

BIOGRAPHICAL SKETCH

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NAME: Joshi, Trupti Ph.D

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

POSITION TITLE: Professor & Senior Associate Dean of Informatics and Population Analytics

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
B. J. Medical College, Pune, India	Bachelor of Medicine, Bachelor of Surgery (M.B.B.S.)	01/2000	Medicine and Surgery
Bioinformatics Center, University of Pune, India	Advanced Diploma in Bioinformatics (A.D.B.)	08/2001	Bioinformatics
UT-ORNL Graduate School of Genome Science & Technology, University of Tennessee, Knoxville	Master of Science, Life Sciences (M.S.)	07/2003	Bioinformatics
MU Informatics Institute, University of Missouri, Columbia	Doctor of Philosophy, Informatics (Ph.D.)	05/2013	Bioinformatics

A. Personal Statement

I am the Senior Associate Dean for Informatics & Population Analytics with the Joan C. Edwards School of Medicine at Marshall University and a Professor within the Department of Biomedical Sciences. I also currently have an Adjunct faculty appointment with Department of Biomedical Informatics, Biostatistics and Medical Epidemiology at University of Missouri, where I have previously held joint and core faculty appointments with the Institute for Informatics and Data science, Department of Computer Science and Department of Plant Science and Technology. My rigorous interdisciplinary training with degrees in both clinical medicine and bioinformatics, as well as broad based leadership experience and dedication to mentoring, I have the passion and motivation to seamlessly connect the biomedical, clinical and translational informatics domains at Marshall University. I have over 22+ years of experience working in academia, collaborations with multi-disciplinary researchers and several Industry partners. My expertise is in the areas of bioinformatics and its application to plants sciences, animal sciences, health informatics and biomedical fields. In my previous role at the University of Missouri, I developed a unique appreciation for the challenges faced by rural communities and the important value of collaborative research programs aimed at underserved communities and underutilized institutions.

In particular, my work leading and participating in multi-disciplinary teams has positioned me well to provide leadership and mentoring for the INBRE and COBRE programs amongst others. I am the Principal Investigator of the NIH-funded West Virginia IDeA Network of Biomedical Research Excellence (WV-INBRE), where I oversee the state-wide network composed primarily of new investigators and students at primarily undergraduate institutions (PUIs) across West Virginia (WV), with the focus on enhancing the education and training opportunities in biomedical research and fostering research growth in WV. Currently, I also lead the development

of Soybean Knowledge Base (SoyKB), a comprehensive web resource for bridging translational genomics and molecular breeding in soybeans and Knowledge Base Commons (KBCommons) universal framework for enabling similar capabilities for all organisms including plants and crops; animals and pets; human and diseases; and microbes and viruses. Over the past few decades, I have conducted research in many areas of computational biology and bioinformatics, including development of computational methodologies and data analysis pipelines using HPC and cloud based resources, multiomics data integration methods, machine learning and deep learning methods such as G2PDeep for biomarker identification, IMPRes algorithm for *in silico* hypothesis generation and application of translational bioinformatics tools and frameworks towards advances in precision medicine, precision agriculture, and genomic epidemiology including Covid. I have published more than 175 peer-reviewed publications in reputed peer-reviewed journals and conferences (h-Index: 52, i10-Index: 120 and over 13,418 citations according to Google Scholar) and co-developed several bioinformatics software. My research lab has expertise in high throughput multiomics analytics and data integration for bulk / single cell RNAseq transcriptomics, proteomics, metabolomics, epigenomics, and regulatory networks. We have developed several machine learning for biomarker identification, deep learning methods (G2PDeep and IRnet) for phenotype prediction, single cell based regulation prediction (CrossMP), computational methods for *in silico* hypothesis generation using pathways (IMPRes) and web-based multiomics data integration frameworks (KBCommons), many of which have been applied for biomedical research in cancers, cardiovascular, kidney diseases, eye diseases and are directly applicable and expandable for conducting research on cancer immunoprevention and treatments. Interdisciplinary training in informatics, data science and AI have been an integral part of my lab's focus for student and personnel development.

Ongoing and recently completed projects that I would like to highlight include:

5P20GM103434-25

Joshi (PI)

08/01/24 – 07/31/29

West Virginia IDeA Network of Biomedical Research Excellence (WV-INBRE)

2343815

Mittler (PI), Role: Co-PI

04/01/24-03/31/28

Rapid cell-to-cell and plant-to-plant responses to abiotic stress

2232889

Calyam (PI), Role: Co-PI

01/01/23 – 12/31/25

CICI: UCSS: Trusted Resource Allocation in Volunteer Edge-Cloud Computing Workflows

MU-SCIDRP

Whiting (PI)

05/01/2024 – 04/30/2025

Neuro-ophthalmic biomarkers in a canine model of amyotrophic lateral sclerosis

DE-SC0023142

Cahoon (PI), Role: Co-PI

09/01/22-09/30/27

B5: Bigger Better Brassicaceae Biofuels and Bioproducts

AOC23380006

Joshi (PI)

07/01/22-03/27/26

Bioinformatics and Data Science Infrastructure Development for Genomic Epidemiology

2110017

Mittler (PI), Role: Co-PI

06/01/21-05/31/26

RESEARCH-PGR: Developing novel strategies to enhance the tolerance of crops to a combination of drought and heat stress

Citations

1. Shuai Zeng, Duolin Wang, Juexin Wang, Dong Xu, Trupti Joshi. G2PDeep: a Deep-learning Based Webserver for Phenotype Prediction and Genome-Wide Association Study. *Nucleic Acids Research*, 2021. gkab407, <https://doi.org/10.1093/nar/gkab407>
2. Jing Zhou, Yuexu Jiang, Yue Huang, Qionglin Wang, Jussuf T. Kaifi, Eric T. Kimchi, Chiswili Yves Chabu, Zhenguo Liu, Trupti Joshi, Guangfu Li. Single-cell RNA sequencing to characterize the response of pancreatic cancer to anti-PD-1 immunotherapy. *Translational Oncology*. 2022 Jan;15(1):101262. doi: 10.1016/j.tranon.2021.101262.
3. Yuexu Jiang, Duolin Wang, Shuai Zeng, Manish Immadi, Yen On Chan, Jing Zhou, Dong Xu, Trupti Joshi. IRnet: Immunotherapy response prediction using pathway knowledge-informed graph neural network. *Journal of Advanced Research*. 2024 Aug 7: S2090-1232(24)00320-5. doi: 10.1016/j.jare.2024.07.036.
4. Lyu, Zhen, Sabin Dahal, Shuai Zeng, Juexin Wang, Dong Xu, and Trupti Joshi. 2024. "CrossMP: Enabling Cross-Modality Translation between Single-Cell RNA-Seq and Single-Cell ATAC-Seq through Web-Based Portal" *Genes* 15, no. 7: 882. <https://doi.org/10.3390/genes15070882>

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2025 – Present	Senior Associate Dean, Informatics & Population Analytics, Joan C. Edwards School of Medicine, Marshall University
2025 – Present	Professor, Department of Biomedical Sciences, Joan C. Edwards School of Medicine, Marshall University
2025 – Present	Adjunct Faculty, Department of Biomedical Informatics, Biostatistics and Medical Epidemiology, University of Missouri, Columbia
2024 – 2025	Associate Professor, Department of Biomedical Informatics, Biostatistics and Medical Epidemiology, University of Missouri, Columbia
2017 – 2024	Assistant Professor, Department of Biomedical Informatics, Biostatistics and Medical Epidemiology (earlier Health Management and Informatics), University of Missouri, Columbia
2015 – 2020	Director, Translational Bioinformatics, School of Medicine – Medical Research Office, University of Missouri, Columbia
2015 – 2017	Assistant Research Professor, Department of Molecular Microbiology and Immunology, University of Missouri, Columbia
2015 – Present	Adjunct Faculty, Department of Computer Science, University of Missouri, Columbia
2015 – Present	BioNEXUS Regional Bioinformatics Conference Planning Subcommittee Member.
2015 – 2015	Great Lakes Bioinformatics Conference (GLBIO) 2015 Program Committee Member.
2014 – 2025	Graduate Student Masters Committee, University of Missouri, Columbia.
2014 – 2025	Interdisciplinary Plant Group (IPG) Faculty, University of Missouri, Columbia.
2014 – 2025	Curriculum Committee Member, Informatics Institute, University of Missouri, Columbia.
2014 – Present	Doctoral Faculty, Informatics Institute, University of Missouri, Columbia.
2014 – 2025	Associate Director, Digital Biology Laboratory, University of Missouri, Columbia.
2013 – 2015	Assistant Research Professor, Department of Computer Science, University of Missouri, Columbia
2013 – 2025	Core Faculty MU Informatics Institute, University of Missouri, Columbia
2010 – 2013	Research Scientist and Lab Manager, Digital Biology Laboratory, University of Missouri, Columbia
2005 – 2010	Research Associate and Lab Manager, Digital Biology Laboratory, University of Missouri, Columbia

2005 – 2013	Reviewer for ISMB 2005, CSB 2005, and RECOMB 2013 Conferences.
2005 – Present	Member of International Society for Computational Biology.
2003 – 2005	Programmer/Analyst and Lab Manager, Digital Biology Laboratory, University of Missouri, Columbia
2003 – 2003	Bioinformatics Consultant, Ceres Inc.
2002 – 2003	Graduate Research Assistant, Oak Ridge National Laboratory
2002 – 2002	Scientific Operations Intern, Celera Genomics
2001 – 2002	Graduate Research Assistant, University of Tennessee-Knoxville
2001 – 2001	Bioinformatics Software Development, University of Pune, India
2000 – 2001	Resident Medical Intern, Ruby Hall Hospital and Y.C.M.Hospital, Pune, India

Honors

2023	Bond Life Science Center (LSC) 2023 Most Collaborative Faculty Recognition, Columbia, MO.
2016	College of Engineering “Special Academic Appointment Faculty”, MO Honor Award, Columbia, MO.
2013	First place in Biological Merit Poster Presentation for MCBIOS 2013 Conference, Columbia, MO.
2012	APBioNet Travel Grant for InCoB 2012 Conference, Bangkok, Thailand.
2012	Graduate Professional Council (GPC) Travel Award for APBC 2012 Conference, Columbia, MO.
2011	Informatics Day 2011 Poster Award, Columbia, MO.
2005	Travel Award for GO Annotation Camp, Stanford, CA.
2001	J. N. Tata Endowment Scholarship for higher education abroad, India.
2001	India Foundation Scholarship for higher education abroad, India.
2000	Bioinformatics Merit Scholarship, Department of Biotechnology, Government of India.
1994	Merit Rank Holder, Maharashtra State Higher Secondary Board Examination, Pune, India.

C. Contributions to Science

1. Many genome scale datasets are now generated in biomedical and biological experimental studies, but the datasets are largely complex and diverse, making it difficult to integrate data and draw inferences for validation and testing. This has made informatics an essential component of get a complete systems biology understanding of any organism. With my expertise and strong interdisciplinary collaborative research with faculty and researchers from plant science, animal science, biomedical and other domains over 18+ years, I have developed and contributed several cutting edge and innovative computational methodologies and data integration developments that have helped advance the science and the way genomics and translational systems biology studies are conducted in the biological and biomedical areas. The publications below highlight some of my interdisciplinary research spanning from studies in mouse models to human subjects and integrating transcriptomics and Chip-seq studies in understanding the underlying molecular mechanisms.
 - a. Khalyfa A, Marin JM, Sanz-Rubio D, Lyu Z, Joshi T, Gozal D. Multi-Omics Analysis of Circulating Exosomes in Adherent Long-Term Treated OSA Patients. *Int J Mol Sci.* 2023 Nov 8;24(22):16074. doi: 10.3390/ijms242216074.
 - b. Tarak Srivastava, Daniel P. Heruth, R. Scott Duncan, Mohammad H. Rezaiekhalthigh, Robert E. Garola, Lakshmi Priya, Jianping Zhou, Varun C. Boinpelly, Jan Novak, Mohammed Farhan Ali, Trupti Joshi, Uri S. Alon, Yuexu Jiang, Ellen T. McCarthy, Virginia J. Savin, Ram Sharma, Mark L. Johnson, and Mukut Sharma. Transcription factor β -catenin plays a key role in fluid flow shear stress mediated glomerular injury in solitary kidney. *Cells.* 2021 May 19;10(5):1253. doi: 10.3390/cells10051253.
 - c. Alexei Stuckel, Wei Zhang, Xu Zhang, Shuai Zeng, Urszula Dougherty, Reba Mustafi, Qiong Zhang, Elsa Perreand, Tripti Khare, Trupti Joshi, Diana West-Szymanski, Marc Bissonnette, Sharad Khare. Enhanced CXCR4 expression associates with increased gene body 5-hydroxymethylcytosine modification but not decreased promoter methylation in colorectal cancer. *Cancers (Basel).* 2020 Mar; 12(3): 539. doi: 10.3390/cancers12030539.
 - d. Majumder K, Wang J, Boftsi M, Fuller MS, Rede JE, Joshi T, Pintel DJ. Parvovirus minute virus of mice interacts with sites of cellular DNA damage to establish and amplify its lytic infection. *eLife.* 2018;7:e37750.

2. In addition to the contributions described above, over the years I have conducted active research and led several publications that have applied the informatics techniques towards advancing the plant science research and improvement in crop production. My contributions in the development of widely used Soybean Knowledge Base (SoyKB) web resource with more than 500+ registered users both domestic and international, has revolutionized the way genome sequence information and largescale resequencing data is being utilized along with other multi-omics datasets in the improvement of soybean molecular breeding. We have further expanded similar capabilities to other organisms via KBCommons framework. We have generated resequencing datasets for 1000+ soybean genomes and also developed a SNP and Indel analysis Pegasus workflow that utilizes HPC and cloud technology resources in collaboration with Cyverse, making the analysis and data sharing via SoyKB extremely fast and efficient. This is enabling researchers to easily generate and access datasets in the era of Big Data and leading to a vast repository of data being contributed to the public domain to advance science for generations to come.
 - a. Shuai Zeng, Zhen Lyu, Siva Ratna Kumari Nariseti, Dong Xu and Trupti Joshi. Knowledge Base Commons (KBCommons) v1.1: a universal framework for multi-omics data integration and biological discoveries. *BMC Genomics* 2019, 20(Suppl 11):947. doi.org/10.1186/s12864-019-6287-8.
 - b. Y. Jiang, D. Wang, D. Xu and T. Joshi. A Dynamic Programming Approach to Integrate Gene Expression Data and Network Information for Pathway Model Generation. *Bioinformatics*. 2019 Jun 6. pii: btz467. doi: 10.1093/bioinformatics/btz467.
 - c. Joshi T, Fitzpatrick MR, Chen S, Liu Y, Zhang H, Endacott RZ, Gaudiello EC, Stacey G, Nguyen HT, Xu D. Soybean Knowledge Base (SoyKB): A web resource for integration of soybean translational genomics and molecular breeding. *Nucleic Acids Research*. 2014. Jan;42(Database issue):D1245-52. doi: 10.1093/nar/gkt905.
 - d. Mary Galli, Arjun Khakhar, Zefu Lu, Zongliang Chen, Sidharth Sen, Trupti Joshi, Jennifer L. Nemhauser, Robert J. Schmitz, and Andrea Gallavotti. The DNA binding landscape of the maize auxin response factor family. *Nature Communications*. *Nature Communications*. 2018. Volume 9, Article number: 4526 (2018).
3. Biggest challenges faced by researchers and our collaborators is the lack of many robust, easy to use computational and informatics methods that can be used by students and scientists with non-informatics background in their everyday research. To ease this problem and provide a solution, I have co-developed several methodologies for gene function prediction and gene regulatory network analysis that can be applied in many different organisms. The publications below highlight some of my work in the areas mentioned above that have been widely utilized in plant and animal science domains.
 - a. Juexin Wang, Anjun Ma, Qin Ma, Dong Xu, Trupti Joshi. Inductive inference of gene regulatory network using supervised and semi-supervised graph neural networks. *Computational and Structural Biotechnology Journal*. Volume 18, 2020, Pages 3335-3343. <https://doi.org/10.1016/j.csbj.2020.10.022>
 - b. Shuai Zeng, Mária Škrabišová, Zhen Lyu, Yen On Chan, Kristin Bilyeu, and Trupti Joshi. SNPviz v2.0: A web-based tool for enhanced haplotype analysis using large scale resequencing datasets and discovery of phenotypes causative gene using allelic variations. 2020 IEEE International Conference on Bioinformatics and Biomedicine (BIBM) (2020): 1408-1415.
 - c. Sadia Akter, Dong Xu, Susan C. Nagel, John Bromfield, Katherine Pelch, Gilbert B. Wilshire and Trupti Joshi. Machine Learning Classifiers for Endometriosis Using Transcriptomics and Methyloomics Data. *Frontier Genetics*. 2019. doi: 10.3389/fgene.2019.00766.
 - d. Yang Liu, Duolin Wang, Fei He, Juexin Wang, Trupti Joshi, Dong Xu. Phenotype prediction and genome-wide association study using deep convolutional neural network of soybean. *Frontier Genetics*. 22 November 2019. <https://doi.org/10.3389/fgene.2019.01091>

Complete List of Published Work in My Bibliography:

<https://www.ncbi.nlm.nih.gov/myncbi/trupti.joshi.2/bibliography/public/>