

## **MKU-Industry Consultancy Cell “Bioinformatics Consultancy Services”**

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### **Prelude:**

I have fifteen years of expertise in the field of “Bioinformatics and Computational genomics” with cutting edge technologies. I have developed variety of standalone computational tools and web-servers for biological applications. I did biological data analysis for research groups from multiple institutions which are evident from the publications. I intend to provide bioinformatics solutions to the postgraduates, researchers, faculty members and entrepreneurs. I am committed to give professional consultancy services to meet the highest quality and degree of precision required by above target groups.

### **Objectives:**

Our main objective is “Analysis of High-throughput datasets in Biology” for biological interpretations. I am able to offer Bioinformatics services in the following fields with the available hardware and open source softwares.

- ❖ Genomics
- ❖ Transcriptomics
- ❖ Next Generation Sequencing Data analysis
- ❖ Whole Genome assembly & annotation
- ❖ Microarray Data Analysis
- ❖ Epigenomics
- ❖ Phylogenomics
- ❖ Toxicogenomics
- ❖ Metabolomics
- ❖ Pathway analysis

- ❖ RNA structure analysis
- ❖ Biomarker identification
- ❖ MLST typing of pathogens
- ❖ Evolutionary dynamics of viruses
- ❖ **Network analysis**
- ❖ Microbiome, meta-genomics, and environmental genetics
- ❖ Machine learning **for biological applications**
- ❖ Graphics and visualization **of bioinformatics results for publications**
- ❖ Analysis of high-throughput large datasets in Biology

**Available Infrastructure for Bioinformatics solutions:**

- ✓ HP Z4 series workstation (Linux)
- ✓ HP ENVY Phoenix workstation (Linux)
- ✓ HP Clients (3 Nos)
- ✓ HP Laptop
- ✓ Compaq Laptop
- ✓ HP MFP 1536 dnf
- ✓ UGC-INFLIBNET internet access to literature
- ✓ 3 KVA UPS
- ✓ 1 KVA UPS
- ✓ **Open source software's compatible with Linux/Unix platforms**

**Mode of operation:**

1. Above target clients **may** approach us and discuss their proposed project
2. We will associate with them to develop a computational protocol, possibly from our earlier analysis pipelines or new pipelines
3. We will provide the suitable computational tools/resources and analysis services (research contract basis) to get the fruitful results
4. After analysis we will deliver the computational results in the universally accepted formats (Ex. followed by GenBank/DDBJ/EMBL)
5. Project completion report will be delivered to the clients with proper interpretation on the results.