

CFA2.7 Course Title: introduction to transcriptome and proteomic data analysis

Modality: Advance Training Course

Dates:

28 and 29 November 2018 from 10 to 14h and 15 to 19h

30 November 2018 from 10 to 14h

Duration:

Theoretical-practical lectures: 20h

Location: Videoconference room TORRE-CACTI Building, University of Vigo

Academic coordinators:

Name	Institution	e-mail
Paloma Morán	Universidade de Vigo	paloma@uvigo.es
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Lecturers:

Name	Institution	e-mail
Carlos Canchaya Sánchez	Universidade de Vigo	ccanchaya@gmail.com
Ángel Pérez Diz	Universidade de Vigo	angel.p.diz@uvigo.es

General description:

The aim of this theoretical and practical course is to provide theoretical background and insight in methodologies commonly used for transcriptome and proteome analysis, and to provide hands-on experience turning primary data into information that can be used for biological interpretation. The course will be focused on marine organisms although It can be also useful to a wide range of species.

Contents:

Short theoretical introductory lectures will cover current HTS platforms, their applications in biology, the principles of downstream data analysis, and key terms and concepts in proteomics, including basic strategies of separation, quantification and identification of proteins. The practical sessions will include *de novo* transcriptomics workflow for differential expression using RNA-Seq and functional annotation by means of gene ontologies, and for proteomics, 2-DE and shotgun MS/MS data analysis. Following a proteogenomics approach, data from transcriptomics and proteomics will be used in complementary ways.

Teaching methodologies:

Theoretical lectures and practical *in situ* bioinformatic work.

Evaluation system:

Take home exercises and final exam

Brief CV of the lecturers:

Carlos Canchaya is associate professor at University of Vigo, Spain. His expertise area is Comparative Genomics and has large experience in structural genomics and genome sequencing projects in bacteriophages, food bacteria, and eukaryotes. He is currently working on the genome sequencing of the Mediterranean mussel (*Mytilus galloprovincialis*) and he is interested in marine mollusks and their adaptations to the environment.

Ángel Pérez Diz is associate professor at University of Vigo, Spain. His research interests are mainly focused on evolutionary biology, specifically in understanding the functional consequences of genetic changes, the molecular mechanisms underlying the processes of adaptation and ultimately speciation, and basic knowledge about reproductive biology including mechanisms of reproductive isolation in marine organisms. To advance in this direction he is currently using proteogenomic approaches and integrating results from different omics data. See publication record in:

Google Scholar: <https://scholar.google.es/citations?user=tx2DZnYAAAAJ&hl=es>.

ResearchGate: https://www.researchgate.net/profile/Angel_Perez_Diz2