GENOMICS AND PROTEOMICS APPLIED TO INFECTIOUS DISEASES

CU characterization:

CU name:

Genomics and Proteomics Applied to Infectious Disease

Scientific area acronym:

BM

Duration:

Semiannual

Working hours:

78

Contact hours:

28

ECTS:

3

Observations:

Mandatory CU

Teacher in charge and respective teaching load in the CU:

Ricardo Parreira - 4,5 hours

Other teachers and respective teaching load in the CU:

Celso Cunha – 1.5 hours
Ana Domingos – 4.5 hours
Fátima Nogueira – 1.5 hours
Ana Paula Arez – 1.5 hours
Sandra Antunes - 6 hours

Intended learning outcomes (knowledge, skills and competences to be developed by the students):

1. Acquisition of basic knowledge regarding the general concepts and technical features of some of the techniques (including DNA and RNA sequencing, recombinant protein production and purification, and assessment of protein/protein and protein/nucleic acid interactions).

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Intended learning outcomes (knowledge, skills and competences to be developed by the students): (continuation)

2. Demonstration of the ability for a critical assessment/analysis of the potential/limits of the different described techniques.

3. Recognition of the limits/potential of the different genomics/proteomics techniques applied to the study of specific infectious diseases or their vectors.

Syllabus:

I. Introduction to (automated) sequencing technologies for DNA fragments and complete genomes: Sanger vs NGS (Next Generation Sequening).

II. Production of recombinant proteins in prokaryotic and eukaryotic hosts and their purification.

III. Interactions between proteins and between them and nucleic acids.

IV. Functional Genomics, DNA Microarrays and RNA Sequencing.

V. Use of techniques in the field of Genomics and Proteomics to study: proteomics approach in the study of the tick vector and diseases associated with ticks, erythrocyte enzymopathies and their effects on malaria infection, determinants of resistance in P. falciparum to anti-malarial drugs, and the study of Hepatitis D virus infections and liver cancer.

Teaching methodologies (including assessment):

Due to (i) the multitude of technical specificities of experimental approaches in the field of genomics and proteomics and (ii) the heterogeneous and incipient training of students at the Master, they limit the successful implementation of classes with a practical component. Thus, the experience of previous years led us to choose to increase the theoretical training component, distributed by formal classes and scientific seminars, to the detriment of the theoretical-practical component. However, the close connection that this curricular unit has with that of Bioinformatics, characterized by a strong practical component, and dealing with genomic analysis, should be highlighted. The tutorial orientation component is still privileged in the present CU.

Considering the small number of ECTS associated with this CU, the assessment will be based exclusively on the result of a Boolean written exam (True/False). Attendance of 2/3 of the classes is mandatory.

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References for consultation / mandatory existence:

- Arthur, L. (2012). Introduction to Genomics, 2nd ed. Oxford University Press, UK.
- Arthur, L. (2010). Introduction to Protein Science, 2nd ed. Oxford University Press, UK.
- Josip, L. (2011). Introducing Proteomics: From Concepts to Sample Separation, Mass Spectrometry and Data Analysis. Wiley-Blackwell, UK.

The recommended bibliography will additionally include scientific articles that will cover, more specifically, each of the presented themes.