

Course Presentation

Introduction to Bioinformatics for Biomedical Research

UEB – VHIR

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Outline

- Where are we?
- What do we do?
- Why this course
- Goals
- Methodology
- Contents

Where we are located

Where are we?



Our web at VHIR's web site

Statistics and Bioinformatics Unit (UEB)

Presentation

Team

Services

Teaching

Publications

Rates

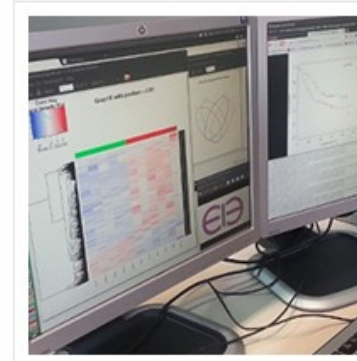
Service Request

The Statistics and Bioinformatics Unit (UEB) was created in 2008 in order to **promote the use and development of modern statistical and bioinformatics resources on research** performed in its environment.

Nowadays, the Statistics and Bioinformatics Unit includes the former Support Unit in Methodology for Biomedical Research (USMIB) and, as part of the Scientific and Technical Support Area of the Vall d'Hebron Research Institute, has the mission to provide expert advice, services and training for clinical and biomedical research.

The main objectives of the UEB are:

- To provide statistical, methodological and bioinformatics support for clinical and biomedical research, mainly in our center but also to the rest of the community.
- To contribute to training in statistics and bioinformatics for clinical and biomedical research, by conducting its own courses and participating in formal training in the VHIR's area.
- To carry out innovation and development activities in the field of statistics and bioinformatics, particularly in anything that could revert in an improvement of the procedures and services provided by the Unit.



More information:

- [UEB's presentations on Slideshare](#)

► Presentation

► Academic Research Organization (ARO)

► Biobank

► Laboratory Animal Service

► High Technology Unit (UAT)

► **Statistics and Bioinformatics Unit (UEB)**

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► Support Unit for Clinical Research (USIC)

► BioCores BCN

What we do

We provide support in ...

Clinical Data analysis

- Biostatistical Analysis
- Clinical Trials
- CRF development (Redcap)
- Epidemiological studies
- *Data Management for Clinical Trials*

Omics Data Analysis & Bioinformatics

- Gene Expression Analysis
- Methylation
- Metagenomics
- Exome sequencing
- Integrative Omics
- Database / applicationsn development
- High performance Computing (HPC) services

Training

- Short Workshops
- Courses
- Official training (MSc)
- Students in practice

Consulting

- Sample size
- Experimental design
- GRANT review
- Statistical parts of papers

Short consultations (< 3hrs) are free

Other services budgeted according our rates:

<http://ueb.vhir.org/Services>

Why this course

- Current biomedical research often has to do (either as “Input” or “output”) with massive quantities of biological information
- Some of this requires sophisticated tools of methods
- Other can be managed with basic knowledge of simple tools
- Researchers and/or technicians must know
 - How to deal with basic problems
 - How to recognize complex situations
 - How to communicate with specialists and understand their questions, proposals and work.

“Hiring a statistician/bioinformatician after the data has been collected is like hiring a physician when a patient is in the morgue: She might be able to tell you what went wrong , but she is unlikely to be able to fix it”

R.A. Fisher

Objectives

- Main objective is providing a (biased) overview of some of the most commonly used bioinformatics methods and tools in biomedical research.
- At the end of the course you should ...
 - Have an overview of the main areas of bioinformatics.
 - Recognize some problems whose solution requires a bioinformatical approach.
 - Identify the right methods to deal with these problems.
 - Be familiar with some of the existing tools to solve these problems.
 - Know when to ask for a bioinformatician's help and understand the solution proposed.

Methodology

- This is an applied **bioinformatics course**.
- Most work based on examples & real data
- Intended for non-programmers:
 - Most tools presented will have a GUI
 - We will do an introduction to R because doing Bioinformatics also means some *scripting*.
- We have a program but there may be others:
Ask questions and make suggestions to improve it or change it “on the fly”.

Methodology (II)

- This is an on-line synchronic course
 - We are not located on the same room
 - But we work together at the same time.
- We make our best to communicate fluidly, add examples and exercises to keep the class dynamic.
- We ask you to avoid as much as possible to stay hidden below the screen
 - Show yourselves, Participate, Ask questions and suggestions
- It's a new situation but communication need not be neither less nor worse, only different :-)

Contents

- **Session 1**

- Course presentation. Introduction to Bioinformatics
- Introduction to R (I)

- **Session 2**

- Introduction to R (II)
- Databases in Molecular Biology

- **Session 3**

- Genomic browsers: Ensembl and UCSC
- Omics data repositories: GTEx, GEO, TCGA, etc.

- **Session 4**

- Introduction and applications of Next Generation Sequencing
- Managing NGS data with Galaxy.

- **Session 5**

- Sequencing preprocessing and management
- Introduction to minor variant analysis

Contents (II)

- **Session 6**
 - Case study I: Minor variant analysis with Galaxy
- **Session 7**
 - Introduction to Omics Data Analysis
 - Important ideas in RNA-seq data analysis.
- **Session 8**
 - Case Study II: RNA-seq data analysis
- **Session 9**
 - Methods and tools for Biological Significance Analysis.
- **Session 10**
 - Case Study III: Biological Significance Analysis.

Course Web site

https://uebvhir.github.io/Course_Bioinformatics_2020.html

Curs de Bioinformàtica per a la Recerca Biomèdica



Informació del curs

Objectius

La recerca biomèdica moderna necessita sovint fer servir informació de diverses menes; per exemple sobre estructures, seqüències, anotacions o funcions de diferents tipus d'entitats i components biològics. Molta d'aquesta informació es troba disponible en bases de dades públiques i el domini de les eines per accedir-hi i recuperar-ne la informació necessària és una habilitat cada cop més imprescindible entre els investigadors en biomedicina. L'objectiu principal d'aquests curss és proporcionar una perspectiva general dels principals recursos bioinformàtics que poden resultar d'utilitat en el dia a dia de la recerca biomèdica o la pràctica clínica. El seu enfoc és aplicat i el que es persegueix és dotar als investigadors i professionals de la biomedicina de conceptes i eines per saber quan -i com- cal fer servir cadascun d'aquests recursos, o quan és millor buscar suport més especialitzat.

- The course has no specific materials
 - Slides in web site before session
 - Software
 - Online tools
 - R & Bioconductor in class computers
 - Links and resources from the web
 - [List of journals and books](#)
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Expected output

- At the end of the course you should be able to
 - Recognize a variety of bioinformatics problems
 - Know how to solve some of them using online bioinformatic tools or adapting R scripts provided in the course (or found in the web).
 - Recognize more complex situations and the resources (or people) needed to deal with them