Vall d'Hebron
Institut de Recerca

Course Presentation

Intrroduction to Bioinformatics for Biomedical Research

UEB – VHIR

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Outline

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

Where are we

Our web at VHIR's web site

Statistics and Bioinformatics Unit (UEB)

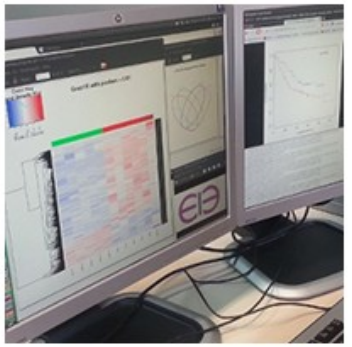
Presentation | Team | Services | Teaching | Publications | Rates | Service Request

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)
Presentation
Team
Services
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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 curse you should ...
  - Have an overview of the main areas of bioinfomatics.
  - 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
  - Although we will show programming examples
- We have a program but there may be others: Ask questions and make suggestions to improve it or change it "on the fly".

Contents

- **Session 1**
  - Introduction to Bioinformatics
  - Databases and tools for recovering information from DB
- **Session 2**
  - Next Generation Sequencing Technologies
  - NGS Data Quality. Managing NGS data with Galaxy.
- **Session 3**
  - Biological Significance Analysis. Analysis of "gene lists"
- **Session 4**
  - Omics data analysis overview.
  - RNA-seq data analysis with Bioconductor
- **Session 5**
  - Introducing clinical Bioinformatics.
  - Searching for minor variants associated with disease

Course Web site

https://uebvhir.github.io/bioinformatica2018.html

Materials

- 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
    -

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.
  - Recognize more complex situations and the resources (or people) needed to deal with them