<div align="center">**Training Course- 2 (Advanced)**
<u>Bioinformatics for molecular biologists</u></div>

Introduction:
Bioinformatics is mathematical, statistical and computing methods that aim to solve biological problems using DNA and amino acid sequences and related information. Thus, Bioinformatics involves the integration of computers, software tools, and databases in an effort to address biological questions. Each of these important areas in bioinformatics aims to understand complex biological systems. Each of these important areas in bioinformatics aims to understand complex biological systems.

Beneficiaries: Scientists, researchers, undergraduate students and post graduate students who are interested in biological and computational research. This includes medical, veterinary, agricultural, aquaculture , many other biology related fields.

Duration: This intensive training course will be held during five successive days, 10 hours per day. During this course they will be able to have good understanding of some useful bioinformatics tools to be applied in their own research.

Day-1: Using Nucleotide Sequence Databases

- Retrieving GenBank entries without accession numbers
- Using a Gene-Centric Database
- Working with Whole-Genome Databases
- Working with complete viral genomes
- Working with complete bacterial genomes
- More bacterial genomics at TIGR
- Microbes from the environment at DoE
- Exploring the Human Genome
- Finding out about the Ensembl project

- Reading into Genes and Genomes
- Making Use (and Sense) of GenBank
- Making sense of the GenBank entry of a prokaryotic gene
- Making sense of the GenBank entry of an eukaryotic mRNA
- Making sense of a GenBank eukaryotic genomic entry
- Working with related GenBank entries

Using Protein and Specialized Sequence Databases

- The Cross-References
- The Keywords
- The Features
- Finally, the sequence itself
- Finding Out More about Your Protein
- Finding out more about "modified amino acids
- Some advanced biochemistry sites
- Finding out more about biochemical pathways
- Finding out more about protein structures
- Finding out more about major protein families

- From Translated ORFs to Mature Proteins
- ORFs: What you see is NOT what you get
- A personal final destination for each protein
- A combinatorial diversity of folds and functions
- Reading a Swiss-Prot Entry
- Deciphering the EGFR Swiss-Prot entry
- General information about the entry
- Name and origin of the protein
- The References
- The Comments

Day-2 :Working with Protein 3-D Structures

- Beyond This Chapter
- Finding proteins with similar shapes
- Finding other PDB viewers
- Classifying your PDB structure
- Doing homology modeling
- Folding proteins in a computer
- Threading sequences onto PDB structures
- Looking at structures in movement
- Predicting interactions

- From Primary to Secondary Structures
- Predicting the secondary structure of a protein sequence
- Predicting additional structural features
- From the Primary Structure to the 3-D Structure
- Retrieving and displaying a 3-D structure from a PDB site
- Guessing the 3-D structure of your protein
- Looking at sequence features in 3-D

Day 3 : Working with RNA

- Using PatScan to look for RNA patterns
- Finding the "New" RNAs: miRNAs and siRNAs
- Doing RNA Analysis for Free over the Internet
- Studying evolution with ribosomal RNA
- Finding the small, non-coding RNA you need
- Generic RNA resources

- Predicting, Modeling and Drawing RNA Secondary Structures
- Using Mfold
- Interpreting mfold results
- Forcing interaction in mfold
- Searching Databases and Genomes for RNA Sequences
- Finding tRNAs in a genome

Building Phylogenetic Trees

- Knowing what's what in your tree
- Displaying your phylogenetic tree
- Doing Phylogeny for Free over the Internet
- Finding online resources
- Finding generic resources
- Collections of orthologous genes

- Finding Out What Phylogenetic Trees Can Do for You
- Preparing Your Phylogenetic Data
- Choosing the right sequences for the right tree
- Preparing your multiple sequence alignment
- Building the Kind of Tree You Need
- Computing your tree