

I. Vita

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AREA OF EXPERTISE / INTERESTS

Bioinformatics and Computational Biology: Highly successful track record of integrating biology and bigdata science with over 14 years' experience in bioinformatics, computational biology, and scientific programming. In-depth knowledge of bioinformatics data analysis tools and databases, information management, and integration to support diverse activities essential for organismal improvement and genomics-enabled studies.

Research: Data science; Next-generation sequencing (data analysis, alignment, assembly, annotation); Computational modeling of *-omics* bigdata; Systems biology, develop algorithms to study intra- and inter-species interaction networks (*e.g. host-pathogen interactions*), predict Gene Regulatory Networks; Metagenomics (*e.g. rhizosphere microbiome interacting with the host*); Computational genomics. Develop workflows to facilitate data mining; Develop and maintain scientific software / tools.

Computational skills: Unix/Linux shell scripting; Machine learning techniques (Support Vector Machines, Artificial Neural Networks); Statistical & mathematical modeling of biological data; Bayesian statistics; Develop algorithms combining similarity-search, Hidden Markov Models (HMMs) and Artificial Intelligence; Implementation as web-based software / databases / visualization tools using R, PERL, HTML, PHP and CGI-PERL. Hands-on experience in a range of bioinformatics tools/packages (BLAST, FASTA, InterProScan, Psi-Blast, BlastClust, CD-hit, HMM-Pfam, Gene Ontology *etc.*); Sequence analysis (homology search, pathway analysis, subcellular localization, PSSM, motif, domain search); Phylogenetics (MEGA, PHYLIP, ClustalW); Databases (NCBI, UniProt, KEGG, STRING, Pathguide, IntAct).

ACADEMIC APPOINTMENTS & PROFESSIONAL EXPERIENCE

- Assistant Professor (Bioinformatics), Utah State University (USU), Logan, Utah, USA [July 2017 - present]
- Director, Bioinformatics Facility, Center for Integrated BioSystems (CIB), Utah State University (USU), Logan, Utah, USA [July 2017 - present]
- Adjunct Assistant Professor, Computer Science, Utah State University (USU), Logan, Utah, USA [July 2017 - present]
- Director, High-Performance Computing | Bioinformatics Facility, Institute for Integrative Genome Biology (IIGB), Botany & Plant Sciences, University of California, Riverside (UCR), California, USA [July 2014 - May 2017].
- Faculty [Research Scientist (bioinformatics/metagenomics)], National Institute for Microbial Forensics & Food and Agricultural Biosecurity (NIMFFAB), Department of Biochemistry & Molecular Biology, Oklahoma State University (OSU), Stillwater, Oklahoma, USA [March 2011 - June 2014].
- Postdoctoral Research Fellow, Bioinformatics Lab, Plant Biology Division, The Samuel Roberts Noble Foundation, Ardmore, Oklahoma, USA [April 2007 - March 2011].

- Project Assistant, Bioinformatics Center, Institute of Microbial Technology (IMTECH-CSIR), Chandigarh, India [January 2005 - March 2007].
- Research Associate, CSK HP Agricultural University, Palampur, Himachal Pradesh, India [August 2001 - December 2004].
- Junior Research Fellow, CSK HP Agricultural University, Palampur, Himachal Pradesh, India [March 2001 - August 2001].
- Marketing Officer, Nunhems-Proagro Seeds Pvt. Ltd., New Delhi, India [September 1998 - October 2000].
- Scientific Assistant (Tea Breeding), Institute of Himalayan Bioresource Technology (IHBT-CSIR), Palampur, India [April 1996 - May 1997].

EDUCATION

Noble Foundation, Ardmore (OK), USA	Bioinformatics	Postdoctoral Fellow	2007-11
Dr. B.R. Ambedkar University, India	Plant Breeding & Genetics	Ph.D.	2006
Sikkim Manipal University, India	Bioinformatics	PGDBI	2004
CSK HP Agricultural University, India	Plant Breeding & Genetics	M.Sc.	1998
CSK HP Agricultural University, India	Agriculture	B.Sc.	1995

RESEARCH GRANT SUPPORT

Total career research grant funding to date: \$1,524,048

Role	Career Grant Awards			USU Grant Awards		
	External	Internal	Total	External	Internal	Total
PI	\$260,314	\$476,832*	\$737,146	\$160,314	\$373,332 [#]	\$533,646
Co-PI / Co-PD	\$611,022	\$175,880	\$786,902	-	\$75,880	\$75,880
Across all roles	\$871,336	\$652,712	\$1,524,048	\$160,314	\$449,212	\$609,526

* includes start-up funds of \$53,500 at OSU, and \$353,332 at USU

[#] includes start-up funds of \$353,332 at USU

List of funded projects: (as Principal Investigator)

- Source: Office of Research, RGS (USU)
Title: Promoting Sustainability in Nitrogen Cycling: Artificial Intelligence to Explore Diversity of Enzymes involved with Nitrification and Mineralization in Agricultural Soils
Investigators: **R. Kaundal**, J. Norton
Funding: \$20,000
Grant period: 1 year (Jul 2019 - Jun 2020)
- Source: Utah Agricultural Experiment Station (UAES), USU
Title: Advancing Agricultural Research *via* Bioinformatics and High-Performance Computing: a systems approach to modeling of complex - OMICS bigdata and tool development
Investigators: **R. Kaundal**
Funding: TBD
Grant period: 5 years (Nov 2019 - Oct 2024)
- Source: Oklahoma Center for the Advancement of Science & Technology (OCAST)
Title: *i*PMNET: a Bioinformatics System for Predicting Genome-wide Plant-Microbe interactions Network
Investigators: **R. Kaundal**
Funding: \$100,000
Grant period: 2 years (Nov 2012 - Jun 2015)

- Source: Oklahoma State University (Provost Office)
Title: *iCREST - interdisciplinary* Center for Research Excellence in Science & Technology (Bioinformatics & Computational Biology)
Investigators: **R. Kaundal**, S. Kak, B. Fathepure, G. Kakani
Funding: \$50,000
Grant period: 1 year (Sep 2011 - Aug 2012)
- Source: Oklahoma Agricultural Experimental Station (OAES), Office of the Vice President for Research and Technology, and the Office of the Provost and Sr. Vice President; OSU
Title: Bioinformatics at NIMFFAB / BMB (*start-up*)
Investigators: **R. Kaundal**
Funding: \$53,500
Grant period: 3 years (Mar 2011 - Jun 2014)
- Source: National Science Foundation (NSF EPSCoR, Track II)
Title: Tri-state BRICNET: a Bioinformatics Research Inspired Cyber NETwork
Investigators: **R. Kaundal et al**; total 20 participants from various universities / institutes of 3 states; I led the scientific component on Oklahoma side
Partner states: Oklahoma, Kansas, Missouri
Funding: \$6M total; \$2M for each state
Grant period: 3 years
Status: White paper selected by the Oklahoma EPSCoR committee; not successful with NSF.

(as Co-PI)

- Source: Utah Agricultural Experiment Station (UAES), USU
Title: Genomic Content and Structure of the Bovine Major Histocompatibility Complex
Investigators: A. Thomas, **R. Kaundal**
Funding: \$75,880
Grant period: 1.5 years (Jul 2019 - Dec 2020)
- Source: United States Department of Agriculture (USDA, SCRI-CAP)
Title: Design and Delivery of Therapeutic Proteins for HLB Protection
Investigators: New Mexico Consortium, Inc. (PI, G. Gupta, Los Alamos National Laboratory), M. Roose, **R. Kaundal**, Ed Stover, N. McRoberts, D. Ullman, *et al.*
Funding: \$7M (funded \$493,011 to UCR, *Bioinformatics part transferred to USU as new subaward = \$160,314*)
Grant period: 3 years (2016 - 2019) [submitted for 5 years; funded for first 2 years, *extension submitted*]
- Source: United States Department of Agriculture (USDA, NIFA)
Title: Forensic Plant Pathology - Enhancing U.S. Crop Biosecurity through Multidisciplinary Graduate Education, Experience and Research
Investigators: J. Fletcher, A. Wayadande, **R. Kaundal**, U. Melcher, R. Allen, F. Ochoa-Corona, L. Ma, C. Garzon
Funding: \$261,000
Grant period: 5 years (2012 - 2017)
- Source: National Science Foundation (NSF, Information & Intelligent Systems)
Title: MCBIOS Conference on Computational Biology and Bioinformatics
Investigators: C. Zhang, **R. Kaundal**, A. Perkins, D. Knisley, C. Compadre
Funding: \$17,325
Grant period: 1 year (May 2014 - Apr 2015)
- Source: Oklahoma State University (Provost Office)
Title: Entangled Genomes: an interdisciplinary program in the ecology and evolution of genomic interactions

Investigators: M. Fishbein, D. Brunson, **R. Kaundal**, K. Baum, H.K. Dai, M. Anderson, A. Doust, B. Fathepure, J. Fletcher, C. Greenwood, P. Hoyt, P. Jeyasingh, B. Luttbeg, S. Marek, U. Melcher, M. Palmer, K. Scheets, J. Steets, M. Tobler, L. Watson, A. Wayadande, G. Wilson, M. Yang, L. Zhu

Funding: \$50,000

Grant period: 1 year (Sep 2011 - Aug 2012)

- Source: Oklahoma State University (Provost Office)
Title: Phase II of the Bioinformatics Graduate Certificate Program: an interdisciplinary training workshop
Investigators: P. Hoyt, L. Zhu, **R. Kaundal**, S. Hartson, A. Doust, P. Canaan, H.K. Dai, D. Brunson, M. Fishbein
Funding: \$50,000
Granting period: 1 year (Sep 2011 - Aug 2012)
- Source: North Central Research Association (NCRA) of Agricultural Experiment Station Directors
Title: Biochemistry & Genetics of plant-fungal interactions
Investigators: Multi-state US NCRA grant; myself as one of the Collaborators
Granting period: 5 years (Oct 2013 - Sep 2018)

Pending proposals:

Grants pending review: **1** (NIH), **2** (USDA).

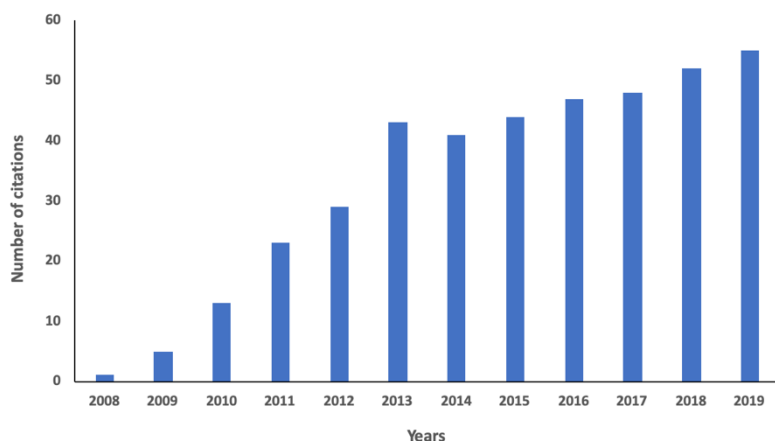
PUBLICATIONS

(* indicates the corresponding author, *italic* font indicates contribution by bioinformatics staff member supervised by me, underlined font indicates contribution by an undergraduate student mentored, and *underlined italic* font indicates contribution by a graduate student mentored by me. ^s denotes equal contributions, and ^ indicates contribution by students of a collaborator mentored by me).

Research Productivity

	Career (2005 to 2019)	USU (2017 to 2019)
Papers published / accepted	20	7
Editorials	4	0
Software developed	15	10
Other manuscripts submitted (in revision / preparation)	10	10
Conference presentations (oral / poster)	56	27
Book chapters / Bulletins	3	0
Invited lectures	28	3
Dissertations	3	1
Copyrights	1	0

Distribution of Google Scholar citations



	All	Since 2014
Citations	413	290
h-index	9	9
i10-index	9	9

Under review (4); In preparation (6): 10

- Loaiza, C.D. and **Kaundal, R***. 2019. PredHPI: an integrated web server platform for the detection and visualization of host-pathogen interactions using sequence-based methods. *Bioinformatics* (in review).
- Carman, J.G., Sherwood, D.A., Gao, L., Lacey, J.A., Arias, M.M de., Dwivedi, K.K., Pattanayak, J., Klein, P., Bhat, B.V., Price, B.J., **Kaundal, R.**, Stevens, J.R., Jamison, M. and Kowallis, B.M. 2019. Inducing asexual gametophyte formation (apomeiosis) in *Arabidopsis*, *Boechera* and *Vigna* by pharmacologically modifying energy and stress signaling pathways. *Proc. Natl. Acad. Sci.* (invited paper, *in review*).
- **Kaundal, R***, Duhan, N., Acharya, B., Pudussery, M.V., Ferreira, J.F.S., Suarez, D.L. and Sandhu, D*. 2019. Comparative leaf and root transcriptomics study of alfalfa (*Medicago sativa* L.) reveals novel genotype-specific salt tolerance mechanisms. *Scientific Reports*, Nature (in review).
- Moley, L., [^], Jones, R., **Kaundal, R.**, Thomas, A., Benninghoff, A. and Isom, C. 2019. Gene expression and DNA Methylation patterns of high and low apoptosis porcine SCNT blastocysts. *In review*.
- Mohammadi, M^S., Smith, E^S., Stanghellini, M. and **Kaundal, R***. 2019. Complete genome sequence of *Pythium brassicum* P1, an oomycete root pathogen: insights into its host specificity to *Brassicaceae*. *PLOS Pathogens*.
- Duhan, N., Meshram, M., Loaiza, C.D. and **Kaundal, R***. 2019. citSATdb: genome wide Simple Sequence Repeats (SSR) marker database of citrus species for germplasm characterization and improvement. *Frontiers in Plant Science* (in preparation).
- Sahu, S.S., Kaundal, A., Rojas, C.M., Lee, S., Weirick, T., Mysore, K.S. and **Kaundal, R***. 2019. An integrated approach for deciphering genome-scale plant-pathogen interaction networks: *in silico* modeling and experimental validation. *The Plant Cell* (in preparation).
- Loaiza, C.D. and **Kaundal, R***. 2019. An integrated *in silico* approach to decipher genome-scale Citrus and HLB host-pathogen interactions. *Horticulture Research* (in preparation).
- Loaiza, C.D., Duhan, N. and **Kaundal, R***. 2019. GreeningDB: an integrated resource, database and prediction server, of host-pathogen interactions and comparatomics of citrus and citrus greening disease, HLB. *Horticulture Research* (in preparation).
- Weirick, T., Moncrief, R., Fathepure, B.Z., Mahalingam, R. and **Kaundal, R***. 2019. LigPred: a comprehensive prediction system for the identification and classification of enzymes related to the synthesis and degradation of lignin. *Bioenergy Research* (in preparation).

Published: 20

- Loaiza, C.D., Duhan, N., Lister, M. and **Kaundal, R***. 2019. *In silico* prediction of host-pathogen protein interactions in melioidosis pathogen *Burkholderia pseudomallei* and human reveals novel virulence factors and their targets. *Briefings in Bioinformatics* (DOI: [10.1093/bib/bbz162](https://doi.org/10.1093/bib/bbz162)).
- Sahu, S.S., Loaiza, C.D. and **Kaundal, R***. 2019. Plant-mSubP: a computational framework for the prediction of single- and multi-target protein subcellular localization using integrated machine learning approaches. *AoB Plants* (DOI: [10.1093/aobpla/plz068](https://doi.org/10.1093/aobpla/plz068)).
- Sharma, B., Batz, T.A., **Kaundal, R.**, Kramer, E.M., Sanders, U.R.[^], Mellano, V.J., Duhan, N. and Larson, R.B. 2019. Developmental and molecular changes underlying the vernalization-induced transition to flowering in *Aquilegia coerulea* (James). *Genes* **10**(10): 734.
- Phatak, S.[^], Thomas, A., **Kaundal, R.**, Jones, R., Hintze, K. and Benninghoff, A. 2019. Impact of the Total Western Diet for Rodents on Colon Mucosal Gene Expression in a Multigenerational Murine Model of Colitis-associated Colorectal Cancer. *Current Developments in Nutrition* **3**(S1): nzz030.OR04-03-19.
- Tello, D., Gil, J., Loaiza, C.D., Riascos, J.J., Cardozo, N. and Duitama, J. 2019. NGSEP3: accurate variant calling across species and sequencing protocols. *Bioinformatics* **pii**: btz275.

- Sandhu, D., Puduserry, M., **Kaundal, R.**, Suarez, D.L., Kaundal, A. and Sekhon, R.S. 2018. Molecular characterization and expression analysis of the Na⁺/H⁺ exchanger gene family in *Medicago truncatula*. *Functional & Integrative Genomics* **18**(2): 141-153.
- Moley, L.[^], Jones, R., **Kaundal, R.**, Thomas, A., Benninghoff, A. and Isom, S.C. 2018. Gene expression analysis and DNA methylation patterns of porcine somatic cell nuclear transfer blastocysts with high and low incidence of apoptosis. *Reproduction, Fertility and Development* **31**(1): 128-128.
- Volz, D.C., Leet, J.K., Altomare, D., Chen, A., Stapleton, H.M., *Katiyar, N.*, **Kaundal, R.**, Yu, Y. and Wang, Y. 2016. Tris(1,3-dichloro-2-propyl)phosphate induces Genome-wide hypomethylation within early Zebrafish embryos. *Environmental Science & Technology* **50**(18): 10255-10263.
- *Sahu, S.S., Weirick, T.* and **Kaundal, R.***. 2014. Predicting genome-scale Arabidopsis-*Pseudomonas syringae* interactome using domain and interolog-based approaches. *BMC Bioinformatics* **15**(S11): S13.
- *Weirick, T., Sahu, S.S., Mahalingam, R.* and **Kaundal, R.***. 2014. LacSubPred: predicting subtypes of Laccases, an important lignin metabolism-related enzyme class, using *in silico* approaches. *BMC Bioinformatics* **15**(S11): S15.
- **Kaundal, R.***, *Sahu, S.S., Verma, R.[^]* and *Weirick, T.* 2013. Identification and characterization of plastid-type proteins from sequence-attributed features using machine learning. *BMC Bioinformatics* **14**(S14): S7.
- Ahmed, F., **Kaundal, R.** and Raghava, G.P.S. 2013. PHDcleav: a SVM based method for predicting human Dicer cleavage sites using sequence and secondary structure of miRNA precursors. *BMC Bioinformatics* **14**(S14): S9.
- **Kaundal, R.**, Saini, R. and Zhao, P.X. 2010. Combining machine learning and homology-based approaches to accurately predict subcellular localization in Arabidopsis. *Plant Physiology* **154**(1): 36-54.
- Benedito, V.A., Li, H., Dai, X., Wandrey, M., He, J., **Kaundal, R.**, Torres-Jerez, I., Gomez, S.K., Harrison, M.J., Tang, Y., Zhao, P.X. and Udvardi, M.K. 2010. Genomic inventory and transcriptional analysis of *Medicago truncatula* transporters. *Plant Physiology* **152**(3): 1716-1730.
- **Kaundal, R.** and Raghava, G.P.S. 2009. RSLpred: predicting subcellular localization of rice proteins combining compositional and evolutionary information. *Proteomics* **9**(9): 2324-2342.
- **Kaundal, R.**, Kapoor, A.S. and Raghava, G.P.S. 2006. Machine learning techniques in disease forecasting: a case study on rice blast prediction. *BMC Bioinformatics* **7**(1): 485.
- **Kaundal, R.*** and Sharma, B.K. 2006. Genotype x environment interaction and stability analysis for yield and other quantitative traits in maize (*Zea mays* L.) under rainfed and high rainfall valley areas of the sub-montane. *Research on Crops* **7**(1): 171-180.
- Kapoor, A.S. and **Kaundal, R.** 2007. Development of weather based forewarning systems for rice blast. *Himachal Journal of Agricultural Research* **33**(2): 211-217.
- **Kaundal, R.** and Kapoor, A.S. 2005. Virulence pattern of *Pyricularia grisea* in district Kangra of Himachal Pradesh. *Himachal Journal of Agricultural Research* **31**(2): 170-172.
- **Kaundal, R.*** and Sharma, B.K. 2005. Genetic variability and association studies for different yield components over the environments in elite cultivars of *Zea mays* L. *Himachal Journal of Agricultural Research* **31**(1): 31-38.

Editorials: 4

- Wren, J.D., Toby, I., Hong, H., Nanduri, B., **Kaundal, R.**, Dozmorov, M.G. and Thakkar, S. 2016. Proceedings of the 2016 MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference. *BMC Bioinformatics* **17**(S13): 356.

- Wren, J.D., Dozmorov, M.G., Burian, D., Perkins, A., Zhang, C., Hoyt, P. and **Kaundal, R.** 2014. Proceedings of the 2014 MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference. *BMC Bioinformatics* **15**(S11): 11.
- Wren, J.D., Dozmorov, M.G., Burian, D., **Kaundal, R.**, Perkins, A., Perkins, E., Kupfer, D.M. and Springer, G.K. 2013. Proceedings of the 2013 MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference. *BMC Bioinformatics* **14**(S14): S1.
- Wren, J.D., Dozmorov, M.G., Burian, D., **Kaundal, R.**, Bridges, S. and Kupfer, D.M. 2012. Proceedings of the 2012 MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference. *BMC Bioinformatics* **13**(S15): S1.

BIOINFORMATICS SOFTWARE DEVELOPED: 15

- **deepHPI** (<http://bioinfo.usu.edu/deepHPI/>): a Deep Learning framework for the prediction / characterization of host-pathogen protein interactions and visualization
- **NECminer** (<http://bioinfo.usu.edu/NECminer/>): a comprehensive bioinformatics system to investigate the diversity of enzymes in soil metagenomes; prediction and characterization of nitrification-related enzymes
- **Plant-mSubP** (<http://bioinfo.usu.edu/Plant-mSubP/>): a highly accurate webserver for predicting single- and multi-localized proteins in the plant systems
- **PredHPI** (<http://bioinfo.usu.edu/PredHPI/>): an integrated web server platform for the detection and visualization of host-pathogen interactions using sequence-based methods
- **citSATdb** (<http://bioinfo.usu.edu/citSATdb/>): a citrus microsatellite markers database, and central resource for citrus genic and non-genic Simple Sequence Repeats (SSRs)
- **GreeningDB** (<http://bioinfo.usu.edu/GreeningDB/>): a database of host-pathogen interactions and studying comparatomics of citrus and citrus greening disease (HLB)
- **AP-iNET** (<http://bioinfo.usu.edu/AP-iNET/>): a bioinformatics system for predicting and visualizing genome-wide Protein Interaction Networks (PINs) in the *Arabidopsis-Pseudomonas syringae* model interaction system
- **LacSubPred** (<http://bioinfo.usu.edu/lacsubpred/>): a two-phase classification system to characterize various laccase subtypes using unsupervised and supervised learning approaches, a useful resource to the biofuel community
- **LigPred** (<http://bioinfo.usu.edu/ligpred/>): a comprehensive prediction system for the identification and classification of enzymes related to the synthesis and degradation of lignin
- **PLpred** (<http://bioinfo.usu.edu/PLpred/>): this online tool first identifies a query protein to be a plastid or non-plastid one and then, classifies the identified plastid proteins further into four categories *viz.* Chloroplast, Chromoplast, Amyloplast or Etioplast proteins
- **AtSubP** (<http://bioinfo3.noble.org/AtSubP/>): a highly accurate Arabidopsis Subcellular Localization predictor
- **RSLpred** (<https://webs.iiitd.edu.in/raghava/rslpred/>): a highly accurate Rice Subcellular Localization predictor
- **RB-Pred** (<https://webs.iiitd.edu.in/raghava/rbpred/>): a first of its kind worldwide, this server forecasts rice leaf blast severity based on the weather parameters for general use to plant pathologists and farming community
- **DoBlast** (<http://bioinfo.okstate.edu:8080/doblast/>): a parallelized BLAST server for genome-scale annotations; large-scale sequence data analysis could be finished in minutes using automated parallel computing

- **Project** (<https://webs.iiitd.edu.in/raghava/rs|pred/project.html>): Given a protein sequence / accession number, this tool searches for high hydrophobicity window in the query sequence when a suitable pattern is made to search by the user (e.g. AL???LW pattern). The high hydrophobicity window is defined with the Kyte-Doolittle score schema based on the user-customizable search pattern, user-customizable window size and score threshold value.

BOOK CHAPTERS / BULLETINS / DISSERTATIONS: 6

- Moley, L.A. ^ 2019. *Gene expression and DNA methylation patterns of high and low apoptosis porcine SCNT blastocysts* (doctoral dissertation). Utah State University, Logan (UT), USA
- Azad, R.K., Mishra, N., Ahmed, F., **Kaundal, R.*** 2013. *Bioinformatics approaches to deciphering alien gene transfer: a comprehensive analysis*. In: Pratap, A. and Kumar, J. (Eds.) *Alien Gene Transfer in Crop Plants: Innovations, Methods and Risk Assessment*, Vol I. Springer Business and Science Media, USA (*invited chapter*).
- Reddy, C.S., Susheela, K., Kapoor, A.S., **Kaundal, R.**, Krishnaiah, N.V., Mishra, B., Ramakrishna, Y.S., Prasad, Y.G., Reddy, D.Y. and Prabhakar, M. 2004. *Forewarning Rice Blast in India*; Technical Bulletin No. 9, 2004-2005, Directorate of Rice Research, Rajendranagar, Hyderabad (AP), India, 46 pp.
- Contributed full chapter on rice blast forewarning in the book entitled “*Weather based forewarning for crop pests and diseases*”; Kalyani Publishers, New Delhi, India
- **Kaundal, R.** 2006. *Genetic analysis of yield components and blast resistance vis-à-vis identification of molecular markers for blast resistance in rice (Oryza sativa)* (Doctoral dissertation). Dr. B.R. Ambedkar University (*formerly Agra University*), Agra (UP), India
- **Kaundal, R.** 1998. Stability analysis for yield and some other quantitative characters in elite varieties of maize (*Zea mays* L.) (Master’s thesis). CSK Himachal Pradesh Agricultural University, Palampur (HP), India

PAPERS / ABSTRACTS PRESENTED / PUBLISHED IN SYMPOSIA / CONFERENCES: 56

2020

1. Duhan, N., Meshram, M., Loaiza, C.D. and **Kaundal, R.*** 2020. citSATdb: Genome-Wide Simple Sequence Repeats (SSR) Marker Database of Citrus Species for Germplasm Characterization and Crop Improvement. *Plant and Animal Genomes conference XXVIII* (PAG international); San Diego (CA), USA; Jan 11-15. Oral and poster presentation
2. Loaiza, C.D., Duhan, N. and **Kaundal, R.*** 2020. GreeningDB: a Database of Protein Features and Protein-Protein Interactions of the Bacteria causing HLB. *Plant and Animal Genomes conference XXVIII* (PAG international); San Diego (CA), USA; Jan 11-15. Poster presentation
3. Acharya, B.A., **Kaundal, R.**, Duhan, N., Pudussery, M., Ferreira, J.F.S., Suarez, D.L. and Sandhu, D. 2020. Dissecting salt tolerance mechanism in alfalfa using RNA-seq analysis of a tolerant and a sensitive genotype. *Plant and Animal Genomes conference XXVIII* (PAG international); San Diego (CA), USA; Jan 11-15. Poster presentation

2019

4. Phatak, S. ^, Thomas, A., **Kaundal, R.**, Jones, R., Hintze, K. and Benninghoff, A. 2019. Impact of the Total Western Diet for Rodents on Colon Mucosal Gene Expression in a Multigenerational Murine Model of Colitis-associated Colorectal Cancer. *NUTRITION 2019, American Society for Nutrition conference*; Baltimore (MD), USA; Jun 8-11. Oral presentation, OR04-03-19
5. Phatak, S. ^, Thomas, A., **Kaundal, R.**, Jones, R., Hintze, K. and Benninghoff, A. 2019. Impact of the Total Western Diet for Rodents on Colon Mucosal Gene Expression in a Multigenerational Murine Model of

Colitis-associated Colorectal Cancer. *NUTRITION 2019, American Society for Nutrition conference*; Baltimore (MD), USA; Jun 8-11.

- ^ student won 1st place in poster presentation (Diet & Cancer Research interest section)
- 1st place in ‘Three minutes thesis’ presentation competition
- Won travel award from Federation of American Societies for Experimental Biology (FASEB)

6. Phatak, S.[^], Thomas, A., **Kaundal, R.**, Jones, R., Hintze, K. and Benninghoff, A. 2019. Impact of the Total Western Diet for Rodents on Colon Mucosal Gene Expression in a Multigenerational Murine Model of Colitis-associated Colorectal Cancer. *The Animal, Dairy and Veterinary Sciences Summer Student Research Symposium*; Utah State University (USU), Logan (UT), USA; Aug 07.
 - ^ 1st place in flash talk presentation
7. Sharma, B., Batz, T., **Kaundal, R.**, Mellano, V. and Sanders, U.[^]. 2019. Developmental, and Genetic Changes in Shoot Apical Meristem During Transition to Flowering in *Aquilegia coerulea*. *14th Annual Science Research Symposium*; California State Polytechnic University, Pomona (CA); Apr 26
8. Loaiza, C.D. and **Kaundal, R***. 2019. Prediction of Host-Pathogen protein-protein interactions using machine learning. *The Annual Student Research Symposium*; Utah State University (USU), Logan (UT), USA; Apr 10-11. Oral presentation
9. Lister, M., Larson, R.B. and **Kaundal, R***. 2019. Centralizing Bioinformatics via High-Performance Computing: Applications, Opportunities, and Challenges in the Era of Large-scale -Omics Data. *The Annual Student Research Symposium*; Utah State University (USU), Logan (UT), USA; Apr 10-11
10. Ediriweera, U. and **Kaundal, R***. 2019. Computational Prediction of Host-Pathogen Protein Interactions in Melioidosis pathogen *Burkholderia pseudomallei* and Human reveals novel Virulence Factors and Infectivity Mechanisms. *The Annual Student Research Symposium*; Utah State University (USU), Logan (UT), USA; Apr 10-11. Oral presentation
11. Lister, M., Larson, R.B. and **Kaundal, R***. 2019. High-Performance Computing for Bioinformatics and the Challenges of Big -OMICS Data. *The Annual Engineering Research Week, College of Engineering*; Utah State University (USU), Logan (UT), USA; Apr 09
12. Ediriweera, U. and **Kaundal, R***. 2019. Computational Prediction of Host-Pathogen Protein Interactions in Melioidosis pathogen *Burkholderia pseudomallei* and Human reveals novel Virulence Factors and Infectivity Mechanisms. *The Annual Engineering Research Week, College of Engineering*; Utah State University (USU), Logan (UT), USA; Apr 09
13. Lister, M., Larson, R.B. and **Kaundal, R***. 2019. High-Performance Computing for Bioinformatics and the Challenges of Big -OMICS Data. *The Annual Plants, Soils, and Climate Showcase, College of Agriculture and Applied Sciences*; Utah State University (USU), Logan (UT), USA; Apr 02. Oral presentation
14. **Kaundal, R***, Duhan, N., Acharya, B., Pudussery, M.V., Ferreira, J.F.S., Suarez, D.L. and Sandhu, D*. 2019. Comparative transcriptomics study of alfalfa (*Medicago sativa* L.) reveals novel genotype-specific salt tolerance mechanisms. *The Annual Plants, Soils, and Climate Showcase, College of Agriculture and Applied Sciences*; Utah State University (USU), Logan (UT), USA; Apr 02. Oral presentation
15. Loaiza, C.D. and **Kaundal, R***. 2019. Deciphering plant-pathogen interactomes: a study on citrus greening disease. *The Annual Plants, Soils, and Climate Showcase, College of Agriculture and Applied Sciences*; Utah State University (USU), Logan (UT), USA; Apr 02. Oral presentation
16. Ediriweera, U. and **Kaundal, R***. 2019. Computational Prediction of Host-Pathogen Protein Interactions in Melioidosis pathogen *Burkholderia pseudomallei* and Human reveals novel Virulence Factors and Infectivity Mechanisms. *The 16th MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; University of Alabama, Birmingham (AL), USA; Mar 28-30. Oral presentation

17. Loaiza, C.D. and **Kaundal, R***. 2019. An integrated *in silico* approach to explore Citrus and HLB host-pathogen interactions. *The Plant and Animal Genome XXVII International Conference (PAG)*; Town and Country Hotel, San Diego (California), USA; Jan 12-16
18. Moley, L.A.[^], Jones, R., **Kaundal, R.**, Thomas, A.J., Benninghoff, A.D. and Isom, C. 2019. Gene expression analysis and DNA methylation patterns of porcine SCNT blastocysts with high and low incidence of apoptosis. *The 45th Annual International Embryo Transfer Society Conference*; Sheraton Hotel, New Orleans (LA), USA; Jan 20-23. Both oral and poster presentation accepted (*Peer reviewed*)

2018

19. Loaiza, C.D. and **Kaundal, R***. 2018. PredHPI: an integrated web-server platform for the prediction and visualization of host-pathogen interactions. *The 16th Annual Rocky Mountain Bioinformatics Conference*; Viceroy Hotel, Aspen/Snowmass (CO), USA; Dec 6-8. Both oral and poster presentation accepted
20. Mohammadi, M^S., Smith, E^S., Stanghellini, M. and **Kaundal, R***. 2018. Complete genome sequence of *Pythium brassicum* P1, an oomycete root pathogen: insights into its host specificity to *Brassicaceae*. *The XVth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; Mississippi State University, Starkville (MS), USA; March 29-31 (*Invited presentation*)
21. Sahu, S.S., Loaiza, C.D. and **Kaundal, R***. 2018. Plant-mSubP: a computational framework for the prediction of single and multi-location protein subcellular localization using integrated machine learning approaches. *The XVth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; Mississippi State University, Starkville (MS), USA; March 29-31
22. Sahu, S.S., Loaiza, C.D. and **Kaundal, R***. 2018. Plant-mSubP: a computational framework for the prediction of single and multi-target protein subcellular localization using integrated machine learning approaches. *Plants, Soils, and Climate Student Showcase; College of Agriculture and Applied Sciences (CAAS)*; Utah State University, Logan (UT), USA; March 19
23. Batz, T., **Kaundal, R.**, Mellano, V. and Sharma, B. 2018. Molecular and Morphological Analysis of the Floral Transition in *Aquilegia coerulea*. *The 99th Annual Pacific Division meeting of AAAS (American Association for the Advancement of Science)*; California State Polytechnic University, Pomona (CA), USA; June 12-15. Published in the *Proceedings of the Pacific Division of the AAAS*, Vol. 37, Part I
24. Moley, L.A.[^], Jones, R., **Kaundal, R.**, Thomas, A.J., Benninghoff, A.D. and Isom, C. 2018. RNA-Seq analysis of porcine SCNT blastocysts with high and low incidence of apoptosis. *The 51st Annual Meeting of the Society for the Study of Reproduction (SSR)*; Hilton New Orleans Riverside, New Orleans (LA), USA; July 10-13
25. Moley, L.A.[^], Jones, R., **Kaundal, R.**, Thomas, A.J., Benninghoff, A.D. and Isom, C. 2018. Gene expression analysis and DNA methylation patterns of porcine SCNT blastocysts with high and low incidence of apoptosis. *The 7th Annual ADVS Student Research Symposium*; Utah State University, Logan (UT), USA; August 08 (*Oral presentation*)
26. Sandhu, D., Cornacchione, M.V., Pudussery, M., Kaundal, A., **Kaundal, R.**, Ferreira, J.F.S. and Suarez, D.L. 2018. Genetic analysis of salinity responses in *Medicago* genotypes. Punjab Agricultural University (PAU), Ludhiana (Punjab), India; Jan 15 (*Invited presentation*)

2017

27. Sandhu, D., Pudussery, M., **Kaundal, R.** and Suarez, D.L. 2017. Molecular analysis of the Na⁺/H⁺ exchanger gene family and its role in salt stress in *Medicago truncatula*. *The ASA, CSSA & SSSA International Annual Meetings*; Tampa (Florida), USA; Oct 22-25
28. Kupsco, A., Leet, J.K., Altomare, D., Chen, A., Stapleton, H.M., *Katiyar, N.*, **Kaundal, R.**, Yu, Y., Wang, Y. and Volz, D.C. 2017. Transcriptome and DNA Methylome profiling of early Zebrafish embryos exposed to Tris (1,3-dichloro-2-propyl) phosphate. *56th Annual Meeting and ToxExpo, Society of Toxicology*; Baltimore (Maryland), USA; Mar 12-16

2016

29. Kupsco, A., Leet, J.K., Altomare, D., Chen, A., Stapleton, H.M., *Katiyar, N.*, **Kaundal, R.**, Yu, Y., Wang, Y. and Volz, D.C. 2016. Transcriptome and DNA Methylome profiling of early Zebrafish embryos exposed to Tris (1,3-dichloro-2-propyl) phosphate. *International Symposium & Workshop: Fish and amphibian embryos as alternative models in toxicology and teratology*; Aulnay-sous-Bois/Paris, France; Dec 01-02
30. Kupsco, A., Leet, J.K., Altomare, D., Chen, A., Stapleton, H.M., *Katiyar, N.*, **Kaundal, R.**, Yu, Y., Wang, Y. and Volz, D.C. 2016. Transcriptome and DNA Methylome profiling of early Zebrafish embryos exposed to Tris (1,3-dichloro-2-propyl) phosphate. *Toxicoepigenetics: The interface of Epigenetics and Risk assessment, Society of Toxicology meeting*; Tysons (Virginia), USA; Nov 02-04
31. **Kaundal, R.***, *Hayes, J., Katiyar, N.* and *Liu, T.* 2016. Centralizing bioinformatics via High-Performance Computing: applications, opportunities, and challenges in the era of large-scale -Omics data. *Plant and Animal Genomes conference XXIV* (PAG international); San Diego (CA), USA; Jan 09-13

2015

32. **Kaundal, R.***, *Hayes, J., Katiyar, N.* and *Pham, V.* 2015. Centralizing bioinformatics via High-Performance Computing: applications, opportunities, and challenges in the era of large-scale -Omics data. The *XIIth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; University of Arkansas, UAMS, Little Rock (AR), USA; March 13-14
33. *Sahu, S.S., Hayes, J.* and **Kaundal, R.*** 2015. Computational prediction of single and multi-target protein subcellular localization using machine-learning approach. The *XIIth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; University of Arkansas, UAMS, Little Rock (AR), USA; March 13-14

2014

34. *Sahu, S.S., Kaundal, A., Rojas, C.M., Lee, S., Weirick, T., Mysore, K.S.* and **Kaundal, R.*** 2014. Computational prediction and experimental validation of host-pathogen protein-protein interactome: a case study on *Arabidopsis thaliana - Pseudomonas syringae* model system. *American Society of Plant Biologists (ASPB) meeting*; Portland, Oregon, USA; July 12-16
35. *Weirick, T., Sahu, S.S., Mahalingam, R.* and **Kaundal, R.*** 2014. Predicting subtypes of laccases, an important lignin metabolism-related enzyme class, with machine learning. The *XIth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; Oklahoma State University, Stillwater (OK), USA; March 6-8
36. *Sahu, S.S., Weirick, T.* and **Kaundal, R.*** 2014. Prediction of *Arabidopsis-Pseudomonas syringae* interactome based on domain and interolog based approaches. The *XIth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; Oklahoma State University, Stillwater (OK), USA; March 6-8

2013

37. *Moncrief, R., Weirick, T.* and **Kaundal, R.*** 2013. Deciphering genome-scale host-pathogen Protein Interaction Networks using Artificial Intelligence and its applicability to select agents. *International Plant Genomics Congress*; St. Louis (MO), USA; Sep 23-24
38. *Sahu, S.S., Weirick, T., Moncrief, R.* and **Kaundal, R.*** 2013. A Bioinformatics Approach to Predict Host-Pathogen Protein-Protein Interactions Network. *BMB Annual Research Symposium*; OSU Stillwater (OK), USA; September 19
39. *Weirick, T., Fathepure, B.Z., Mahalingam, R.* and **Kaundal, R.*** 2013. LigPred: a Comprehensive Prediction System for the Identification and Classification of Enzymes Related to the Synthesis and Degradation of Lignin. *NSF EPSCoR Annual Bioenergy Conference*; Oklahoma State University, Stillwater (OK), USA; April 23

40. Weirick, T., Fathepure, B.Z., Mahalingam, R. and **Kaundal, R***. 2013. LigPred: a Comprehensive Prediction System for the Identification and Classification of Enzymes Related to the Synthesis and Degradation of Lignin. *Biochemistry & Molecular Biology Annual Research Symposium*; Oklahoma State University, Stillwater (OK), USA; September 19
41. **Kaundal, R*** and Verma, R[^]. 2013. PLpred: a bioinformatics system for the identification and classification of plastid type proteins. The *Xth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; University of Missouri, Columbia (MO), USA; April 5-6
42. Moncrief, R. and **Kaundal, R***. 2013. Bioinformatics Approaches to Deciphering Host-Pathogen Protein Interaction Networks (PINs). The *Xth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; University of Missouri, Columbia (MO), USA; April 5-6
43. Sahu, S.S. and **Kaundal, R***. 2013. Predicting Multi-target Protein Subcellular Localization combining homology and Machine Learning Approaches. The *Xth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; University of Missouri, Columbia (MO), USA; April 5-6
44. Ahmed, F., **Kaundal, R.** and Raghava, G.P.S. 2013. PHDcleav: a SVM-based method for predicting human Dicer cleavage sites using sequence and secondary structure of miRNA precursors. The *Xth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; University of Missouri, Columbia (MO), USA; April 5-6
45. Moncrief, R. and **Kaundal, R***. 2013. Artificial Intelligence-based prediction of plant host-pathogen protein interaction networks in select agents. *Gordon Research Conferences (Chemical & Biological Terrorism Defense)*; Ventura Beach Marriott, Ventura (CA), USA; March 9-10 (**invited talk** and poster)
46. Weirick, T., Fathepure, B.Z., Mahalingam, R. and **Kaundal, R***. 2013. LigPred: a Comprehensive Prediction System for the Identification and Classification of Enzymes Related to the Synthesis and Degradation of Lignin. *NSF EPSCoR Bioinformatics Workshop*; Arkansas State University, Little Rock (AR), USA; March 3-5
47. Kelley, R. and **Kaundal, R***. 2013. Bioinformatics Approaches to Deciphering Genome-wide Host-Pathogen Protein Interaction Networks. *OSU Annual Research Week & Symposium (2013)*; Oklahoma State University, Stillwater (OK), USA; Feb 20-21
48. Weirick, T., Fathepure, B.Z., Mahalingam, R. and **Kaundal, R***. 2013. LigPred: a Comprehensive Prediction System for the Identification and Classification of Enzymes Related to the Synthesis and Degradation of Lignin. *OSU Annual Research Week & Symposium (2013)*; Oklahoma State University, Stillwater (OK), USA; Feb 20-21

2012

49. Kelley, R. and **Kaundal, R***. 2012. Bioinformatics Approaches to Deciphering Genome-wide Host-Pathogen Protein Interaction Networks. *Biochemistry & Molecular Biology Annual Research Symposium (2012)*; Oklahoma State University, Stillwater (OK), USA; Sep 20-21
50. Verma, R[^] and **Kaundal, R***. 2012. A Support Vector Machine-based prediction method to classify the plastid and non-plastid type proteins. The *IXth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference*; University of Mississippi, Oxford (MS), USA; Feb 17-18

2010

51. **Kaundal, R.** and Zhao, P.X. 2010. A systematic approach to predicting organism-specific subcellular localization suggests species-specific sorting patterns. The 18th Annual International Conference on *Intelligent Systems for Molecular Biology (ISMB)*; Boston (MA), USA; July 10-14

2009

52. **Kaundal, R.** and Zhao, P.X. 2009. ASLpred: Arabidopsis Subcellular Localization predictor. *American Society of Plant Biologists (ASPB) meeting*; Honolulu, Hawaii Islands, USA; July 18-22

2008

53. **Kaundal, R.** and Zhao, P.X. 2008. An integrated prediction system for protein subcellular localization in Arabidopsis. *Plant and Animal Genomes conference XVI (PAG meeting)*; San Diego (CA), USA; Jan 12-16

2004

54. A.S. Kapoor and **R. Kaundal**. 2004. Development of weather based forewarning models for rice blast in Himachal Pradesh. *The 56th Annual meeting and National Symposium on Crop Surveillance: Disease Forecasting and Management*; Division of Plant Pathology, Indian Agricultural Research Institute (IARI), New Delhi; Feb 19-21
55. A.S. Kapoor and **R. Kaundal**. 2004. Development of weather-based forecasting models for rice neck blast in Himachal Pradesh. *National Symposium on Emerging Trends in Plant Disease Management*; Department of Plant Pathology, CSK Himachal Pradesh Agricultural University, Palampur, India; Nov 09-10

2002

56. Kapoor, A.S., **Kaundal, R** and Pratap, A. 2002. Weather based forewarning of rice blast in H.P. *International Conference on Challenges and Options for Sustainable Development of the Himalayas - Beyond 2002*; CSK Himachal Pradesh Agricultural University (HPAU), Palampur, India; Oct 01-04.

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Rakesh Kaundal and Raghava, G.P.S. RSLpred: a SVM-based method for subcellular localization prediction of rice proteins. SW-3638/2007.

HONORS / AWARDS RECEIVED: 5

- OSU President's Cup for creative interdisciplinarity in *bioinformatics and computational biology*, 2013 (1st prize)
- OSU President's Cup for creative interdisciplinarity on the project "*EDNA: Powerful New Technology for Electronic Diagnostic Nucleic acid Analysis*", 2012 (3rd place)
- Qualified National Eligibility Test (NET-ICAR), 2003 conducted by Indian Council of Agricultural Research (ICAR), New Delhi, India
- Third best award for poster paper presentation (Weather based forewarning of rice blast in H.P.) in the "*International Conference on Challenges and Options for Sustainable Development of the Himalayas-Beyond 2002*" held at CSK HPAU, Palampur, India; Oct 1-4, 2002
- Merit Certificate for securing first rank in the school in Class XII (1991).

INVITED TALKS: 28

1. XVth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference (*featured speaker*), Mississippi State University, Starkville (MS), USA; Mar 31, 2018
2. Institute of Genomics and Bioinformatics, College of Life Sciences, National Chung Hsing University, Taichung (Taiwan); Mar 07, 2018
3. Center for Integrated Biosystems (CIB), College of Agriculture and Applied Sciences, Utah State University, Logan, UT (USA); Apr 13, 2017
4. Department of Computer Engineering and Computer Science, University of Louisville, Louisville, KY (USA); Nov 02, 2016
5. Department of Plant Pathology, North Carolina State University, Raleigh, NC (USA); Apr 04, 2016
6. Computational Life Sciences, Bayer Corporation, Morrisville, NC (USA); Mar 18, 2016

7. XIIIth MCBIOS bioinformatics conference, University of Memphis, Memphis, TN (USA); Mar 04, 2016
8. XIIth MCBIOS conference (*featured speaker*), University of Arkansas / UAMS, Little Rock, AR (USA); Mar 13, 2015
9. Department of Plant Science, South Dakota State University, Brookings, SD (USA); Jun 24, 2014
10. Department of Plant Pathology and Microbiology, Iowa State University, Ames, IA (USA); Apr 10, 2014
11. Center for Science, Technology & Mathematics (NJCSTM), Kean University, Union, NJ (USA); Apr 02, 2014
12. Plant Biology Division 25th Anniversary Symposium, Noble Foundation, Ardmore, OK (USA); Mar 28, 2014
13. Institute for Integrative Genome Biology, University of California, Riverside, CA (USA); Mar 19, 2014
14. Department of Biology, Bowling Green State University, Bowling Green, OH (USA); Feb 27, 2014
15. Plant Genomics Congress (Next-Generation Sequencing), St. Louis, MO (USA); Sep 24, 2013
16. Xth MCBIOS conference, University of Missouri, Columbia, MO (USA); Apr 05, 2013
17. National Bureau of Plant Genetic Resources (NBPGR), New Delhi (India); Dec 10, 2012
18. National Research Center on Plant Biotechnology (NRCPB, IARI), New Delhi (India); Dec 08, 2012
19. Bioinformatics Workshop (NSF), Noble Foundation, Ardmore, OK (USA); April 19-21, 2012
20. IXth MCBIOS annual conference; University of Mississippi, Oxford, MS (USA); Feb 17-18, 2012
21. NSF EPSCoR Track I; Advanced Technology Research Center, OSU, Stillwater, OK (USA); Nov 17, 2011
22. NSF EPSCoR Track II; Oklahoma State Regents for Higher education, Oklahoma City, OK (USA); Nov 16, 2011
23. Technology Pipeline Solutions (Information Technology), MONSANTO, St. Louis, MO (USA); Oct 19, 2010
24. Department of Biochemistry & Molecular Biology, OSU, Stillwater, OK (USA); Sep 26, 2010
25. 30th Annual Crown Gall Conference; Samuel Roberts Noble Foundation, Ardmore OK (USA); Nov 21-22, 2009
26. Department of Biological Sciences, University of North Texas, Denton, TX (USA); May 21, 2009
27. Department of Botany and Microbiology, University of Oklahoma, Norman, OK (USA); Oct 30, 2008
28. ‘Resource Person’ for imparting training to participants in the Department of Biotechnology, Government of India sponsored training program on “*Bioinformatics tools for genome analysis*” organized by Advanced Centre for Hill Bioresources & Biotechnology, CSK HPAU, Palampur (HP) India; July 05-07, 2006.

TEACHING EXPERTISE

Graduate level:

- Course: PSC 6900 (2 credits): Special problems in PSC, Bioinformatics and -omics bigdata mining
University: Department of Plants, Soils, and Climate / CIB, USU, Logan (UT)
Year: 2019 (fall)
- Course: ENTO/PLP 5623 (*co-teaching*): Advanced Biotechnology Methods
University: Department of Entomology & Plant Pathology, OSU, Stillwater (OK)
Year: 2011, 12, 13
- Course: BIOC 5002 (*colloquium*)
University: Department of Biochemistry & Molecular Biology, OSU, Stillwater (OK)

Year: 2011, 12, 13

- Course: BI0006 (2+1); Computational Methods for Sequence Analysis
University: Sikkim Manipal University (SMU), Palampur Center, India
Year: 2004

Undergraduate level:

- **Course:** BIOTECH 522 (1+1); Bioinformatics
University: CSK Himachal Pradesh Agricultural University, Palampur (HP), India
Year: 2003-04.

Guest lectures:

- Course: ADVS 5260 (3 credits): Methods in Biotechnology: Molecular Cloning
University: Department of Animal, Dairy and Veterinary Sciences, USU, Logan (UT)
Year: 2017, 2018
- Course: CS 6900 (1 credit): Research topics presented by CS faculty
University: Department of Computer Science, USU, Logan (UT)
Year: 2018, 2019

Hands-on workshops taught:

- Introduction to R / Bioconductor
- Linux tutorials (basic and advanced)
- Next-generation sequencing data analysis (RNA-seq, ChIP-seq)
- GALAXY (<https://galaxyproject.org/>)

SCIENTIFIC / PROFESSIONAL SERVICES

(A) OSU *i*CREST Center for Bioinformatics (<https://www.facebook.com/iCREST.okstate/>)

- Lead investigator & Founding director of OSU's *interdisciplinary* Center for Research Excellence in Science and Technology (*i*CREST), Bioinformatics & Computational Biology

(B) Editorial Board

- Frontiers in Plant Science, *Associate Editor* (section: Bioinformatics & Computational Biology)
- Frontiers in Genetics, *Associate Editor* (Bioinformatics & Computational Biology)
- Frontiers in Bioengineering and Biotechnology, *Associate Editor* (Bioinformatics & Computational Biology)
- BMC Bioinformatics (*conference papers*), *Associate Editor*
- Journal of Plant Biochemistry and Biotechnology, *Editor*
- Board member, MCBIOS (*elected through nomination followed by voting*); 2012-15

(C) Reviewer

- Manuscript reviewer for: *Briefings in Bioinformatics*, *BMC Bioinformatics*, *PLoS ONE*, *PLoS Pathogens*, *BMC Genomics*, *Plant OMICS*, *Molecular Biology Reports*, *OMICS: a Journal of Integrative Biology*, *Journal of Plant Biochemistry and Biotechnology*, *Journal of Computational Biology and Bioinformatics Research*, *Computers in Biology and Medicine*

(D) Organizing International Conferences

- Invited workshop host / Speaker (*Next-generation sequencing data analysis*), XIIIth MCBIOS conference, University of Memphis; Mar 3-5, 2016
- Session Chair (*Next-generation sequencing*), XIIth MCBIOS conference, University of Arkansas / UAMS; Mar 12-14, 2015
- **Conference Chair**, MCBIOS 2014 (<http://www.mcbios.org/>); hosted at OSU, Stillwater (March 6-8)

- Session Chair (computational biology), Xth MCBIOS conference, University of Missouri; Apr 06, 2013
- Member, Program Committee, *International Symposium on Network Enabled Health Informatics, Bio-Medicine and Bioinformatics (HI-BI-BI)*; Aug 27-28, 2012
- Member, Program Committee, *ACM International Conference on Bioinformatics and Computational Biology 2010*
- Invited to chair two sessions in the above ACM-BCB international conference; Aug 02-04, 2010

(E) Organizing workshops

- 7 Next-generation sequencing data analysis workshops (<http://facility.bioinformatics.ucr.edu/workshops>), IIGB (UCR); **2014**: Dec 5-8; **2015**: Jan 27, Sep 30; **2016**: Feb 12, Mar 04, Mar 11, Jun 30
- Organized a comprehensive 1-week Bioinformatics workshop at OSU; August 13-17, 2012
- Computational Biology workshop; Noble Foundation, Ardmore (OK); October 02, 2009
- 1-day Bioinformatics workshop; Noble Foundation, Ardmore (OK); June 20, 2007

(F) Judging

- MCBIOS-JMP Young Scientist Award Competition (Postdoc and student categories); XVth MidSouth Computational Biology & Bioinformatics Society (MCBIOS) annual conference; Mississippi State University, Starkville (MS), USA; Mar 29-31, 2018
- State Science Fair, California Science Center, Los Angeles (CA); May 23-24, 2016
- XIIIth MCBIOS conference; University of Memphis, Memphis (TN); Mar 03-05, 2016
- XIIth MCBIOS conference; University of Arkansas / UAMS, Little Rock (AR); Mar 12-14, 2015
- Xth Annual BMBGSA Research Symposium; Oklahoma State University, Stillwater; Sep 19-20, 2013
- Xth MCBIOS annual conference; University of Missouri, Columbia (MO); Apr 5-6, 2013
- OSU Research Week & Symposium; Oklahoma State University, Stillwater; Feb 20-22, 2013
- IXth MCBIOS annual conference; University of Mississippi, Oxford (MS); Feb 17-18, 2012
- OSU Research Week & Symposium; Oklahoma State University, Stillwater; Feb 22-23, 2012

(G) Postdoctoral Research Fellow supervised: 1**(H) Bioinformatics full-time staff supervised: 3** (1 Bioinformatics Scientist, 1 Systems Administrator, 1 Senior Statistician / Programmer)**(I) Students supervised: 20**

Current:

- Naveen Duhan (Ph.D. student), Department of Plants, Soils, and Climate / CIB, USU
- Cristian D Loaiza (master's student), Department of Plants, Soils, and Climate / CIB, USU
- Nikhil S. Kurivella (master's student), Department of Computer Science, USU
- Matthew Lister (Linux systems administrator, undergrad), Department of Computer Science, USU
- Suyash Mhetre (master's student, GRA worker), Department of Management Information Systems, Huntsman School of Business, USU
- Kaige Zhang, Ph.D. (Research Assistant), Department of Computer Science, USU

Completed:

- Udarika Ediriweera (master's student), Department of Computer Science, USU
- Robyn Kelley (master's student), Department of Biochemistry & Molecular Biology, OSU
- Tyler Weirick (master's student), Department of Biochemistry & Molecular Biology, OSU
- Eric Smith (Ph.D. student, *co-supervised*), Department of Entomology, UCR
- Kalpana Varala (MS hourly student), Management Information Systems, Spears School of Business, OSU

- Andrew J Walters (Undergraduate Research Fellow), Department of Biological Engineering, USU
- Alex Beeston (Undergraduate Research Fellow), Department of Biological Engineering, USU
- Caleb Smith (undergraduate student), Department of Electrical & Computer Engineering, USU
- Raul Ramirez (undergraduate student), Department of Computer Science, USU
- Viet Pham (undergraduate student), Department of Computer Science, UCR
- Thomas Liu (undergraduate student), Department of Computer Science, UCR
- Joel Gomez (undergraduate student), Department of Computer Science, UCR
- Kenny Luu (undergraduate student), Department of Computer Science, UCR
- Austin Leong (undergraduate student), Department of Computer Science, UCR

(J) Membership of Scientific Societies

- Sigma Xi: The Scientific Research Society
- MidSouth Computational Biology and Bioinformatics Society (MCBIOS)
- American Society of Plant Biologists (ASPB)
- International Society for Computational Biology (ISCB), *life member*.

MEDIA CONTRIBUTIONS

TV: OState TV; March 6-8, 2014: Conference Chair, MCBIOS bioinformatics
(<http://www.ostate.tv/?play=15FA764F-E504-23D0-A7DC-BD5E031B64F7>)

Magazine: O'COLLY; September 12, 2012: Tech approach to genomes
(http://www.ocolly.com/opinion/columns/article_6fd88860-fc99-11e1-a92c-001a4bcf6878.html)

Internet:

- i*Plant collaborative; August 17, 2012: Summer workshop in bioinformatics
(<https://pods.iplantcollaborative.org/wiki/display/Events/2012+OSU+Summer+Workshop+in+Bioinformatics>)
- YouTube video: Organized distinguished Sirny lecture
(<https://www.youtube.com/watch?v=5SYIhjhGg44>) Hosted world-renowned expert, Dr. Eugene Koonin (NCBI), in the field of evolutionary and computational biology.

Dated: Dec 10, 2019
Place: Logan, Utah (USA)

(Rakesh Kaundal)