SWADHA SINGH

Computational Biology | Bioinformatics
+1-650-260-8147 | swadha22@gmail.com | LinkedIn

EDUCATION

Doctor of Philosophy- Quantitative & Systems Biology   Merced, CA
University of California, Merced   *Jan 2017 – Oct 2022(expected)*

Master of Science - Quantitative & Systems Biology   Merced, CA
University of California, Merced   *Jan 2017 – June 2020*

Master of Science – Bioinformatics   Allahabad, India
University of Allahabad, India   *July 2012 – July 2014*

Bachelor of Science – Applied Science   Allahabad, India
University of Allahabad, India   *July 2009 – July 2012*

WORK EXPERIENCE

➢ **University of California, Merced**   *Jan 2017 – present*
Graduate Student Researcher   *PI: Dr. Scott Roy and Dr. Diana Chu*
Histones are proteins that package the DNA. I study histone variants in nematodes:

- Project-1: To understand the Histone H2A variant incorporation dynamics before and after fertilization in *C.elegans*;
  - o Developed custom **ChIP-seq** processing pipeline and deployed on university HPC for quality control, genome alignment, peak-calling, pean annotation using fastx toolkit, Bowtie2, SAMTOOLS, MACS2, chipseeker, chippeakAnno etc.
  - o Developed custom **RNAseq** automated pipeline, for quality control/adapters removal, genome alignment, and differential expression analysis for RNAseq using fastx toolkit, STAR, HTseq and DESeq2 etc.
  - o Designed and implemented computational workflow to correlate ChIP and RNAseq data to understand tissue specific nature of the histone H2A variants in *C. elegans*.
  - o Conceptualized and correlated our ChIP and RNAseq data with already published post translational modification states for active/inactive genes.

- Project 2- [To reconstruct the evolutionary history of *C. elegans's* histone H2A variants in Nematodes](#);
  - o Created an automated workflow and leveraged the intron position conservation to trace the origins and evolution of the H2A variants (HTZ-1, HTAS-1 and HIS-35) in 126 reported nematode genomes.
  - o Used BASH, PERL and Python programming languages to build the overall datamining and evolutionary analysis workflow which incorporates the tools BLAST, CLUSTALW, MUSCLE, IQ-TREE and deployed them on the University HPC.

- Project 3- To characterize the evolutionary loss and replacement of core histones (H2A, H2B, H3 and H4) in the *C. elegans'* relatives *C. monodelphis* and *Diploscapter pachys*.
  - o Used BASH, PERL and Python programming languages to build the overall workflow.

➢ **San Francisco State University**   *May 2016-Dec 2017*
Volunteer   *PI: Dr. Diana Chu*
I used genetic analysis to understand how chromosome architecture and dynamics influence gene expression and male fertility in the model organism *C. elegans,* and to determine if worms with a mutant H2A histone (HTAS-1 and HTZ-1 gene) are infertile.

Volunteer   *PI: Dr. Scott Roy*
Analyzed Hi-C (high-throughput chromosome conformation capture) data to study the whole chromatin architecture of various eukaryotes, to test the hypothesis that splicing of rare 'minor' type introns are facilitated by clustering of these introns (and their host genes) in the 3D genome.

➢ **Project Assistant, National Botanical Research Institute, Lucknow, India**   *Oct 2014-Aug 2015*
Project Assistant II   *PI: Dr. Samir Sawant*
I assessed the impact of stress conditions on the chromatin-interactome network of *Arabidopsis thaliana*. I have analyzed the RNAseq data and correlated it with the Hi-C (high-throughput chromosome conformation capture) data in this study.

➢ **Indian Institute of Toxicology Research, Lucknow, India**   *June 2014 - Sept 2014*
Summer Intern.   *PI: Dr. Vikas Srivastava*
Performed screening, validation, and confirmation of the presence of single nucleotide polymorphism (SNPs) in two strains of laboratory mouse (*Mus musculus*): C57BL/6 and BALB/c to find whether the strains are maternally imprinted or paternally imprinted.

➢ **University of Allahabad, India**   *July 2012-July 2014*
Graduate Student Researcher   *PI: Dr. Dwijendra Gupta*
Evaluated six machine learning algorithms for their efficiency to classify "Riboswitches". For determining effective classifier, the algorithms were compared on the statistical measures of specificity, sensitivity, accuracy, F-measure and receiver operating characteristic (ROC) plot analysis.

Independent Graduate Student Researcher
Facilitated an *in-silico* analysis of Sirt2 from *Schistosoma mansoni* to determine its structures, conformations, and interactions with inhibitors.

➢ **National Agri - Food Biotechnology Institute, Mohali, India**   *June 2013-July 2013*
Summer Intern.   *PI: Shrikant Mantri*
Performed reference gene-based mapping & clustering of the newly added sequences of *Triticum aestivum* in UniGene database to find Single Nucleotide Polymorphism in the sequences.

BIOINFORMATICS & COMPUTATIONAL SKILLS

- Next Generation Sequencing Data Analysis.
- Performed high-throughput data analysis by making pipelines.
- Programming language: Python, Perl, R, BASH.
- Operating System: Linux(Ubuntu), CentOS, Windows.
- Microsoft office (Visual basics scripting (Macros))

PUBLICATIONS

- Singh R, **Singh S**, Pandey PN. 2016. In-silico analysis of Sirt2 from *Schistosoma mansoni*: Structures, conformations, and interactions with inhibitors. Journal of Biomolecular Structure & Dynamics 34(5):1042-51.
- **Singh S** and Singh R. 2017. Application of supervised machine learning algorithms for the classification of regulatory RNA riboswitches. Briefings in Functional Genomics 16(2):99-105.
- Yadav VK, **Singh S,** et al. 2022. Stress conditions modulate the chromatin interactions network in Arabidopsis. Frontiers in Genetics 12:799805.
- **Singh S**, Chu D, Roy S. 2022. Nematode histone H2A variant evolution reveals diverse histories of retention and loss and evidence for conserved core-like variants. (Submitted to PLOS Genetics: PGENETICS-D-22-00786).
- **Singh S**, Tabuchi T, Roy S, Chu D et.al. Histone H2A variant incorporation dynamics before and after fertilization in *C. elegans*. (*in prep.*)

AWARDS & GRANTS

- Graduate Student Award | AY 2018-2019 | UC Merced $9446

- Origins of Intron-Exon Structures
  - ❖ National Science Foundation (NSF:1616878) | 2016-2021 $539,862.00

- Defining transcriptional and post-transcriptional regulatory mechanisms of the paternal histone variant HTAS-1 in germ cell and embryo development.
  - ❖ National Science Foundation (NSF: STC DBI-1548297) | 2016-2021 $24,000,000.00
  - ❖ National Science Foundation (NSF: MCB RUI 1817611) | 2018-2022 $656,826.00
  - ❖ National Institutes of Health (NIH: NICHD1R03HD093990A1)

TEACHING EXPERIENCE

- BIO-001 Lab (Spring 2017) Two sections, 30 students each.
  Taught the major concepts in biology including origin of life, evolution, DNA, genes and genomes. Principles and patterns of inheritance, biotechnology, biodiversity, earth systems, environments and disease relationships in addition to ecosystem structures, function, nutrient cycles, pollution, and genotypes to phenotypes.

- BIO-002 Lab (Fall 2017) Two sections, 30 students each.
  Familiarized students with fundamental techniques, materials and equipment pertinent to molecular biology practices. Provided hands-on experience on methodologies for studying biological systems and their molecular components to improve the application of engineering principles to solve bioengineering and biochemical engineering problems. Laboratory practices were described in the context of the application of Biotechnology to medicine, bioremediation, raw material production, biofuels, and agriculture. Discussed the ethical and societal considerations as well.

- BIO 002 Discussion (Spring 2018). Three sections, 30 students each.
  Conducted discussions among students to introduce them to the molecules and molecular processes underlying life. Gave them an overview of structures and chemical properties of biological macromolecules. Familiarized the students with the principles of molecular and cell biology to increase the understanding of biological systems, and to improve the application of engineering principles to solve bioengineering and biochemical engineering problems. Topics include an introduction to the cell, the structure, function and metabolism of the main biomolecules, DNA replication, transcription and translation, control of gene expression, an introduction to molecular biotechnology: recombinant DNA, connections between molecular biology and disease, ethical considerations in DNA manipulation.

PROFESSIONAL REFERENCE ON REQUEST