Ishwor Thapa

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Education

Doctor of Philosophy, Biomedical Informatics, University of Nebraska at Omaha, 2025.

Thesis: *Democratizing design and implementation of agent-based modeling in biomedicine*

Advisor: Dr. Dario Ghersi, M.D., Ph.D.

Master of Science, Computer Science, University of Nebraska at Omaha, 2009.

Thesis: *Identifying and assessing the impact of refactoring by mining version repositories.*

Advisor: Dr. Harvey Siy, Ph.D.

Bachelor of Engineering, Computer Engineering, Tribhuvan University, 2005.

Experience

Software Application Developer at Bioinformatics Core Facility   10/2009 - till date

School of Interdisciplinary Informatics, College of IS&T, University of Nebraska at Omaha, NE

▷ Delivered core-related services to biomedical researchers at various institutions to analyze biomedical data and understand molecular mechanisms underlying different biological phenomena.

▷ Managed servers by installing/upgrading/configuring a wide range of bioinformatics software tools.

▷ Collaborated with different researchers to run and customize bioinformatics pipelines for omics-based analysis.

▷ Assisted both graduate and undergraduate students in the BMI and BIOI programs with their research and capstone projects and co-authored research papers.

▷ Engaged in recruitment and outreach activities, including mentoring in the high school internship program and delivering training workshops for high school teachers organized by the College of IS&T.

▷ Engaged in grant writing, manuscript preparation, and participation in international conferences.

Research Collaborator   04/2025 - till date

Department of Urology, Mayo Clinic, Rochester, MN

Graduate Assistant   01/2009 - 05/2009

Department of Computer Science, University of Nebraska at Omaha, NE

Student Worker: Java Web Application Developer   03/2008 - 01/2009

Mathbio Research Group, Department of Mathematics, University of Nebraska at Omaha, NE

Software Developer   01/2006 - 08/2007

Sambad project, Madan Puraskar Pustakalaya, Nepal

Teaching/Mentoring Experience

1. Designed and developed a course module on Python scripting for data visualization.

2. Created hands-on exercises for bioinformatics modules covering: (a) high-throughput sequencing workflows using Galaxy, (b)structural bioinformatics, and (c) data visualization.

3. Assisted in workshop activities involving K–12 teachers and students from other colleges in Nebraska.

4. Organized and supervised bioinformatics workshops and summer programs, mentoring both high school students from Nebraska and international partner institutions.

Grants and Awards

1. Key Personnel, Bioinformatics analysis of EVs RNA cargo, *Mayo Clinic*, 12/15/24-12/14/26.

2. Key Personnel, Data analysis in cancer informatics, *Mayo Foundation for Medical Education and Research*, 4/1/23-10/1/24.

3. Key Personnel, New data analytics approaches, *Mayo Clinic*, 5/1/21-4/30/22.

4. Technical Administrator, E-PACERR: Enhancing Professionalism, Advocacy and Capacity for Excellence in Responsible Bioinformatics Research, *NIH*, 4/1/21-3/31/24.

Technical Skills

Programming: R, Python, Perl, Java, Matlab, C and C++.

Systems Administration: Linux (Debian/RPM), Windows Server

Infrastructure & Cloud: HPC (Slurm), GCP, Azure, AWS, Docker

Operating Systems: Linux (Debian/RPM), Mac OS, Microsoft Windows.

Bioinformatics Tools

Genomics & Variant Calling: Local/global aligners, Bowtie2, BWA, SAMtools, BEDtools, FreeBayes, GATK

Transcriptomics: STAR, DESeq2, HTSeq, EdgeR, featureCounts, Seurat

Epigenomics: ATAC-seq, DNA methylation, ChIP-seq

Proteomics: MaxQuant, Proteome Discoverer, Mascot, EBI PRIDE

Microbiome & Metagenomics: QIIME 2, DADA2, MetaPhlAn, HUMAnN

Structural Biology: ChimeraX

Visualization, Pipelines & Workflow: Tablet, IGV, Cytoscape, Snakemake, Nextflow, Galaxy

Service

1. Member of International Society for Extracellular Vesicles

2. Previously a member of The Maverick Club of Bioinformatics at UNO

3. Reviewed papers for BMC Bioinformatics (BioMed Central), Journal of Computational Biology (Mary Ann Liebert), ISMB conferences, and BioMed Research International (Hindawi Publications).

First author publications

1. I. Thapa, Y. Kim, F. Lucien, and H. Ali, "A knowledge graph model for analyzing micrornas in extracellular vesicles data," in *Proceedings of the 14th International Conference on Complex Networks and their Applications*, 2025

2. I. Thapa, Y. Kim, F. Lucien, and H. Ali, "Reproducible gating for high-resolution flow cytometric characterization of extracellular vesicles in next-generation biomarker studies," in *Proceedings of the 18th International Joint Conference on Biomedical Engineering Systems and Technologies - BIOSIGNALS*, pp. 1020–1027, INSTICC, SciTePress, 2025

3. I. Thapa and D. Ghersi, "Modeling preferential attraction to infected hosts in vector-borne diseases," *Frontiers in Public Health*, vol. 11, p. 1276029, 2023

4. I. Thapa and H. Ali, "A multiomics graph database system for biological data integration and cancer informatics," *Journal of Computational Biology*, vol. 28, no. 2, pp. 209–219, 2021

5. I. Thapa and H. Ali, "A new graph database system for multi-omics data integration and mining complex biological information," in *Computational Advances in Bio and Medical Sciences*, Springer, 2020

6. I. Thapa, H. S. Fox, and D. R. Bastola, "Transcriptome analysis of hiv-1 virus in understanding the effect of antiretroviral drugs (cart) and methamphetamine on the virus," in *Proceedings of the 2015 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pp. 962–968, IEEE, 2015

7. I. Thapa, H. S. Fox, and D. Bastola, "Coexpression network analysis of mirna-142 overexpression in neuronal cells," *BioMed research international*, vol. 2015, 2015

8. I. Thapa, S. Bhowmick, and D. R. Bastola, "A comparison between hierarchical clustering and community detection method in the collection of gene targets for molecular identification of pathogenic fungi," in *Proceedings of the 2012 IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW)*, pp. 756–761, IEEE, 2012

9. I. Thapa and H. Siy, "Assessing the impact of refactoring activities on the jhotdraw project," in *Proceedings of the 2010 ACM Symposium on Applied Computing*, pp. 2369–2370, ACM, 2010

10. I. Thapa, *Identifying and assessing the impact of refactoring by mining version repositories*. University of Nebraska at Omaha, 2009

Other Publications

11. S. Kim, I. Thapa, and H. Ali, "A novel computational approach for the mining of signature pathways using species co-occurrence networks in gut microbiomes," *BMC microbiology*, vol. 24, no. Suppl 1, p. 490, 2024

12. C. J. Pecka, I. Thapa, A. B. Singh, and D. Bastola, "A computational approach to demonstrate the control of gene expression via chromosomal access in colorectal cancer," *BioMedInformatics*, vol. 4, no. 3, pp. 1822–1834, 2024

13. S. Kim, I. Thapa, and H. H. Ali, "A robust network model for studying microbiomes in precision agriculture applications," in *International Conference on Computational Science*, pp. 58–71, Springer, 2024

14. R. Ahmad, B. Kumar, I. Thapa, G. A. Talmon, J. Salomon, A. E. Ramer-Tait, D. K. Bastola, P. Dhawan, and A. B. Singh, "Loss of claudin-3 expression increases colitis risk by promoting gut dysbiosis," *Gut Microbes*, vol. 15, no. 2, p. 2282789, 2023

15. R. Ahmad, B. Kumar, I. Thapa, R. L. Tamang, S. K. Yadav, M. K. Washington, G. A. Talmon, S. Y. Alan, D. K. Bastola, P. Dhawan, *et al.*, "Claudin-2 protects against colitis-associated cancer by promoting colitis-associated mucosal healing," *The Journal of Clinical Investigation*, vol. 133, no. 23, 2023

16. M. Beaver, D. Noe, I. Thapa, H. Ali, J. Snowden, T. Kielian, and G. L. Skar, "Bacteria commonly associated with central nervous system catheter infections elicit distinct csf proteome signatures," *Frontiers in Neurology*, vol. 14, p. 1102356, 2023

17. R. Lama Tamang, B. Kumar, S. M. Patel, I. Thapa, A. Ahmad, V. Kumar, R. Ahmad, D. F. Becker, D. Bastola, P. Dhawan, *et al.*, "Pyrroline-5-carboxylate reductase-2 promotes colorectal carcinogenesis by modulating microtubule-associated serine/threonine kinase-like/wnt/β-catenin signaling," *Cells*, vol. 12, no. 14, p. 1883, 2023

18. F. Clark, A. Gil, I. Thapa, N. Aslan, D. Ghersi, and L. K. Selin, "Cross-reactivity influences changes in human influenza a virus and epstein barr virus specific cd8 memory t cell receptor alpha and beta repertoires between young and old," *Frontiers in Immunology*, vol. 13, p. 1011935, 2023

19. Y. Kim, E. Van Der Pol, A. Arafa, I. Thapa, C. J. Britton, J. Kosti, S. Song, V. B. Joshi, R. M. Erickson, H. Ali, *et al.*, "Calibration and standardization of extracellular vesicle measurements by flow cytometry for translational prostate cancer research," *Nanoscale*, vol. 14, no. 27, pp. 9781–9795, 2022

20. F. Lucien, Y. Kim, J. Qian, J. J. Orme, H. Zhang, A. Arafa, F. Abraha, I. Thapa, E. J. Tryggestad, W. S. Harmsen, *et al.*, "Tumor-derived extracellular vesicles predict clinical outcomes in oligometastatic prostate cancer and suppress antitumor immunity," *International Journal of Radiation Oncology* Biology* Physics*, vol. 114, no. 4, pp. 725–737, 2022

21. S. Gowrikumar, M. Primeaux, K. Pravoverov, C. Wu, B. C. Szeglin, C.-E. G. Sauve, I. Thapa, D. Bastola, X. S. Chen, J. J. Smith, *et al.*, "A claudin-based molecular signature identifies high-risk, chemoresistant colorectal cancer patients," *Cells*, vol. 10, no. 9, p. 2211, 2021

22. N. Perumal, R. K. Kanchan, D. Doss, N. Bastola, P. Atri, R. Chirravuri-Venkata, I. Thapa, R. Vengoji, S. K. Maurya, D. Klinkebiel, *et al.*, "Mir-212-3p functions as a tumor suppressor gene in group 3 medulloblastoma via targeting nuclear factor i/b (nfib)," *Acta neuropathologica communications*, vol. 9, pp. 1–19, 2021

23. M. Beaver, D. Lagundzin, I. Thapa, J. Lee, H. Ali, T. Kielian, and G. L. Skar, "Cutibacterium acnes central nervous system catheter infection induces long-term changes in the cerebrospinal fluid proteome," *Infection and immunity*, vol. 89, no. 4, pp. e00531–20, 2021

24. R. K. Kanchan, N. Perumal, P. Atri, R. Chirravuri Venkata, I. Thapa, D. Klinkebiel, A. M. Donson, D. Perry, M. Punsoni, G. Talmon, *et al.*, "Mir-1253 exerts tumor suppressive effects in medulloblastoma via inhibition of cdk6 and cd276 (b7-h3)," *Brain Pathology*, 2020

25. M. L. Hale, I. Thapa, and D. Ghersi, "Funset: an open-source software and web server for performing and displaying gene ontology enrichment analysis," *BMC Bioinformatics*, vol. 20, no. 1, p. 359, 2019

26. L. Zhang, I. Thapa, C. Haas, and D. Bastola, "Multiplatform biomarker identification using a data-driven approach enables single-sample classification," *BMC bioinformatics*, vol. 20, no. 1, p. 601, 2019

27. S. Kim, I. Thapa, L. Zhang, and H. Ali, "A novel graph theoretical approach for modeling microbiomes and inferring microbial ecological relationships," *BMC genomics*, vol. 20, no. 11, pp. 1–13, 2019

28. S. Chugh, S. Barkeer, S. Rachagani, R. K. Nimmakayala, N. Perumal, R. Pothuraju, P. Atri, S. Mahapatra, I. Thapa, G. A. Talmon, *et al.*, "Disruption of c1galt1 gene promotes development and metastasis of pancreatic adenocarcinomas in mice," *Gastroenterology*, 2018

29. C. Thompson, S. Kumar, D. Ghersi, R. Chirravuri, I. Thapa, L. Smith, and S. Batra, "Analysis of clinical significance of muc4 isoforms in pancreatic cancer patients using tcga rna-seq dataset," in *PANCREAS*, vol. 46, pp. 1440–1440, LIPPINCOTT WILLIAMS & WILKINS TWO COMMERCE SQ, 2001 MARKET ST, PHILADELPHIA, PA 19103 USA, 2017

30. S. Kim, I. Thapa, G. Lu, L. Zhu, and H. H. Ali, "A systems biology approach for modeling microbiomes using split graphs," in *Proceedings of the 2017 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pp. 2062–2068, IEEE, 2017

31. S. Sharma, K. Karri, I. Thapa, D. Bastola, and D. Ghersi, "Identifying enriched drug fragments as possible candidates for metabolic engineering," *BMC Medical Genomics*, vol. 9, no. 2, p. 46, 2016

32. O. Bonham-Carter, I. Thapa, S. From, and D. Bastola, "A study of bias and increasing organismal complexity from their post-translational modifications and reaction site interplays," *Briefings in bioinformatics*, p. bbv111, 2016

33. J. K. Banwait, S. P. Dougherty, I. Thapa, and D. K. Bastola, "Guilt-by association approach to identify novel human aging-related genes using protein domains," in *Proceedings of the 2015 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pp. 301–304, IEEE, 2015

34. A. Balasubramanya, I. Thapa, D. Bastola, and D. Ghersi, "A novel approach to identify shared fragments in drugs and natural products," in *Proceedings of the 2015 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pp. 575–580, IEEE, 2015

35. J. Warnke-Sommer, I. Thapa, and H. Ali, "Next generation sequence assembler mis-assembly of phage genomes with terminal redundancy," in *Proceedings of the 2015 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pp. 1102–1108, IEEE, 2015

36. S. V. Yelamanchili, B. Morsey, E. B. Harrison, D. Rennard, K. Emanuel, I. Thapa, D. Bastola, and H. Fox, "The evolutionary young mir-1290 favors mitotic exit and differentiation of human neural progenitors through altering the cell cycle proteins," *Cell death & disease*, vol. 5, no. 1, p. e982, 2015

37. P. C. Iwen, I. Thapa, and D. Bastola, "Review of methods for the identification of zygomycetes with an emphasis on advances in molecular diagnostics," *Laboratory Medicine*, vol. 42, no. 5, pp. 260–266, 2015

38. S. Charntikov, S. T. Pittenger, I. Thapa, D. R. Bastola, R. A. Bevins, and G. Pendyala, "Ibudilast reverses the decrease in the synaptic signaling protein phosphatidylethanolamine-binding protein 1 (pebp1) produced by chronic methamphetamine intake in rats," *Drug & Alcohol Dependence*, vol. 152, pp. 15–23, 2015

39. O. Bonham-Carter, I. Thapa, and D. Bastola, "Evidence of post translational modification bias extracted from the trna and corresponding amino acid interplay across a set of diverse organisms," in *Proceedings of the 5th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, pp. 774–781, ACM, 2014

40. K. D. Cooper, I. Thapa, C. Cortes, Z. Eriksen, D. R. Bastola, and H. Ali, "On mining biological signals using correlation networks," 2013

41. K. A. Bryant, T. C. Van Schooneveld, I. Thapa, D. Bastola, L. O. Williams, T. J. Safranek, S. H. Hinrichs, M. E. Rupp, and P. D. Fey, "Kpc-4 is encoded within a truncated tn4401 in an incl/m plasmid, pne1280, isolated from enterobacter cloacae and serratia marcescens," *Antimicrobial agents and chemotherapy*, vol. 57, no. 1, pp. 37–41, 2013

42. R. Khazanchi, K. Dempsey, I. Thapa, and H. Ali, "On identifying and analyzing significant nodes in protein-protein interaction networks," in *Proceedings of the 2013 IEEE 13th International Conference on Data Mining Workshops (ICDMW)*, pp. 343–348, IEEE, 2013

43. K. Dempsey, I. Thapa, D. Bastola, and H. Ali, "Functional identification in correlation networks using gene ontology edge annotation," *International journal of computational biology and drug design*, vol. 5, no. 3-4, pp. 222–244, 2012

44. D. R. Bastola, S. McGrath, S. Bhowmick, and I. Thapa, "A comparison of computational approaches in the molecular identification of pathogenic organisms," in *Proceedings of the 2012 IEEE Second International Conference on Healthcare Informatics, Imaging and Systems Biology (HISB)*, pp. 73–73, IEEE, 2012

45. M. Lyon, M. V. Wilson, K. A. Rouhier, D. J. Symonsbergen, K. Bastola, I. Thapa, A. E. Holmes, S. M. Sikich, and A. Jackson, "Image analysis of detechip®–a molecular sensing array," in *Advances in Computer Science, Engineering & Applications*, pp. 145–158, Springer, 2012

46. T. Helikar, B. Kowal, A. Madrahimov, M. Shrestha, J. Pedersen, K. Limbu, I. Thapa, T. Rowley, R. Satalkar, N. Kochi, *et al.*, "Bio-logic builder: a non-technical tool for building dynamical, qualitative models," *PloS one*, vol. 7, no. 10, p. e46417, 2012

47. K. Dempsey, I. Thapa, D. Bastola, and H. Ali, "Identifying modular function via edge annotation in gene correlation networks using gene ontology search," in *Proceedings of the 2011 IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW)*, pp. 255–261, IEEE, 2011

48. S. Dhakhwa, P. A. Hall, G. B. Ghimire, P. Manandhar, and I. Thapa, "Sambad–computer interfaces for non-literates," in *International Conference on Human-Computer Interaction*, pp. 721–730, Springer, Berlin, Heidelberg, 2007