Sagnik Banerjee

BIOINFORMATICS SCIENTIST

Education_____

Iowa State University   *Ames, IA*
PHD IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY, MINOR IN STATISTICS   *Aug. 2016 – Feb. 2022*
- Thesis: Novel approaches to annotate gene structures, decipher protein interactions and compress alignment data
- Advisors: Dr. Carson M. Andorf, Dr. Karin S Dorman

Jadavpur University   *Kolkata, India*
ME IN COMPUTER SCIENCE AND ENGINEERING   *Aug. 2012 – Jun. 2014*
- Thesis: A consensus approach towards prediction of protein secondary structures
- Advisor: Dr. Mita Nasipuri
- GPA: 9.22/10

Institute of Engineering & Management   *Kolkata, India*
B. TECH IN COMPUTER SCIENCE AND ENGINEERING   *Aug. 2008 – Jun. 2012*
- Advisor: Dr. Tamal Chakrabarti
- GPA: 9.02/10

Research Experience_____

Applied Bioinformatics Scientist at Bristol Myers Squibb   *San Diego*
INFORMATICS AND PREDICTIVE SCIENCES   *Sept. 2021 – Present*
- Established platform to assess the accuracy of human gene insertions in mouse genome
- Detected multiple novel genomic expansion loci for AML patients
- Conducted analysis of single-cell data from various modalities to better understand epigenetics of pancreatic neuro-endocrine tumors
- Designed algorithm to simulate reads from single-cell RNA-Seq data sequenced on 10X platform to perform mutation calling
- Compared long reads data from NanoPore and PacBio to determine applicability to diverse scenarios
- Performed bioinformatics analysis of genome sequence data to find structural changes caused due to gene knockouts and gene knock ins and estimated off target effects

Intern at Bristol Myers Squibb   *Remote*
BIOINFORMATICS AND COMPUTATIONAL GENOMICS INTERN   *Jun. 2021 – Aug. 2021*
- Improved the accuracy of cell type predictions to 99% using single-cell RNA-Seq data
- Constructed an architecture to train and test models with new data

Oak Ridge Institute for Science and Education, USDA-ARS   *Ames, IA*
BIOINFORMATICS AND COMPUTATIONAL BIOLOGY GRADUATE RESEARCH ASSISTANT   *Jan. 2018 – Sept. 2021*
- Improved the structural annotation of >1200 genes in Arabidopsis thaliana by employing changepoint detection from short-read coverage data
- Collaborated with researchers to find >100 temporally significant novel fungal effectors from RNA-Seq data using computational approaches in 3 different pathosystems
- Illustrated the relevance of gene counts to infer regulatory properties of 20,000 genes in Arabidopsis thaliana using machine learning through a collaborative venture
- Explored over 5 assemblers to assemble fungal genomes from short-read data and evaluated their performance
- Formulated deep learning and machine learning models to detect incorrect gene assemblies
- Expedited and improved the extent of compression of short-read alignments by over 30%

- Presented posters at 2 symposia and 5 conferences
- Delivered research talks at 2 student symposia and 5 conferences
- Received 1 award from Publons for placing in the top 1% of reviewers in Molecular Biology and Genetics on Publons global reviewer database
- Wrote 3 technical manuscripts for publication in peer-reviewed journals and over 10 abstracts for international conferences

Department of Plant Pathology and Microbiology, Iowa State University
Ames, IA

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY GRADUATE RESEARCH ASSISTANT   *May. 2017 – Jul. 2019*

- Investigated statistical models leading to the discovery of >400 novel phasiRNAs in barley leaves infected with blumeria
- Designed an optimized computational pipeline, called **NGPINT**, that was used to detect over 100 novel protein interactions from next generation interaction screening (NGIS) data
- Assessed the efficacy of various normalization methods for analyzing NGIS data and participated in designing the pipeline **Y2H-SCORES** to prioritize candidate interactors for secondary validations
- Identified over 200 novel genes involved in regulatory activity in the barley-blumeria patho-system
- Presented poster at 2 symposiums and 2 conferences
- Received 2 awards from Elsevier for reviewing more than 75 papers
- Wrote 1 grant application requesting funding for epigenetics research
- Mentored 1 first-year student in the Bioinformatics & Computational Biology program
- Delivered 2 lectures on expectation maximization using gene counts estimation as an example at a graduate level biostatistics course

Department of English, Iowa State University
Ames, IA

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY GRADUATE RESEARCH ASSISTANT   *May 2017 – Aug. 2017*

- Generated predictive models to assess writer's native language from essay samples written in English
- Performed comparative analysis and helped produce reports outlining results

Department of Computer Science and Engineering, Jadavpur University
Kolkata, India

GRADUATE RESEARCH ASSISTANT   *Jan. 2013 – Dec. 2014*

- Advanced the understanding of post-translational modifications by incorporating 40 high quality physico-chemical properties of amino acids as features
- Investigated the importance of physico-chemical properties in assessing disordered regions of proteins
- Mentored 2 students pursuing masters in academic capacity

Teaching Experience_____

Graduate Teaching Assistant
Ames, IA

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY PROGRAM, IOWA STATE UNIVERSITY   *Jan. 2019 – May 2019*

- Delivered two lectures on gene count estimation. Prepared study materials and homework assignment
- Supported instructor with test administration, curriculum development and assignment grading

Graduate Teaching Assistant
Ames, IA

DEPARTMENT OF GENETICS, DEVELOPMENTAL AND CELL BIOLOGY, IOWA STATE UNIVERSITY   *Jan. 2019 – May 2019*

- Combined hands-on-training with weekly lectures to demonstrate human anatomy with feline specimens and skeletal models
- Devised mnemonic tools to better help students memorize terms and pathways
- Monitored student performance by administering weekly tests

Assistant Professor
Kolkata, India

DEPARTMENT OF ELECTRONICS & COMM. ENGN, INSTITUTE OF ENGINEERING & MANAGEMENT   *Jul. 2015 – Jul. 2016*

- Applied innovative teaching methods to encourage student learning objectives.
- Evaluated and supervised student activities and performance levels to provide reports on academic progress.
- Helped struggling students by providing support outside of classrooms and consistently checking in on progress.
- Performed research to serve as basis for academic writing for publication.
- Mentored and recommended students for future degrees

Assistant Professor *Kolkata, India*
DEPARTMENT OF COMPUTER SCIENCE & ENGN., TECHNO INDIA BATANAGAR *Jan. 2015 – Jul. 2015*
- Delivered lectures and facilitated classroom discussions on various engineering topics
- Organized day-long workshops to train students on current industry practices

Graduate Teaching Assistant *Kolkata, India*
DEPARTMENT OF COMPUTER SCIENCE & ENGN., JADAVPUR UNIVERSITY *Jan. 2019 – May 2019*
- Optimized learning plans and quantified student progress through test administration and supported instructor with curriculum development and assignment grading

Research Projects_____

Constructing Predictive Approaches to Identify Cell Types *Remote*
BRISTOL-MYERS SQUIBB *Sept. 2021 – Present*
- Created machine learning models to predict cell types using single-cell RNA-Seq data for individual tissue types
- Identified less informative features by contrasting inter class variance with intra-class mean

Generation of Consensus Gene Annotation from Multiple RNA-Seq Samples *Ames, IA*
IOWA STATE UNIVERSITY *Jan. 2021 – Present*
- Devised deep learning methods to detect merged gene models and applied changepoint detection to improve their structures
- Used different techniques to merge gene annotation constructed from multiple RNA-Seq samples across a multitude of diverse tissue types and conditions.

Fast Compression of Short Read Alignments *Ames, IA*
IOWA STATE UNIVERSITY *Jan. 2021 – Present*
- Achieved 31% better compression than other state-of-the-art compressors within 66% of time
- Reduced storage requirement by preserving short read mapping location and re-coding the CIGAR to represent mismatches, insertions and deletions
- Accelerated compression and decompression by coding the algorithm in C

Deciphering regulatory associations of *Arabidopsis thaliana* genes *Ames, IA*
IOWA STATE UNIVERSITY *Jan. 2019 – Present*
- Designed predictive models, using machine learning, to characterize regulatory behavior of genes
- Alleviate poor performance by accounting for technical correlations among gene sequences

Mining putative effectors of *Phakopsora Pachyrhizi* using both long- and short- reads *Ames, IA*
IOWA STATE UNIVERSITY *Jan. 2019 – Sept. 2020*
- Processed sequence data from PacBio platform to generate full-length transcripts expressed in soybean leaves infected with *Phakopsora pachyrhizi* over a time-course
- Improved the sequence quality of full-length transcripts by correcting them with paired-ended short reads
- Executed LOCALIZER and APOPLASTP to predict subcellular localization of candidate effectors
- Compared results with other isolates to detect novel effectors in each critical time point of infection

Constructing accurate eukaryotic gene structures from expression data & proteins *Ames, IA*
IOWA STATE UNIVERSITY *Jan. 2018 – Apr. 2021*
- Designed a pipeline, called **FINDER**, to automatically download short reads from NCBI and annotate gene structures from assembled transcripts with no manual intervention
- Applied statistical changepoint analysis to modify gene boundaries and detect more genes
- Integrated gene prediction module with expression analysis to discover more genes
- Extended the gene repertoire by including tissue-specific transcripts in the final annotation
- Asserted the efficacy **FINDER** on model and non-model organisms

Identifying host targets of powdery mildew effector proteins

Ames, IA

IOWA STATE UNIVERSITY

Aug. 2017 – Sept. 2020

- Engineered a novel pipeline, called **NGPINT**, to detect fusion reads from NGIS data, perform differential abundance estimation and subsequent visualization of candidate interactors
- Assessed five normalization techniques to remove technical artifacts and at the same time preserve biological variance

Detection of phasiRNAs on Barley-Blumeria infectome

Ames, IA

IOWA STATE UNIVERSITY

May. 2017 – Dec. 2018

- Implemented hyper-geometric distribution to detect phasiRNAs from short-read expression data
- Resulted in the detection of novel phasiRNAs involved in infection kinetics in the barley-blumeria pathosystem

Native language identification shared task project

Ames, IA

IOWA STATE UNIVERSITY

May. 2017 – Aug. 2017

- Improved the performance of native language identification using an ensemble of machine learning classifiers

A consensus-based approach towards protein secondary structure prediction

Kolkata, India

JADAVPUR UNIVERSITY

Jan. 2013 – May. 2014

- Designed an ensemble classifier comprising of multiple support vector machines (SVM) trained with evolutionary features
- Boosted the performance by augmenting the SVMs with other protein secondary structure predictors

An optimized pattern matching algorithm

Kolkata, India

INSTITUTE OF ENGINEERING & MANAGEMENT

Jul. 2011 – May. 2012

- Designed an algorithm which could perform faster string search on compressed data
- Compressed both the text and the pattern using Huffman's algorithm, where the dictionary used for compressing pattern was same as that of the text
- Rewrote Knuth-Morris-Pratt algorithm (KMP) and Boyre Moore (BM) algorithm such that they could match text and patterns represented in the form of bits

Learner's Management System

Kolkata, India

INSTITUTE OF ENGINEERING & MANAGEMENT

Jul. 2011 – May. 2012

- Designed a website which would cater to the daily needs of academia
- Designed an online whiteboard, using HTML5, which could be used for communication between teachers and students
- Added a module which could check a program against a set of previously provided input and output thereby eliminating the need for manual inspection

Creation of a calculator using an 8051 microcontroller

Kolkata, India

ICEE DESIGN TECHNOLOGIES

May. 2011 - Aug. 2011

- Created a basic calculator using an 8051 microcontroller
- Improved the calculator by programming it to solve quadratic equations

Publications

17. **Banerjee S.**, Andorf C.M., ABRIDGE: An ultra-compression software for SAM alignment files. *bioRxiv*   **2022**

16. **Banerjee S.**, Bhandary P., Woodhouse M., Sen T. Z., Wise R. P., Andorf C. M. **FINDER: An automated software package to annotate eukaryotic genes from RNA-Seq data and associated protein sequences.** *BMC Bioinformatics*   **2021**

15. **Banerjee S.,** Velásquez-Zapata V., Fuerst G., Elmore J. M., Wise R. P. **NGPINT: A Next-generation protein-protein inter- action software.** *Briefings in Bioinformatics*   **2020**

14. Velásquez-Zapata V., Elmore J. M., **Banerjee S.**, Dorman K. S., Wise R. P. **Y2H-SCORES: A statistical framework to infer protein-protein interactions from next-generation yeast-two-hybrid sequence data.** *Plos Computational Biology*   **2021**

13. Elmore M., **Banerjee S.**, Pedley K., Ruck A., Whitham S. **De novo transcriptome of** *Phakopsora pachyrhizi* **uncovers putative effector repertoire during infection.** *Physiological and Molecular Plant Pathology*   **2020**

12. Hunt M., **Banerjee S.**, Surana P., Liu M., Fuerst G., Mathioni S., Nettleton D., Wise R. P. **Small RNA discovery in the interaction between barley and the powdery mildew pathogen.** *BMC Genomics*   **2019**

11. Vajjala S., **Banerjee S. A study of N-gram and Embedding Representations for Native Language Identification**. *Proceedings of the 12th Workshop on Innovative Use of NLP for Building Educational Applications*   **2017**

10. **Banerjee S.**, Ghosh D., Basu S., Nasipuri M. **JUPred_SVM: Prediction of Phosphorylation Sites Using a Consensus of SVM Classifier**. *Proceedings of 5th International Conference on Soft Computing for Problem Solving*   **2016**

9. **Banerjee S.**, Ghosh D., Basu S., Nasipuri M. **JUPred_MLP: Prediction of Phosphorylation Sites Using a Consensus of MLP Classifiers**. *Proceedings of the 4th International Conference on Frontiers in Intelligent Computing: Theory and Applications*   **2016**

8. **Banerjee S.**, Guha S., Dutta A., Dutta S. **Improvement of protein disorder prediction by brainstorming consensus**. *International Conference and Workshop on Computing and Communication*   **2015**

7. **Banerjee S.**, Mitra B., Chatterjee A., Santra A., Chatterjee B. **Identification of relevant physico-chemical properties of amino acids with respect to protein glycosylation prediction**. *International Conference and Workshop on Computing and Communication*   **2015**

6. **Banerjee S.**, Basu S., Ghosh D., Nasipuri M. **PhospredRF: Prediction of protein phosphorylation sites using a consensus of random forest classifiers**. *International Conference and Workshop on Computing and Communication*   **2015**

5. **Banerjee S.**, Nag S., Tapadar S., Ghosh S., Guha S., Bakshi S. **Improving protein protein interaction prediction by choosing appropriate physiochemical properties of amino acids**. *International Conference and Workshop on Computing and Communication*   **2015**

4. **Banerjee S.**, Basu S., Nasipuri M. **Big Data Analytics and Its Prospects in Computational Proteomics**. *Information Systems Design and Intelligent Applications*   **2015**

3. **Banerjee S.**, Chakrabarti T., Sinha D. **A Faster Fitness Calculation Method for Genetic Algorithm Based Multiple Protein Sequence Alignment**. *International Journal of Scientific & Engineering Research*   **2013**

2. **Banerjee S.**, Chakrabarti T., Sinha D. **Finding all Occurrences of a Pattern by a Genetic Algorithm based Divide-and- Conquer Method**. *International Journal of Computer Applications*   **2013**

1. **Banerjee S.**, Chakrabarti T., Sinha D. **A Genetic Algorithm Based Pattern Matcher**. *International Journal of Scientific & Engineering Research*   **2013**

Technical Skills

Next Generation System (NGS)	Illumina short-read sequencing, PacBio long-read sequencing, Yeast two-hybrid NGS, RNA-Seq, Ribo Seq, CAGE Seq, RAMPAGE, ATAC Seq, Iso-Seq, ChIP-Seq, AmpliSeq, DNA-Seq
Statistics	Differential gene expression, Gene count normalization, Changepoint detection, Hypothesis testing
Machine learning	Linear/logistic Regression, Clustering, Classification, Cross Validation, Feature Selection, Feature Extraction
Deep learning	Recurrent Neural Networks, Bi-directional Recurrent Neural Networks
Predictive applications	Gene function prediction, Protein secondary structure prediction, Protein post-translational modification prediction, Protein disordered region prediction
Back-end	PHP, JSP, Servlets, MySQL, LAMPP, MAMP
Front-end	HTML5, Wordpress, Javascript
Software design	Version control, GitHub deployment, Code maintenance
Programming Languages	Python (scikit learn, biopython, NumPy, Pandas, Matplotlib, TensorFlow, Keras, PyTorch), R (ggplot2, DESeq2), Unix, C, C++, Prolog, Java, JavaScript, PHP, MySQL, JSP, Perl
Genomics	Short-read alignment (STAR, HiSAT2, Bowtie, OLego), Long-read alignment (STARLong, GMAP), Long-read generation (SMRTLink), PacBio read error correction (Hercules, CoLorMap, HECIL, LorDEC, HALC), Gene annotation (FINDER, BRAKER, MAKER, PASA), Genome annotation, Genome assembly (SOAPdenovo, masurca, Spades, ABySS), Variant calling (GATK, FreeBayes), Epigenetic analysis (MEME), Promoter mining, Similarity search (NCBI-BLAST, DIAMOND, exonerate, Spalign, EMBOSS), High-throughput data manipulation (Samtools, Bamtools, Picard, Bedtools, Bedops)
Transcriptomics	Transcriptome assembly (Trinity, PsiCLASS, CLASS2, Strawberry, Stringtie, Scallop, Velvet, Oasis, Trans-ABySS, SOAPdenovo-Trans), Gene co-expression analysis (WCGNA), Gene count generation (Salmon, RSEM, HTSeq-count), Differential gene analysis (EdgeR, DESeq2), Single-cell transcriptomics (SEURAT)
Proteomics	Protein-protein interaction, Effector mining, Post-translational modification
Genome browsers	IGV, UCSC genome browser, jbrowse, Apollo, Geneious
Biological databases	NCBI SRA, NCBI GEO, EMBL, GenBank, UniProt, Swiss Prot, Ensembl, BioGRID, PDB, PhosphoELM, PhosphoSitePlus, DisProt, SCOP
Miscellaneous skills	High performance computing (SLURM), Pipeline construction, Natural language processing, LaTeX, Molecular Biology, Text analysis, Life sciences, Microsoft office, Microsoft PowerPoint, WPS, Slack, Open office, Eclipse, Jupyter Notebooks, PyCharm
Software containers	Docker, Singularity, Conda
Software workflow managers	Common Workflow Language (CWL), Snakemake, Nextflow

Virtual meetings	Zoom, WebEx, Google meet, Skype
Soft skills	Superior interpersonal skills, Public speaking, Demonstrated collaborative success

Presentations_____

POSTERS

9. Accurate construction of eukaryotic gene structures using FINDER – a fully automated gene annotator
14th GREAT LAKES BIOINFORMATICS CONFERENCE (GLBIO)

Virtual Event

May 2021

8. Applying statistical analysis of read coverage data to improve eukaryotic gene structures using FINDER - a completely automated gene annotator
8th GRADUATE PROFESSIONAL STUDENT CONFERENCE, IOWA STATE UNIVERSITY

Virtual Event

Apr. 2021

7. FINDER: A fully automated pipeline to FIND accurate gene structures from proteins and RNA-Seq expression data
11th ACM CONFERENCE ON BIOINFORMATICS, COMPUTATIONAL BIOLOGY AND HEALTH INFORMATICS

Virtual Event

Sep. 2020

6. FINDER1: an automated gene-annotator from multiple sources of data
28th CONFERENCE ON INTELLIGENT SYSTEMS FOR MOLECULAR BIOLOGY

Virtual Event
Jul. 2020

5. A computational pipeline to identify host targets of fungal virulence proteins using next generation yeast two-hybrid
26th CONFERENCE ON INTELLIGENT SYSTEMS FOR MOLECULAR BIOLOGY

Chicago, IL

Jul. 2018

4. A computational pipeline to identify host targets of fungal virulence proteins using next generation yeast two-hybrid
2018 LOOMIS/CBC SYMPOSIUM & WORKSHOP: GENOME EDITING — PUTTING TOGETHER THE PIECES

Ames, IA

May 2018

3. A computational pipeline to identify host targets of fungal virulence proteins using next generation yeast two-hybrid
1st MIDWEST STATISTICAL MACHINE LEARNING COLLOQUIUM, IOWA STATE UNIVERSITY

Ames, IA

May 2018

2. A computational pipeline to identify host targets of fungal virulence proteins using next generation yeast two-hybrid
5th GRADUATE PROFESSIONAL STUDENT CONFERENCE, IOWA STATE UNIVERSITY

Ames, IA

Apr. 2018

1. A computational pipeline to identify host targets of fungal virulence proteins using next generation yeast two-hybrid
4th ANNUAL BIOINFORMATICS AND COMPUTATIONAL BIOLOGY SYMPOSIUM

Ames, IA

Mar. 2018

TALKS (RESEARCH)

6. Combining expression evidence with predicted structures to enrich gene model repertoire in eukaryotes using FINDER – a fully automated gene annotator
ISCB-AFRICA ASBCB CONFERENCE ON BIOINFORMATICS

Virtual Event

Jun 2021

5. Accurate construction of eukaryotic gene structures using FINDER – a fully automated gene annotator
14th GREAT LAKES BIOINFORMATICS CONFERENCE (GLBIO)

Virtual Event

May 2021

4. Constructing genes from raw RNA-Seq data using FINDER – a fully automated software for eukaryotic gene annotation
7th ANNUAL BIOINFORMATICS AND COMPUTATIONAL BIOLOGY SYMPOSIUM

Virtual Event

Apr. 2021

3. Applying statistical analysis of read coverage data to improve eukaryotic gene structures using FINDER - a completely automated gene annotator
8th GRADUATE PROFESSIONAL STUDENT CONFERENCE, IOWA STATE UNIVERSITY

Virtual Event

Apr. 2021

2. Applying statistical analysis of read coverage data to improve eukaryotic gene structures using FINDER - a completely automated gene annotator
63rd ANNUAL MAIZE GENETICS MEETING

Virtual Event

Mar. 2021

1. A computational pipeline to identify host targets of fungal virulence proteins using next generation yeast two-hybrid
6th ANNUAL BIOINFORMATICS AND COMPUTATIONAL BIOLOGY SYMPOSIUM

Virtual Event

Mar. 2020

INVITED TALKS

2. "Accurate construction of eukaryotic gene structures using FINDER – a fully automated gene annotator" -
RESEARCH TALK AT MINNESOTA STATE UNIVERSITY, DEPARTMENT OF BIOLOGICAL SCIENCES

Virtual Event

Feb. 2022

1. "Tell Me About Yourself" – The First Interview Question
CAREER SERVICE WEBINAR

Virtual Event

Apr. 2021

Achievements_____

Bravo points, received 6000 bravo points as a reward for designing analysis pipeline to assess fidelity of gene editing, Bristol-Myers Squibb	**2022**
Second place, Oral presentation, Graduate Professional Student Research Conference	**2021**
First place, Flash talk, Student seminar, Bioinformatics & Computational Biology Program	**2020**
Travel award, Awarded $150 travel fellowship for coming in 3rd at a peer-evaluated Student Seminar course, Bioinformatics & Computational Biology Program	**2020**
Travel award, Awarded $200 travel fellowship for coming in 2nd at a peer-evaluated Student Seminar course, Bioinformatics & Computational Biology Program	**2018**
Student Poster award, 3rd prize winner for Student Poster Presentation at the 4th Annual Bioinformatics and Computational Biology Symposium	**2018**

Recognized Reviewer, Awarded for completing 70 manuscript reviews between 2015-2017   **2017**

Outstanding Reviewer, Awarded for being within the top 10th percentile of reviewers for the Journal, Applied Soft Computing Journal, Elsevier   **2016**

Certificate of Merit, Awarded Certificate of Merit in Chemistry for being among the top 0.1% of successful candidates, Central Board of Secondary Education, India   **2008**

Central Sector Scholarship, Awarded for exceptional performance in class XII exams, Central Board of Secondary Education, India   **2008**

Mentoring Experience_____

Mentor, Served as a Mentor for Larry Davis, a first year PhD student in Bioinformatics and Computational Biology Program (BCB), Iowa State University   **2018**

Recommender, Provided Letter of Recommendation for Sourav Ghosh, a prospective MS student in the Department of Computer Science and Engineering, Institute of Engineering and Management, Kolkata, India, currently pursuing MS at TU Dresden, Germany   **2017**

Research Advisor, Mentored 12 students in groups of 6 (BS Level) to guide them in achieving the goals laid out for publication and presenting research at scientific conferences   **2015-2016**

Academic Mentor, Mentored 2 graduate students (MS Level) to support their advancement in research activity   **2013**

Leadership Skills & Service_____

Critical review of research manuscripts   *India, USA*
REVIEWER   2013 - present
- 58 research manuscripts in Applied Soft Computing, Elsevier
- 1 research manuscript in PLOS One Computational Biology
- 35 research manuscripts in BMC Genomics
- 20 research manuscripts in BMC Bioinformatics
- 4 research manuscripts in 2021 IEEE 18th India Council International Conference

Presentation Judgement   *Virtual*
SESSION CHAIR
- Served as the session chair for the session titled "Information Theory & Coding" at the Interdisciplinary Research in Technology & Management conference   Feb. 2022

Graduate Professional Student Senate (GPSS)   *Ames, IA*
SENATOR, DEPARTMENT OF PLANT PATHOLOGY AND MICROBIOLOGY   2018 - 2019
- Communicated important information from senate meetings to department faculty and student
- Participated in annual senate elections and volunteered in organizing the annual conference

Bioinformatics and Computational Biology Graduate Student Organization   *Ames, IA*
VICE-PRESIDENT   2017 - 2018
- Assisted participants in 2, one day-long workshops
- Reviewed venue and optimized expenditure while organizing the 4th annual BCB student symposium

State Science and Technology Fair of Iowa   *Ames, IA*
LEAD JUDGE   2019 - 2021
- Selected 5 teams in each of 10 categories from a total of 100 participants
- Evaluated teams from all categories to select the best presentations
- Examined the performance of each project based on novelty, presentation, and response to questions

Women in Science

PRESENTER

- Presented methods to assemble DNA to 30 middle school female students