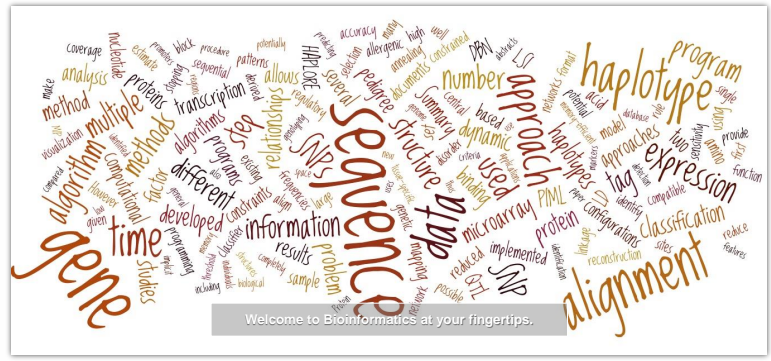


As new genome projects generate large amounts of data, the application of computers is becoming an essential tool in the biological sciences. The need for bioinformatics has arisen from the recent explosion of genomic data, since it provides tools to translate biological data into knowledge.

This website is intended to be a simple guide for those wishing to get started in the bioinformatics world or are curious about this discipline.

To achieve this goal, the website is divided into different sections. One showing an overview of bioinformatics. Two other sections are related with the studies and training and with professional prospects. Finally, a little Perl programming course is included for those intrepid users who want to go beyond.



Welcome to Bioinformatics at your fingertips.

Contents

What is bioinformatics?

If you want to find out what is bioinformatics, this is your place. Take an historical tour, discover the main goals, explore its potential!

What is Bioinformatics?
Bioinformatics is an emerging interdisciplinary area that deals with the application of computers to collection, storage, organization, analysis, manipulation, presentation and distribution of information related to biological or medical data, such as macromolecules like example DNA or protein.
It has evolved to serve as the bridge between observations, tests and the derivation of understanding information about for example processes, factors, and subsequently the application knowledge.

Aims of Bioinformatics
It comprises data in databases (DBMS), bioinformatics register data allowing researchers to access existing information and to submit new data as they are produced. It should be noted that the information stored in these databases is useless until analyzed. So, gene-annotation is an essential task performed by bioinformaticians.
During these years, the data storage in these databases has been growing exponentially. In the following figure, we can see the growth of the International Nucleotide Sequence Database Collection.

Historical landmarks

Here are some of the major landmarks in bioinformatics over the last decades. The data of historical events for both biology and genetics have also been incorporated.

- 1859 Charles Darwin published On the Origin of Species
- 1953 Crick and Watson established the base of genetic inheritance
- 1970 Walter Sattler created the first gene to describe factors located on chromosomes; he observed chromosomal movement during meiosis and developed the chromosomal theory of heredity

In addition, information about other topics of interest, including the human genome sequencing, are included.

Studying and training

Do you want to study bioinformatics but you don't know where? Here you will find the different Spanish universities that offer specific masters in bioinformatics.

direct access to information about the master's programs of six different Spanish universities!

The page also includes other useful resources, such as reference books and up-to-date websites, to deepen the knowledge.

BIOINFORMATIC REVOLUTION
The sequence by Kevin Davies, The 13000 genome by Robert Davies, Genome by Mark Bailey

INTRODUCTION TO BIOINFORMATICS
Introduction to Bioinformatics by John McHardy, Bioinformatics For Dummies by John McHardy, Essential Bioinformatics by John McHardy

COMPUTATIONAL ASPECTS
Algorithms on Strings, Trees and Sequences by Dan Gusfield, Beginning Perl for Bioinformatics by James D. Troup and Leslye Lipson, Practical Computing For Biologists by Steven Brinkley and Casey Dunn

Professional prospects

Here you will get informed about the current state of bioinformatics sector at state level.

Leading institutions in Spain
In Spain there are 10 nodes of scientific centers, which all together perform a national network of research and bioinformatics services. These 10 nodes are coordinated by the **National Bioinformatics Institute (INBI)**.
INBI Bioinformatics and Genomics Group, CIC, Barcelona
INBI Structural Computational Biology Group, CNIC, Madrid
INBI Functional Genomics group, CIPF, Valencia
INBI Molecular Biogenetics in Biotechnology Group, IRB, Barcelona
INBI Bioinformatics and Informatics Technologies Laboratory, UNIA-Málaga
INBI Barcelona Supercomputing Centre, BSC, Barcelona
INBI Biocomputing Unit, CNB, Madrid
INBI Genetic Diversity and Population Genomics Group, UPF, Barcelona
INBI Research Programme on Biomedical Informatics, IISGM-UPF, Barcelona
INBI Genome Analysis Centre, CNAC, Barcelona

What kinds of services are provided by INBI?
Bioinformatics services

And also, the different and varied careers are provided, for finding one which best matches your interest and aspirations.

Bioinformatics careers

Life Science

- Research scientist
- Evolutionary genetics
- Omics sciences (genomics...)

Applications in Agriculture

- Crops
- Food resistance
- Improve nutritional quality
- Protein yield and drought resistant

Applications in Biotechnology

- Human genome sequencing
- Identification of genes
- Identifying gene functions
- Three-dimensional (3D) structure modeling
- Pair-wise genome comparison
- Clonal change

Applications in Computer science

- Database programmer
- Software developer
- Computational biologist
- Network administrator

Applications in Medicine

- Molecular medicine
- Personalized medicine
- Preventative medicine
- Drug discovery
- Vaccine design
- Gene therapy

PROGRAMMING WITH PERL



This section contains a little introductory Perl programming course, one of the most widely used programming languages among bioinformatics.

You can learn easily to program your first scripts, since offers six units with different examples well-developed and exercises to practice. Also, solutions are provided.

- Unit 1 - Using informatics tools in genetics**
 - Why is so useful?
 - Profiles of a bioinformatic
- Unit 2 - My first steps in PERL**
 - What is a programming language?
 - Interpreted vs. compiled source code
 - Why PERL?
 - Installing PERL
 - My first PERL program
- Unit 3 - Variables**
 - Names
 - Variable names
 - Scalars
- Unit 4 - Arrays and hashes**
 - Arrays
 - Hashes
 - File Handling
- Unit 5 - Loops and decisions**
 - If-else-else
 - Comparison operators for numbers and strings
 - Loops
- Unit 6 - Regular expressions**
 - Pattern matching
 - Extraction
 - FASTA format

Select the unit in the menu bar

Choose a unit

Slides with content, examples and exercises

Auto-hideable visible navigation control at right bottom corner

Download the script solutions

```

Unit 3 - Variables
Scalars
Functions
- Returns the length in characters of the value.
- Length
$DNA1 = "AGCTGATAGCTAGCTAG"; #variable defined
$DNA2 = "AGTACAGCTAGTACAGCTAGCTAG";
$DNA3 = $DNA1 . $DNA2; #concatenating
$|ongDNA3 = length($DNA3);
print "The length of the DNA is: ", $|ongDNA3;
    
```

The length of the DNA is: 40