

Introduction to Bioinformatics for Biomedical Research

UEB - VHIR

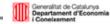
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OUTLINE

1. UEB Presentation

- Who we are?
- What do we do?

2. Course presentation

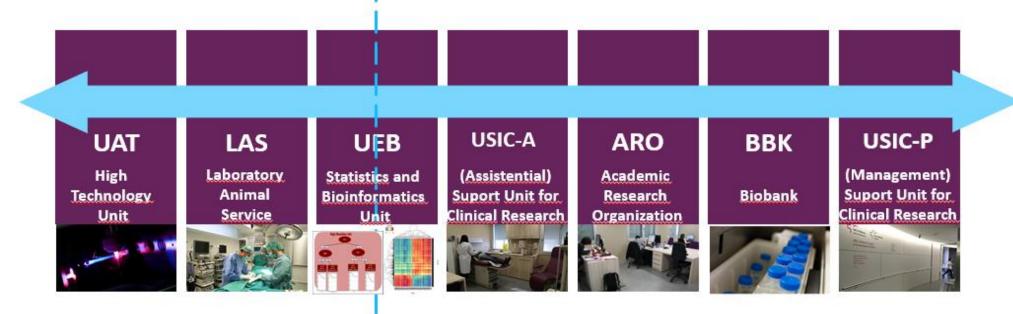
- Why this course?
- Main Goals
- Methodology
- Contents







VHIR's CoreFacilities



BASIC & PRECLINIC

TRANSLATIONAL & CLINIC

Statistical, methodological and bioinformatics support



Innovation and development



http://en.vhir.org/portal1/article_menu_serveis.asp?s=serveis&contenttypeid=43&contentid=1250&t=presentation

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.



- Presentation
- Academic Research Organization (ARO)
- Biobank
- Laboratory Animal Service
- ▶ High Technology Unit (UAT)
- Statistics and Bioinformatics Unit (UEB)

Presentation

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Service Request

- Support Unit for Clinical Research (USIC)
- BioCores BCN



- •Incorporation of new methods & pipelines
- Standarization of workflows and pipelines
- Development of new tools
- Adhesion to quality standards (ISO9001:2015)

2008

Former members:

- -Ricardo Gonzalo
- -Ferran Briansó
- -Xavier de Pedro
- -Israel Ortega
- -Josep Lluís Mosquera





Bioinformatics Platform

Mireia Ferrer Responsible **Bioinformatics**

Esther Camacho Bioinformatics Technician

Projects in Data Science





Head of Unit Santi Pérez-Hoyos

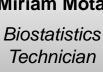
Statistics Platform



Santi Pérez-Hoyos Responsible

Bioestatistics





Anna Sanjuan Biostatistics Technician









We provide support in ...

Clinical Data Analysis

- Biostatistical Analysis
- Clinical Trials
- CRF development (REDCap)
- Epidemiological studies
- Data Management for Clinical Research

Bioinformatics Analysis

- Analysis of omics data (Microarrays, RNA-seq, proteomics and other NGS)
- Single Applications (scRNAseq, HD Flow Cytometry)
- RTqPCR, HT-qPCR
- Variant Analysis
- Biological significance analyses (pathways, networks,...)
- Integrative analyses and biomarker discovery
- High performance computing, development of applications

Consulting and Research Projects

- Sample size
- Experimental design
- GRANT review
- Statistical writing and response to reviewers
- Support for research projects request

Training

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

Short consultations (< 3hrs) are free

Other services budgeted according our rates: http://ueb.vhir.org/Services



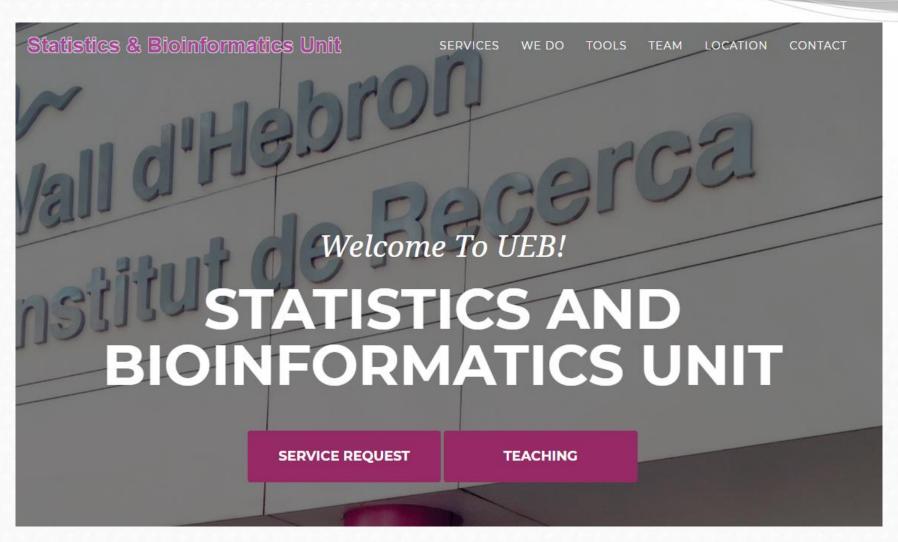
UEB teaching activities:

- Annual scheduled courses:
 - ✓ Basic Statistics for biomedical research
 - ✓ Advanced Statistics for biomedical research
 - ✓ Bioinformatics for biomedical research
- Participation in VHIR Annual Master (Translational Biomedical Research)
- 'On demand' Courses



Statistics Pills





http://ueb.vhir.org/



Where we are?





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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.



Goals and Expected Output

- The main objective is to provide 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 bioinfomatics.
 - Recognize some problems whose solution requires a bioinformatics approach.
 - Recognize a variety of bioinformatics problems
 - Know how to solve some of them using online bioinformatics tools or adapting R scripts provided in the course (or found in the web).
 - 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.



Practical infos

- Classroom course: Aula 101 Pavelló Docent UAB Campus Vall d'Hebron Mòdul Nord.
- Students must bring their own computer.
- 5 Sessions from 9:30-13:50 h

2h (theoretical session) + 20min break + 2h (practical session)

- In each session: Main professor + Support professor
- Certificate of Assistance after the course
 - Sheet of signatures at the end of each class
- Satisfaction Survey will be sent to you after the course
- Any doubts/questions/comments: <u>ueb@vhir.org</u>



Contents

Sessions: 2h + 2h (20 min break)

Session 1 – Monday 20th November

- Introduction to Bioinformatics and Databases for Molecular Biology
- Introduction to R/Rmarkdown and Bioconductor. Hands On

Session 2 – Wednesday 22nd November

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

Session 3 – Monday 27th November

- Introduction to Variant Analysis
- Running a variant analysis workflow on Galaxy. Hands On

Session 4 – Wednesday 29th November

- Introduction to RNA-seq Analysis
- Running a Differential Expression Analysis on R. Hands On

Session 5 – Monday 4th December

- Introduction to Biological Significance Analyses (Pathway Analysis)
- From Gene lists to Pathways. Hands On



Course materials

- Slides posted on UEB's website before each session
- Software
 - Online tools
 - Galaxy webserver
 - Installation instructions for R & RStudio
- Links and resources from the web
 - <u>List of journals and books</u>



Course materials

https://uebvhir.github.io/Course_Bioinformatics_2023.html

Curs de Bioinformàtica per a la Recerca Biomèdica







Informació del curs

Objectius

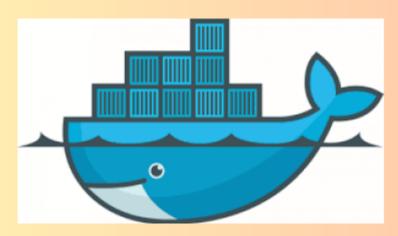
La recerca biomèdica moderna necessita sovint fer servir informació de diverses menes; per exemple sobre estructures, seqüències, anotacions o funcions de diferents tipus d'entitats i components biològics. Molta d'aquesta informació es troba disponible en bases de dades públiques i el domini de les eines 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 curs 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.



Webinar announcement

Thanksgiving Special: How to set up a container in your own computer using DOCKER for reproducible results

Link to webinar



ONLINE in Teams

Presenting: Esther Camacho

Thursday 23/II/23 at I:30pm