Naveen Duhan

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Ᏻ Google Scholar   🌐 https://naveenduhan.com

Summary

› Experienced bioinformatics and computational biology professional with a successful track record of combining biology and big data analytics to support organismal enhancement and genomics-enabled research.

› Knowledge and experience with tools and techniques for Next generation sequencing data analysis, including genome assembly and annotation, RNA-Seq, small RNA sequencing, Digenome, etc.

› Strong foundation in machine learning techniques including Support Vector Machines, deep learning, and Artificial Neural Networks for predictive modeling in bioinformatics.

› Ability to develop and implement algorithms for bioinformatics applications using Linux/Unix environments, command-line tools programming languages such as Python, R, and Perl for data analysis and manipulation.

› Strong problem-solving and critical thinking skills for complex data analysis and interpretation.

Academic Appointments and Professional Experience

Nov,2023 – present	**Research Associate III Bioinformatics**, Animal Disease Research & Diagnostic Laboratory, South Dakota State University, Brookings, SD, USA
Jan, 2019 – Nov, 2023	**Graduate Research Assistant,** Utah State University, Logan, UT, USA
Aug, 2011 – Dec, 2018	**Teaching Assistant Bioinformatics**, School of Agricultural Biotechnology, Punjab Argicultural University, Ludhiana, India
Jul, 2010 – Aug, 2011	**Lecturer Bioinformatics,** Guru Nanak Girls College, Ludhiana, India

Education

2019 – 2023	**Ph.D., Utah State University** **Plant Sciences (Bioinformatics and Computational biology)** **Thesis:** *Machine learning and Data mining in complex genomics big data: developing efficient tools to advance computational systems biology*
2008 – 2010	**M.Sc. Bioinformatics, Punjabi University Patiala, India Thesis:** *In silico prediction of microRNA in Catharanthus roseus and their role in metabolomics*
2005 – 2008	**B.Sc. Biology, Kurukshetra University Kurukshetra, India** Subject: *Zoology, Botany, Chemistry*
2007 – 2008	**Add-on Certificate Diplom, Kurukshetra University Kurukshetra, India** Subject: *Bioinformatics*

Awards

○ **USU Robins Awards finalist for Doctoral Student Researcher of the academic Year 2022-2023**, Utah State University, Logan, UT, USA

○ **Doctoral Student Researcher of the academic Year 2022-2023**, College of Agriculture and Applied Sciences Utah State University, Logan, UT, USA

○ **Doctoral Student Researcher of the academic Year 2022-2023**, Department of Plants, Soils and Climate Utah State University, Logan, UT, USA

Awards (continued)

- 🎗 **Young Scientist Award**, National Conference on Technological Challenges in Social, Environmental, and Agricultural Reforms (TECHSEAR-2017) 9th and 10th September 2017 at IIRR Hyderabad

Grants/Proposals

Current

- 🎗 **Title:** Emerging avian metapneumovirus subgroup A and B in US poultry: development of diagnostic assays and control strategies; **Funding Agency:** Foundation for Food & Agriculture Research; **Role:** Co-PI; **Total Amount:** $300,000; **Time:** 1 Year

Submitted

- 🎗 **Title:** Development of viral vectored vaccines to protect US poultry against avian reovirus infections;Funding Agency: USDA-NIFA; **Role:** Co-PI; **Total Amount:** $649,907; **Time:** 3 Year
- 🎗 **Title:** To study the evolution of emerging avian metapneumovirus subgroups A and B in US poultry and to develop novel virus vectored vaccines against them;Funding Agency: USDA-NIFA; **Role:** Co-PI; **Total Amount:** $649,936; **Time:** 3 Year

Softwares and Webserver Developed

Softwares / Tools (5)

- → **miPyRNA** (https://github.com/navduhan/mipyrna): an automated python package for small RNA sequencing data analysis.
- → **SNVguru** (https://github.com/usubioinfo/snvguru): an automated python package for single nucleotide variation (SNV) analysis.
- → **pySeqRNA** (https://github.com/navduhan/pyseqrna): an automated python package for next-generation sequencing data analysis.
- → **MINpred** (https://bioinfo.usu.edu/minpred/download/minpred.tar.gz): a standalone alignment-free deep learning based tool for nitrogen mineralization enzyme classification.
- → **deepNEC** (https://navduhan@bitbucket.org/navduhan/deepnec.git): a standalone alignment-free deep learning based tool for nitrogen metabolism enzyme classification.

Webserver / Databases (13)

- → **HPInet** (http://bioinfo.usu.edu/hpinet/): a Cereal crops and pathogen prote-protein interaction database. (accessed by ≈ 20 users)
- → **HuPoxNET** (http://bioinfo.usu.edu/hupoxnet/): a database for Human-Monkeypox virus interactome. (accessed by ≈ 20 users)
- → **myDockDB** (http://bioinfo.usu.edu/myDockDB/): a Multiple Myeloma Proteins and Natural Compounds Docking WEB-resource. (accessed by ≈ 20 users)
- → **pySeqRNA** (http://bioinfo.usu.edu/pyseqrna/): complete documentation website for pySeqRNA package. (accessed by ≈ 112 users)
- → **ranchSATdb** (http://bioinfo.usu.edu/ranchSATdb/): a database of ranch animals microsatellite markers (accessed by ≈ 30 users)
- → **TritiKBdb** (http://bioinfo.usu.edu/tritikbdb/): a Host-Pathogen interaction database for understanding Karnal Bunt disease infection mechanisms in Wheat. (accessed by ≈ 540 users)
- → **HuCoPIA** (http://bioinfo.usu.edu/hucopia/): an Atlas of Human vs. SARS-CoV-2 interactome and the comparative analysis with other Coronaviridae family viruses. (accessed by ≈ 60 users)

Softwares and Webserver Developed (continued)

→ **deepNEC** (http://bioinfo.usu.edu/deepNEC/): an integrated web server platform for the prediction of nitrogen metabolism-related enzymes using deep learning. (accessed by ≈ 700 users)

→ **deepHPI** (http://bioinfo.usu.edu/deepHPI/): a Deep Learning framework for the prediction of host-pathogen protein interactions and visualization. (accessed by ≈ 1.03K users)

→ **GreeningDB** (http://bioinfo.usu.edu/GreeningDB/): a database of host-pathogen interactions and studying comparatomics of citrus and citrus greening disease (HLB). (accessed by ≈ 828 users)

→ **covidTracker** (http://bioinfo.usu.edu/covidTracker/): a COVID 19 disease infection statistics tracker. (accessed by ≈ 8200 users)

→ **legumeSSRdb** (http://bioinfo.usu.edu/legumeSSRdb/): a Legume species microsatellite markers database. (accessed by ≈ 712 users)

→ **citSATdb** (http://bioinfo.usu.edu/citSATdb/): a Citrus species microsatellite markers database. (accessed by ≈ 530 users)

Research Interests

To achieve my research goals, I intend to follow a multidisciplinary research strategy combining computational and molecular biology. My interests are divided into the following categories:

- Integrating multi-omics data to improve animal, plant and human health / response to environmental changes:

  - Next-generation sequencing (NGS) data analysis: Genome assembly, RNA-seq, ChiP-seq, Single Cell RNA-seq, Var-seq, Digenome, metagenomes *etc*.
  - Genome-scale functional annotation: develop novel algorithms to predict biochemical pathways and structure/function analyses
  - Development of new pipelines, tools and improvement for existing pipelines for NGS data analysis

- Artifical Intelligence (Machine Learning) based computational modeling to analyze large-scale sequence data

- System biology (*integrating phenotypic, genotypic, and environmental data*):

  - Host-pathogen interactions
  - Protein-protein interactions: both at intra- and inter-species level
  - Metabolic pathway analysis, gene regulatory networks

- Develop prediction tools / web servers / databases to aid research community in the above areas of interest.

Teaching Experience

Uath State University, Logan, UT, USA

- **PSC 4150/6150:** Bioinformatics and Big Data Mining

Punjab Agricultural University, Ludhiana, India

Graduate Level

- **Biotech 509:** Bioinformatics Tools and Their Application in Agriculture

- **Biotech 607:** Advances in Bioinformatics

Undergraduate Level

- **Biotech 307:** Introduction to Bioinformatics

- **Biotech 401:** Introduction to Genomics and Proteomics

- **Biotech 404:** Computational Biology

- **Biotech 499:** In-house Training

Research Publications

I have **27 publications** in international peer-reviewed journals, including **9 first author** articles. My **h-index = 8, i10-index = 7**, and **total citations = 182** (as per Google Scholar Citations).

$^\$$ denotes equal contribution, <u>underlined</u> typeface indicates an undergraduate student mentored, and <u>*underlined*</u> *italic* typeface indicates a graduate student mentored.

Journal Articles

1 Kataria, R., **Duhan, N.**, & Kaundal, R. (2024). Navigating the human-monkeypox virus interactome: Hupoxnet atlas reveals functional insights. *Frontiers in Microbiology*, Accepted.

2 Kaur, S., Seem, K., **Duhan, N.**, Kumar, S., Kaundal, R., & Mohapatra, T. (2024). Comparative mirnome and transcriptome analyses reveal the expression of novel mirnas in the panicle of rice implicated in sustained agronomic performance under terminal drought stress. *Planta*, *259*(6), 128.
🔗 https://doi.org/10.1007/s00425-024-04399-x

3 Luqman, M., **Duhan, N.**, Temeeyasen, G., Selim, M., *Jangra, S.*, & Mor, S. (2024). Geographical expansion of avian metapneumovirus subtype b: First detection and molecular characterization of avian metapneumovirus subtype b in us poultry. *Viruses*, *16*, 508.
🔗 https://doi.org/10.3390/v16040508

4 **Duhan, N.** & Kaundal, R. (2024). RSLpred2: An integrated web server for the annotation of Rice proteome subcellular localization using deep learning. *Rice*, Accepted.

5 Kaur, S., Seem, K., **Duhan, N.**, Kumar, S., Kaundal, R., & Mohapatra, T. (2023). Transcriptome and physio-biochemical profiling reveals differential responses of rice cultivars at reproductive-stage drought stress. *International Journal of Molecular Sciences*, *24*(2), 1002.
🔗 https://doi.org/10.3390/ijms24021002

6 **Duhan, N.**, Kaur, S., & Kaundal, R. (2023). ranchSATdb: A genome-wide simple sequence repeat (SSR) markers database of livestock species for mutant germplasm characterization and improving farm animal health. *Genes*, *14*(2), 1481. 🔗 https://doi.org/10.3390/genes14071481

7 **Duhan, N.** & Kaundal, R. (2023). HuCoPIA: An atlas of Human vs. SARS-CoV-2 interactome and the comparative analysis with other coronaviridae family viruses. *Viruses*, *15*(2), 492.
🔗 https://doi.org/10.3390/v15020492

8 Kataria, R., **Duhan, N.**, & Kaundal, R. (2022). Computational systems biology of Alfalfa–bacterial blight host-pathogen interactions: Uncovering the complex molecular networks for developing durable disease resistant crop. *Frontiers in Plant Science*, *12*, 807354.
🔗 https://doi.org/10.3389/fpls.2021.807354

9 Kaundal, R., Loaiza, C. D., **Duhan, N.**, & Flann, N. (2022). deepHPI: A comprehensive deep learning platform for accurate prediction and visualization of host–pathogen protein–protein interactions. *Briefings in Bioinformatics*, *23*(3), bbac125. 🔗 https://doi.org/10.1093/bib/bbac125

10 Mahalingam, R., **Duhan, N.**, Kaundal, R., Smertenko, A., Nazarov, T., & Bregitzer, P. (2022). Heat and drought induced transcriptomic changes in barley varieties with contrasting stress response phenotypes. *Frontiers in Plant Science*, *13*, 4652. 🔗 https://doi.org/10.3389/fpls.2022.1066421

11 Rutigliano, H. M., Thomas, A. J., Umbaugh, J. J., Wilhelm, A., Sessions, B. R., Kaundal, R., **Duhan, N.**, Hicks, B. A., Schlafer, D. H., White, K. L., & J., D. C. (2022). Increased expression of pro-inflammatory cytokines at the fetal–maternal interface in bovine pregnancies produced by cloning. *American Journal of Reproductive Immunology*, *87*(3), e13520. 🔗 https://doi.org/10.1111/aji.13520

12 **Duhan, N.**, Kataria, R., & Kaundal, R. (2022). TritiKBdb: A functional annotation resource for deciphering the complete interaction networks in wheat-karnal bunt pathosystem. *International Journal of Molecular Sciences*, *23*(13), 7455. 🔗 https://doi.org/10.3390/ijms23137455

13 **Duhan, N.**, Norton, J. M., & Kaundal, R. (2022). deepNEC: A novel alignment-free tool for the identification and classification of nitrogen biochemical network-related enzymes using deep learning. *Briefings in Bioinformatics*, *23*(3), bbac071. 🔗 https://doi.org/10.1093/bib/bbac071

14 Kaundal, R., **Duhan, N.**, Acharya, B. R., Pudussery, M. V., Ferreira, J. F., Suarez, D. L., & Sandhu, D. (2021). Transcriptional profiling of two contrasting genotypes uncovers molecular mechanisms underlying salt tolerance in alfalfa. *Scientific Reports*, *11*(1), 5210. 🔗 https://doi.org/10.1038/s41598-021-84461-w

15 Loaiza, C. D., **Duhan, N.**, & Kaundal, R. (2021). GreeningDB: A database of host–pathogen protein–protein interactions and annotation features of the bacteria causing huanglongbing hlb disease. *International Journal of Molecular Sciences*, *22*(19), 10897. 🔗 https://doi.org/10.3390/ijms221910897

16 Loaiza, C. D., **Duhan, N.**[$], Lister, M., & Kaundal, R. (2021). 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*, *22*(3), bbz162. 🔗 https://doi.org/10.1093/bib/bbz162

17 **Duhan, N.** & Kaundal, R. (2021a). LegumeSSRdb: A comprehensive microsatellite marker database of legumes for germplasm characterization and crop improvement. *International Journal of Molecular Sciences*, *22*(21), 11350. 🔗 https://doi.org/10.3390/ijms222111350

18 Malhotra, P. K., Verma, G., Sidhu, G. S., & **Duhan, N.** (2020). Epigenomics: Role, approaches and applications in plants. *JAPS, Journal of Animal and Plant Sciences*, *30*(5), 1071–1082. 🔗 https://doi.org/10.36899/JAPS.2020.5.0122

19 **Duhan, N.** & Kaundal, R. (2020b). pySeqRNA: An automated python package for rna sequencing data analysis. *f1000research*. 🔗 https://doi.org/10.7490/f1000research.1118314.1

20 **Duhan, N.**, Meshram, M., Loaiza, C. D., & Kaundal, R. (2020a). citSATdb: Genome-wide simple sequence repeat (ssr) marker database of citrus species for germplasm characterization and crop improvement. *Genes*, *11*(12), 1486. 🔗 https://doi.org/10.3390/genes11121486

21 *Kaur, K.*, **Duhan, N.**, Singh, J., Kaur, G., & Vikal, Y. (2020). Computational identification of maize miRNA and their gene targets involved in biotic and abiotic stresses. *Journal of biosciences*, *45*, 1–17. 🔗 https://doi.org/10.1007/s12038-020-00106-6

22 Sharma, B., Batz, T. A., Kaundal, R., Kramer, E. M., Sanders, U. R., Mellano, V. J., **Duhan, N.**, & Larson, R. B. (2019). Developmental and molecular changes underlying the vernalization-induced transition to flowering in *Aquilegia coerulea* (James). *Genes*, *10*(10), 734. 🔗 https://doi.org/10.3390/genes10100734

23 Mohanpuria, P., **Duhan, N.**, Sarao, N. K., Kaur, M., & Kaur, M.. (2018). In silico identification and validation of potential microRNAs in Kinnow Mandarin (*Citrus reticulata* blanco). *Interdisciplinary Sciences: Computational Life Sciences*, *10*, 762–770. 🔗 https://doi.org/10.1007/s12539-017-0235-6

24 *Jhinjer, R. K.*, **Duhan, N.**, & Chhuneja, P. (2017). Comparative structure modeling of Glyoxalase ii protein of *Oryza sativa*. *Int. J. Curr. Microbiol. App. Sci*, *6*(8), 1380–1387. 🔗 https://doi.org/10.20546/ijcmas.2017.608.168

25 **Duhan, N.**, Sarao, N., Mohanpuria, P., & Sidhu, M. (2016). In silico identification and characterization of potential miRNAs from *Capsicum annum*. *HortFlora Research Spectrum*, *5*(4), 306–309. 🔗 https://www.cabdirect.org/cabdirect/abstract/20173074226

26 Mohanpuria, P., Sarao, N. K., **Duhan, N.**, Brar, G., Kaur, A., & Singh, K. (2013). Computational identification and characterization of potential mirnas from asiatic cotton (*Gossypium arboreum* l.) *Crop Improv*, *40*(2), 121–128.

27 Omer, A., Singh, S., & **Duhan, N.** (2012). Identification of miRNAs in *C. roseus* and their potential targets. *Bioinformation*, *8*(2), 75. 🔗 https://doi.org/10.6026/97320630008075

Under Review

1 Larson, R., **Duhan, N.**, & Kaundal, R. (2024). *In silico identification of potential drug-like natural compounds for the treatment of multiple myeloma: A comprehensive molecular docking and simulation study* [Frontiers in Chemistry].

2 **Duhan, N.** & Kaundal, R. (2024a). *AtSubP-2.0: An integrated web server for the annotation of arabidopsis proteome subcellular localization using deep learning* [Plant Genome].

3 **Duhan, N.** & Kaundal, R. (2024b). *PRGminer: Harnessing deep learning for the prediction of resistance genes involved in plant defense mechanisms* [Frontiers in Plant Science].

4 **Duhan, N.** & Kaundal, R. (2024c). *pySeqRNA: An all-in-one NGS to spreadsheet Python package for RNA-Seq data, including single, multi-gene quantification and error correction* [Bioinformatics].

Manuals

1 **Duhan, N.**, Chhuneja, P., & Singh, K. (2012). *Introduction to Bioinformatics: A Practical Manual*. School of Agricultural Biotechnology, Punjab agricultural University, Ludhiana. COA/2012/Manual-10.

Abstract / Oral / Conferences

1 **Duhan, N.**, Temeeyasen, G., Luqman, M., Selim, M., Khaled, A., T., S., Jangra, S., & Mor, S. (2024). TrevoDB: A comprehensive resource for turkey orthoreovirus classification and comparative analysis. In *75th North Central Avian Disease Conference*.

2 **Duhan, N.** & Kaundal, R. (2023). PySeqRNA: Pyseqrna: An automated python package for next-generation sequencing data analysis. In *Plant and Animal Genomes Conference 30 (PAG International 2023)*.

3 Kaundal, R., **Duhan, N.**, Acharya, B. R., Pudussery, M. V., Ferreira, J. F., Suarez, D. L., & Sandhu, D. (2022). Transcriptional profiling of two contrasting genotypes uncovers molecular mechanisms underlying salt tolerance in alfalfa. In *The 2022 Conference on Applied Statistics in Agriculture and Natural Resources, Utah State University, Logan, Utah, USA; May 16-19, 2022*.

4 **Duhan, N.** & Kaundal, R. (2022). PySeqRNA: Pyseqrna: An automated python package for next-generation sequencing data analysis. In *The 2022 Conference on Applied Statistics in Agriculture and Natural Resources, Utah State University, Logan, Utah, USA; May 16-19, 2022*.

5 Kataria, R., **Duhan, N.**, & Kaundal, R. (2021a). Computational systems biology of alfalfa-pseudomonas syringae protein-protein interactions: Uncovering the complex molecular networks of host-pathogen interactions to control bacterial blight in alfalfa. In *ASA, CSSA, SSSA International Annual Meeting*.

6 Kataria, R., **Duhan, N.**, & Kaundal, R. (2021b). Translating-omics big data: Comprehensive understanding of host-pathogen interactions to control bacterial blight in alfalfa using computational approaches. In *MOLECULAR PLANT-MICROBE INTERACTIONS* (Vol. 34).

7   **Duhan, N.** & Kaundal, R. (2021b). PySeqRNA: An automated python package for next-generation sequencing data analysis. In *ASA, CSSA, SSSA International Annual Meeting*.

8   **Duhan, N.**, Norton, J. M., & Kaundal, R. (2021). deepNEC: A novel alignment-free tool for the identification and classification of nitrogen biochemical network-related enzymes using deep learning. In *ASA, CSSA, SSSA International Annual Meeting*.

9   Loaiza, C. D., **Duhan, N.**, & Kaundal, R. (2020). GreeningDB: A database of protein features and protein-protein interactions of the Bacteria causing HLB. In *Plant and Animal Genomes Conference XXVIII (PAG International 2020).*

10   Mahalingam, R., Bregitzer, P., **Duhan, N.**, & Kaundal, R. (2020). Transcriptome analysis of barley varieties with contrasting responses to heat, drought and combined heat and drought stress. In *ASA, CSSA, SSSA Annual International Agronomy Meeting*.

11   **Duhan, N.** & Kaundal, R. (2020a). PySeqRNA: An automated python package for next-generation sequencing data analysis. In *The 28th Annual International Conference on Intelligent Systems for Molecular Biology*.

12   **Duhan, N.**, Meshram, M., Loaiza, C. D., & Kaundal, R. (2020b). citSATdb: Genome-wide simple sequence repeat (ssr) marker database of Citrus species for germplasm characterization and crop improvement. In *Plant and Animal Genomes Conference XXVIII (PAG International 2020).*

13   **Duhan, N.**, Norton, J. M., & Kaundal, R. (2020a). deepNEC: A novel alignment-free tool for the identification and classification of nitrogen biochemical network-related enzymes using deep learning. In *The 2020 Annual ASM Intermountain Branch Meeting, American Society of Microbiology*.

14   **Duhan, N.**, Norton, J. M., & Kaundal, R. (2020b). NECminer: A novel alignment-free tool for the identification and classification of nitrification-related enzymes using deep learning. In *The 28th Annual International Conference on Intelligent Systems for Molecular Biology*.

15   Kaundal, R., & **Duhan, N.** (2019). Comparative transcriptomics study of alfalfa (*Medicago sativa* L.) reveals novel genotype-specific salt tolerance mechanisms. In *The Annual Plants, Soils, and Climate Showcase 2019, College of Agriculture and Applied Sciences; Utah State University, Logan, Utah, USA*.

16   Yadav, I. S., Malhotra, P. K., **Duhan, N.**, & Sharma, A. (2016). Functional annotation of sugarcane ESTs using bioinformatics tools. In *International conference on recent trends in bioinformatics and biotechnology for sustainable development, Punjab Agricultural University, Ludhiana, India*.

17   **Duhan, N.**, Sarao, N. K., Mohanpuria, P., Kaur, R., & Sandhu, P. (2014). In silico identification and characterization of potential miRNAs from *Capsicum annuum*. In *National Symposium Crop Improvement for Inclusive Sustainable Development, Punjab Agricultural University, Ludhiana, India 7-9 november 2014*.

18   Jhinjer, R. K., **Duhan, N.**, Yadav, B., & Chunneja, P. (2012). Comparative structure modelling of glyoxalase ii protein of *Oryza sativa*. In *National Symposium on Bioinformatics Feb 02, 2012, Jammu University, Jammu, India*.

19   Kaur, P., **Duhan, N.**, Yadav, B., & Chunneja, P. (2012). In silico detection of simple sequence repeats in expressed sequence tags of wheat. In *National Symposium on Bioinformatics Feb 02, 2012, Jammu University, Jammu, India*.

20   Manchanda, P., **Duhan, N.**, Yadav, B., & Chunneja, P. (2012). In silico prediction of microRNAs from pea (*Pisum sativum*). In *National Symposium on Bioinformatics Feb 02, 2012, Jammu University, Jammu, India*.

21   **Duhan, N.**and Chunneja, P. (2012). In silico identification of *Catharanthus roseus* miRNAs and their role in human metablomics. In *National Symposium on Bioinformatics Feb 02, 2012, Jammu University, Jammu, India*.

22. Verma, L., Yadav, B., **Duhan, N.**, & Chunneja, P. (2012). In silico gene prediction in *Vitis vinifera* using fourth generation tool. In *National Symposium on Bioinformatics Feb 02, 2012, Jammu University, Jammu, India*.

Other Conferences and Workshops

1. International Conference on Sustainable Agriculture for Food and Livelihood Security. [Organized by: Punjab Agricultural University, Ludhiana, India (November 27-29)]. (2012).

2. Research Oriented Techniques in Biotechnology [Conducted by Orbit Biotech Pvt. Ltd. at Guru Nanak Girls College, Ludhiana, India (January 19-25)]. (2011).

3. Bioinformatics Workshop on Proteomics and Genomics [Conducted by Supercomputing Facility for Bioinformatics and Computational Biology, Indian Institute of Technology, New Delhi India (September 16-19)]. (2009).

4. In-silico structure based drug designing of potent inhibitor for tat protein a therapeutic drug target for HIV [ADI Bio-Solution 3B-2 Mohali, India (June 1-30)]. (2009).

Invited Talks

November 22, 2017	LaTeX: A Useful Tool for Scientific Writing and Presentations at *School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana*.
November 1, 2017	Role of Bioinformatics in Conservation and Use in Plant Breeding at Training programme on "Enhancing germplasm use through pre-breeding, evaluation, and frontier" under the *Centre for Advanced Faculty training in Genetics and Plant Breeding, Punjab Agricultural University, Ludhiana*.
February 3, 2017	Open-source computing for young biologists: Overview of Linux Hands-on training on text mining at "Biotechnological platforms for utility production maize" organized at *ICAR-Indian Institute of Maize Research, Ludhiana*.
February 6, 2017	Differential Gene Expression Studies Hands-on training of raw data assembly, identification, and annotation of differential genes "Biotechnological platforms for utility production maize" organized at *ICAR-Indian Institute of Maize Research, Ludhiana*.
August 30, 2016	Computational identification of disease responsive microRNAs "Innovative breeding approaches for the development of climate smart crops" under the *Centre for Advanced Faculty training in Genetics and Plant Breeding, Punjab Agricultural University, Ludhiana*.
August 6-26, 2015	Bioinformatics: A step towards innovation in agriculture.
	Genomic data analysis non-coding RNA identification and their target prediction at Training programme on "Mendelian Genetics to Molecular Genetics in Relevance to Plant Breeding" under the *Centre for Advanced Faculty training in Genetics and Plant Breeding,Punjab Agricultural University, Ludhiana*.
August 23, 2014	Bioinformatics: A step towards innovation at "Milk Genomics workshop" *DAV College Karnal, India*.
August 18, 2014	In silico gene prediction and annotation at *Department of Plant Breeding, Punjab Agricultural University, Ludhiana*.
November 13, 2013	Role of miRNAs in Clinical Research.
	Searching Biological Databases at "Workshop of Bioinformatics and Human Genomics organized by Christian Medical College, Ludhiana" at *School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana*.

Invited Talks (continued)

October 23, 2013	📄	Role of Bioinformatics in Genomics and Primer Designing at *University College, Kurukshetra University, Kurukshetra, India.*
September 27, 2013	📄	In silico gene prediction and annotation at *Department of Plant Breeding, Punjab Agricultural University, Ludhiana.*
March 15, 2013	📄	Protein structure and function prediction at *Department of Biotechnology Kumaun University Nainital, India.*
March 13-14, 2013	📄	Open-source for budding Computational Biologist at "National Symposium and Workshop on Current Advances in Bioinformatics" organized by *Aligarh Muslim University, Aligarh India.*
March 12, 2013	📄	In silico gene prediction and annotation at *Department of Plant Breeding, Punjab Agricultural University, Ludhiana.*

Leadership Skills

- President of the Indian Student Association at Utah State University for the 2021-22 academic session.

Scientific / Professional Services

- Reviewer for the Undergraduate Research and Creative Opportunities (URCO) Grant Program, Utah State University, Logan, UT, 84322

- Served as Moderator and evaluator at Utah State University Research Symposium 2023.

- Designed 8 courses for the Bioinformatics module in B. Tech Biotechnology Degree under Indian Council of Agricultural Research (ICAR) 5th Dean committee for course revision.

- Students Supervised: 20

- Persons trained in Bioinformatics: 10

- Manuscript Reviewer: 7 (*Briefings in Bioinformatics, BMC Genomics, Journal of Plant Biochemistry and Biotechnology, Scientific Reports-Nature, Frontiers in Cell and Developmental Biology, Genes, and Forests*)

Media Contributions

Internet

2021	→	Data Scientists Uncovering Genes that Protect Alfalfa against Salinity Stress. (Read here)

References

1. **Dr. Rakesh Kaundal** (Academic advisor)

   Associate Professor, Bioinformatics; Director, Bioinformatics Facility

   Department of Plants, Soils and Climate

   Center for Integrative BioSystems

   Utah State University, Logan, UT, 84322, USA

   Email: rkaundal@usu.edu

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2. **Dr. Jeanette M. Norton**

   Professor Soil Microbiology/Ecology; Graduate Program Coordinator

   Department of Plants, Soils and Climate

   Utah State University, Logan, UT, 84322, USA

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3. **Dr. Parveen Chhuneja**

   Principal Molecular Geneticist; Director

   School of Agricultural Biotechnology

   Punjab Agricultural University, Ludhiana, Punjab 141002, India

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4. **Dr. Ramamurthy Mahalingam**

   Research Plant Molecular Geneticist

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   Tel: +1 608-890-0300