



BIOINFORMATICS

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What is Bioinformatics?

Bioinformatics represents a new, growing area of science that uses computational approaches to answer biological questions.

- * Use computer technologies and statistical methods.
- * Manage and analyze a huge volume of biological data.

Bioinformatics?

- * Originated from biology and informatics
- * Informatics means analysis of information
- * Bioinformatics is the analysis of biological information

Correlated subjects

- * Biology
- * Biochemistry
- * Molecular biology
- * Microbiology
- * Genetic engineering
- * Mathematics
- * Statistics
- * Computer science

Why Bioinformatics?

- * Analyze huge volume of data
- * Don't need expensive wet lab
- * Same research can be repeated many times
- * No adverse effect
- * Time saving

Bioinformatics brings together

- * Large databases of biological information
- * Computational techniques of analysis
- * Databases
 - Sequence (1D)
 - Genome projects (Human, mouse, Fruit-fly, slime-mould, Pea, Rice, ...)
 - 120,000 protein sequences
- * Molecular Structure (3D)

What Bioinformatics Do?

- * DNA Sequence Analysis
- * Working with a single protein sequence
- * RNA analysis

What Bioinformatics Do?

(DNA Sequence Analysis)

- * Catching Errors
- * Removing vector sequences
- * Computing /verifying restriction map
- * Designing PCR primers
- * Analyzing DNA composition
- * Establishing the G+C content of your sequence
- * Finding internal repeats in your sequence
- * Identifying genome-specific repeats in your sequence
- * Finding protein-coding regions
- * ORFing your DNA sequence
- * Analyzing your DNA sequence with GeneMark
- * Finding internal exons in vertebrate genomic sequences
- * Complete gene parsing for eukaryotic genomes
- * Assembling sequence fragments
- * Managing large sequencing projects

What Bioinformatics Do?

(working with a single protein sequence)

- * Predicting the main physico-chemical properties of a protein
- * Digesting a protein in a computer
- * Doing primary structure analysis
- * Looking for transmembrane segments
- * Looking for coiled-coil regions
- * Predicting Post-translational Modification in your protein
- * Finding known domains in your protein
- * Discovering new domain in your proteins

What Bioinformatics Do?

(RNA Analysis)

- * Structure prediction
- * Function prediction
- * Translation
- * discovery

Practical examples

- * **Genome annotation**
In the context of genomics, annotation is the process of marking the genes and other biological features in a DNA sequence.
- * **Computational evolutionary biology**
build complex computational models of populations to predict the outcome of the system over time track and share information on an increasingly large number of species and organisms.
- * **Biodiversity**
- * **Analysis of gene expression**
- * **Analysis of regulation of the cell cycle**
- * **Analysis of protein expression**
- * **Prediction of protein structure**
- * **Drug design**
- * **Predict function of unknown protein**
- * **Predict reaction of unknown protein with enzymes**
- * **Working with unknown protein in research**

Practical examples

- * **High-throughput image analysis**
 - DNA mapping
 - RFLP
 - Chromosome walking
 - Restriction mapping
 - Fingerprinting
- * **Genetic Disease analysis**
- * **Analysis of mutation in cancer**
- * **Uses of bioinformatics in agriculture**
- * **Application of Remote Sensing and GIS for agriculture**
 - Evolutionary studies
 - Crop improvement
 - Insect resistance
 - Improve nutritional quality
 - Development of Drought resistance varieties

Software & Tools

- * Software tools for bioinformatics range from simple command-line tools, to more complex graphical programs and standalone web-services available from various bioinformatics companies or public institutions.
- * The computational biology tool best-known among biologists is probably BLAST, an algorithm for determining the similarity of arbitrary sequences against other sequences, possibly from curated databases of protein or DNA sequences.
- * BLAST is one of a number of generally available programs for doing sequence alignment. The NCBI provides a popular web-based implementation that searches their databases.

BLAST

- * **B**asic **L**ocal **A**lignment **S**earch **T**ool
- * It is an algorithm for comparing biological sequences information, such as amino acid sequence of different proteins or nucleotides of DNA sequences.
- * BLAST is used to identify library sequences that resembles the query sequences.
- * BLAST is a tool for alignment of sequences.

BLAST

- * BLAST was originally developed by NCBI
- * The NCBI site provides binary files for the following operating systems and platforms.
 - Unix
 - Linux
 - Mac
 - Windows
 - IBM AIX 5.1

FASTA

- * FASTA is a DNA and protein sequence alignment software package.
- * FASTA package contains programs for protein: protein, DNA: DNA, protein: translate DNA, and ordered or unordered peptide searches.
- * A major focus of the package is the calculation of accurate similarity statistics, so that biologists can judge whether an alignment is likely to have accurate by chance.

CONCLUSION

The recent enormous increase in biological data has made it necessary to use computer information technology to collect, organize, maintain, access, analyze the data. Computer speed, memory, exchange of information over the internet has greatly facilitated bioinformatics.

The bioinformatics tools available over the internet are accessible, well developed, fairly comprehensive, and relatively easy to use.

THANKS