] Jie Hou et al. “SAXSDom: Modeling multidomain protein structures using small-angle X-ray scattering data”. In: *Proteins: Structure, Function, and Bioinformatics* 88.6 (2020), pp. 775–787.
- [12] Robert H Paul et al. “Machine learning classification of neurocognitive performance in children with perinatal HIV initiating de novo antiretroviral therapy”. In: *AIDS (London, England)* 34.5 (2020), p. 737.
- [13] Tianqi Wu et al. “Analysis of several key factors influencing deep learning-based inter-residue contact prediction”. In: *Bioinformatics* 36.4 (2020), pp. 1091–1098.
- [14] Cristian Olaya et al. “Identification and localization of Tospovirus genus-wide conserved residues in 3D models of the nucleocapsid and the silencing suppressor proteins”. In: *Virology journal* 16.1 (2019), p. 7.
- [15] Badri Adhikari and Jianlin Cheng. “CONFOLD2: improved contact-driven ab initio protein structure modeling”. In: *BMC bioinformatics* 19.1 (2018), pp. 1–5.
- [16] Badri Adhikari, Jie Hou, and Jianlin Cheng. “DNCON2: improved protein contact prediction using two-level deep convolutional neural networks”. In: *Bioinformatics* 34.9 (2018), pp. 1466–1472.
- [17] Badri Adhikari, Jie Hou, and Jianlin Cheng. “Protein contact prediction by integrating deep multiple sequence alignments, coevolution and machine learning”. In: *Proteins: Structure, Function, and Bioinformatics* 86 (2018), pp. 84–96.
- [18] Barbara Gandolfi et al. “A Novel Variant in CMAH Is Associated with Blood Type AB in Ragdoll Cats”. In: *PloS one* 13.3 (2018), e0194471.
- [19] Jie Hou, Badri Adhikari, and Jianlin Cheng. “DeepSF: deep convolutional neural network for mapping protein sequences to folds”. In: *Bioinformatics* 34.8 (2018), pp. 1295–1303.

- [20] Chen Keasar et al. “An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12”. In: *Scientific reports* 8.1 (2018), pp. 1–18.
- [21] Badri Adhikari and Jianlin Cheng. “Improved protein structure reconstruction using secondary structures, contacts at higher distance thresholds, and non-contacts”. In: *BMC bioinformatics* 18.1 (2017), pp. 1–13.
- [22] Renzhi Cao et al. “QAcon: single model quality assessment using protein structural and contact information with machine learning techniques”. In: *Bioinformatics* 33.4 (2017), pp. 586–588.
- [23] Haiou Li et al. “Deep learning methods for protein torsion angle prediction”. In: *BMC bioinformatics* 18.1 (2017), pp. 1–13.
- [24] Badri Adhikari, Tuan Trieu, and Jianlin Cheng. “Chromosome3D: reconstructing three-dimensional chromosomal structures from Hi-C interaction frequency data using distance geometry simulated annealing”. In: *BMC genomics* 17.1 (2016), pp. 1–9.
- [25] Badri Adhikari et al. “ConEVA: a toolbox for comprehensive assessment of protein contacts”. In: *BMC bioinformatics* 17.1 (2016), pp. 1–12.
- [26] Debswapna Bhattacharya et al. “FRAGSION: ultra-fast protein fragment library generation by IOHMM sampling”. In: *Bioinformatics* 32.13 (2016), pp. 2059–2061.
- [27] Renzhi Cao et al. “Massive integration of diverse protein quality assessment methods to improve template based modeling in CASP11”. In: *Proteins: Structure, Function, and Bioinformatics* 84 (2016), pp. 247–259.
- [28] Barbara Gandolfi et al. “A dominant TRPV4 variant underlies osteochondrodysplasia in Scottish fold cats”. In: *Osteoarthritis and cartilage* 24.8 (2016), pp. 1441–1450.
- [29] C Olaya et al. “Predictive models for tospoviral proteins involved in virion assembly and host defense suppression”. In: *PHYTOPATHOLOGY*. Vol. 106. 12. 2016, pp. 203–203.
- [30] Badri Adhikari et al. “CONFOLD: residue-residue contact-guided ab initio protein folding”. In: *Proteins: Structure, Function, and Bioinformatics* 83.8 (2015), pp. 1436–1449.
- [31] Renzhi Cao et al. “Large-scale model quality assessment for improving protein tertiary structure prediction”. In: *Bioinformatics* 31.12 (2015), pp. i116–i123.
- [32] Jilong Li, Badri Adhikari, and Jianlin Cheng. “An improved integration of template-based and template-free protein structure modeling methods and its assessment in CASP11”. In: *Protein and peptide letters* 22.7 (2015), pp. 586–593.

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