

Badri ADHIKARI

Assistant Professor of Computer Science
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🌐 <https://badriadhikari.github.io/>

Employment

2017 – present 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 (ACEM), Nepal

Research interests

Deep learning and bioinformatics.

Courses taught

2018 – present Artificial Intelligence
2018 – present Deep Learning
2017 – present Advanced Data Structures and Algorithms
2018 Programming and Data Structures (C++ programming)
2015 Data Structures and Algorithms

Select services

2019 – present NSF reviewer
2018 – present Editorial board member for Computational Biology and Bioinformatics, Science Publishing Group
2015 – present Reviewer for PloS One, Bioinformatics, Interdisciplinary Sciences: Computational Life Sciences, IEEE/ACM Transactions on Computational Biology and Bioinformatics, and Computational and Structural Biotechnology, Nature Scientific Reports, PeerJ, and BioData Mining

Select grants and awards

- 2020 \$163,535, National Science Foundation (NSF) CISE, “CRII: III: Deep Learning Methods for Protein Inter-residue Distance Prediction”
- 2019 \$6,450, UMSL Research Award, “Protein Structure Scoring using Deep Learning”
- 2018 \$5,415, UMSL Research Award, “Open source deep learning Python framework for protein contact prediction”

Select publications

1. Adhikari, B. DEEPCON: protein contact prediction using dilated convolutional neural networks with dropout. *Bioinformatics* **36**, 470–477 (2020).
2. Adhikari, B., Hou, J. & Cheng, J. DNCON2: improved protein contact prediction using two-level deep convolutional neural networks. *Bioinformatics* **34**, 1466–1472 (2018).
3. Adhikari, B., Hou, J. & Cheng, J. Protein contact prediction by integrating deep multiple sequence alignments, coevolution and machine learning. *Proteins: Structure, Function, and Bioinformatics* **86**, 84–96 (2018).
4. Adhikari, B. & Cheng, J. Improved protein structure reconstruction using secondary structures, contacts at higher distance thresholds, and non-contacts. *BMC bioinformatics* **18**, 380 (2017).
5. Adhikari, B., Nowotny, J., Bhattacharya, D., Hou, J. & Cheng, J. ConEVA: a toolbox for comprehensive assessment of protein contacts. *BMC bioinformatics* **17**, 1–12 (2016).
6. Adhikari, B., Trieu, T. & Cheng, J. Chromosome3D: reconstructing three-dimensional chromosomal structures from Hi-C interaction frequency data using distance geometry simulated annealing. *BMC genomics* **17**, 886 (2016).
7. Adhikari, B., Bhattacharya, D., Cao, R. & Cheng, J. CONFOLD: residue-residue contact-guided ab initio protein folding. *Proteins: Structure, Function, and Bioinformatics* **83**, 1436–1449 (2015).

Last updated: July 3, 2020