Research Project 1: ***"Bacterial genome analysis of GC skew in order to find compositional bias ness of genes on leading/lagging stand"***
Duration of Project: 5-7 months
Key Technologies: GC skew biasness, Inversion analysis Research

Background: The DNA replication and transcription machinery share a common DNA template and therefore can collide with each other co-directionally or head-on. Replication-transcription collisions can cause replication fork arrest, premature transcription termination, DNA breaks, and recombination intermediates threatening genome integrity. Collisions may also trigger mutations, which are major contributors to genetic disease and evolution. However, the nature and mechanisms of collision-induced mutagenesis remain poorly understood.

Aim: Analysis of inversion and percentage distribution of genes on leading vs. lagging strands across the bacterial domain and classes. Comparative results were achieved when compared with the doriC database. Further visual validation of such Inversions with IGV and genome annotation using Prokka

Research Project 2:***"Prediction of miRNAs within the long non-coding RNAs and search for their targets"***
Duration of Project: 3-4 months
Key Technologies: mRNA silencing, Gene Ontology (GO) enrichment analysis

Background: Characterization of microRNAs (miRNAs/miRs) has become sterling work of transcriptomic biology. Originally miRNA was reported in *C.elegans* and later identified in mammals including humans. It is predicted that miRNAs account for 1-5% of human genome and regulate at least 30% of protein coding genes. Long non-coding RNA (lncRNA) influences post-transcriptional regulation by interfering with the miRNA pathways either by up-regulating or down-regulating them. Here in this study, we hold a hypothesis that maternally expressed 3(MEG3), a long non-coding RNA of about size 1.6Kb, located at chromosome 14q32.2 in humans contain hidden signatures of miRNA genesis and play important function after being processed into their smaller equivalents.

Results: MEG3 gene which encodes for a non-coding RNA, a total of 168 mature miRNAs were predicted using miRbase from six MEG3 transcripts, which include five splice variants and MEG3 primary assembly. Gene Ontology enrichment analysis of target genes was performed using Gorilla and DAVID which advocates pathway and disease association with MEG3. MEG3 was found to be associated with pathways in cancer, tobacco use disorder, bone development, type II diabetes, and in Alzheimer's.

Experience: This particular research helped me to develop inquisitiveness in the subject and thereafter, I am interested in understanding the mechanisms of mRNA fate decisions. The question of 'how does a cell decide to translate, store or degrade an mRNA at a given time' intrigues me as a biological problem. How do cells accomplish this particular task and how did these decisions evolve? such questions are relevant because mRNA fate decisions at the level of translation/decay play a critical role in various cellular processes as well as in diseases such as Cancer and Neurodegenerative disorders such as Alzheimer's and Parkinson's.