Aims
The Bioinformatics course aims to provide the student with knowledge enabling to combine in an integrated way the computer science disciplines with the chemical-biological ones. The computational methods for genomes analysis and processing of signals generated by high-throughput technologies will be illustrated. Also, the analytical techniques of data deriving from transcriptional profiles and genotyping will be faced in order to evaluate the biological function of genes, regulatory sequences and molecular interaction networks present in the genome of prokaryotic and eukaryotic organisms.

Prerequisites
Basic skills in mathematics, computer science and statistics applied to biology, organic chemistry, cell biology, biochemistry, molecular biology, genetics are warmly recommended to attend the Bioinformatics course.

Contents
Introduction to Bioinformatics: the use of bioinformatics in genomic research. Introduction to biological databases: primary databases of nucleotide sequences (EMBL, GenBank and DDBJ), specialized databases (Ensembl / UCSC Genome Browser, LocusLink, RefSeq, SwissProt, Gene Ontology, Pfam, Kegg), and databases of protein sequences and structures. Browsers for bioinformatics. The interrogation systems (SRS and Entrez).
Alignment of nucleic acid sequences and proteins: Concepts and principles of sequence alignment. Sequence homology and similarity. Definition of the score of an alignment. Multiple alignment of sequences. The ClustalW program. Methods of representing a multiple alignment.
Phylogenetic analysis: tree of life, cladograms, phylograms, rooted and unrooted trees, UPGMA, Neighbour-joining, maximum likelihood, parsimony, bootstrapping.
Genomes: mapping, DNA fingerprinting, BAC, genome sequencing methods, WGS, assembly, contigs, scaffolds, draft e finished sequences.
Functional motifs. Search for promoters and genes into genomes. Genome browsers. Functional annotation of genes and genomes. Classification and comparison of protein structures. Inference of protein secondary and tertiary structure. Homology modelling, threading, ab initio methods. Computational methods for the inference of protein interactions. Integrative methods. Protein networks. Databases of molecular interactions, pathways, genetic diseases, SNPs. Text mining. Markov chains and hidden Markov models. Artificial neural networks. genetic algorithms. Docking. Mechanic and Molecular dynamics.

Textbook
Introduzione alla BioInformatica. Attimonelli M., Helmer Citterich, Pesole G., Valle G., Zanichelli.
Teacher's presentations will be made available to students.