CFT6 Course Title: Bioinformatics

Modality: Transversal Training Course

Dates: 5-6/06/2018
First day: 10:00-13:00 / 15:00-17:00; Second day: 10:00-13:00 / 15:00-17:00

Duration:
Lectures: 10 hours

Location: DOMAR Videoconference Room, Torre-CACTI building, Campus As Lagoas-Marcosende, Universidade de Vigo

Language: English

Academic coordinators:

Name	Institution	e-mail
David Posada	Universidade de Vigo	dposada@uvigo.es

Lecturers:

Name	Institution	e-mail
Miguel M. Fonseca	CIIMAR, Universidade de Porto	mig.m.fonseca@gmail.com

General description:
Bioinformatics is an interdisciplinary science that develops and applies computational tools to solve biological problems. The development of technologies such as high-throughput sequencing are allowing the generation of massive volumes of biological data and computational tools have become indispensable in biological data analysis. This course aims to give a practical introduction to programming in bioinformatics. Participants will get hands-on experience on different applications, tools and computer languages (e.g. R) to address relevant biological questions. Topics include: molecular database searching, sequence alignment, DNA and RNA sequencing, molecular phylogenetics. At the end of the course, the participants should be able to do basic analyzes of biological datasets using state-of-the-art computational tools and methods and to find biological information from the data.

Contents:
1) Introduction to Bioinformatics
2) Reproducible research with Markdown syntax
3) Biological databases
4) R language for bioinformatics
5) High-throughput sequencing (DNA and RNA-seq)

6) Molecular phylogenetics

Teaching methodologies:
The philosophy of the course will be "learning by doing", which means that the bioinformatics skills will be mostly taught using practical examples. The classes will take place in a computer room, with brief introductions of the main concepts and tools, followed by hands-on exercises with the computers. Outside the clasroom, students will have to complete several computational assignments. Specific guidelines will be provided for all the tasks and tutoring will be granted throughout the entire course.

Evaluation system:
Student evaluation will have two components:
1) Attendance and class participation (25%): the teacher will assess the participation of each student in classes and in problem solving exercises.
2) Written reports on autonomous computational exercises (75%): retrieving and organizing genomic data; analysis of sequence homology; species identification using genetic data.

Briev CV of the lecturers:
Miguel Mendonça da Fonseca (CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Portugal)

Miguel Fonseca is an assistant researcher at CIIMAR - Interdisciplinary Centre of Marine and Environmental Research from the University of Porto. In 2011, he obtained a Ph.D. degree in Biology from the University of Porto. His research fits within the realm of phylogenomics, comparative genomics, and bioinformatics. His teaching experience ranges from one/two-days courses ("Computational Genomics", University of Porto, Portugal, 2011; "Bioinformatics", Campus do Mar, University of Vigo, Spain, 2014 and 2016) up to 15 days-long courses ("Programming for Evolutionary Biology", University of Leipzig, Germany, 2012 and 2013). His current scientific activities include the development of genomic pipelines for annotation and analysis of mitochondrial genomes of multiple species (freshwater mussels and hummingbirds), or the development and optimisation of genomic pipelines in cluster computers (e.g. building a genomic pipeline for the largest collection of gene families aiming to infer the Tree of Life) or inferring the phylogeny of fatty acid desaturases. He is also involved in high-throughput sequencing projects of freshwater and marine animals.

Some of his representative publications are:
- Fonseca MM, Harris DJ, Posada D. 2014. Origin and length distribution of unidirectional prokaryotic overlapping genes. G3: Genes, Genomes, Genetics 4:19-27.
- Fonseca MM, Brito JC, Paulo OS, Carretero MA, Harris DJ. 2009. Systematic and phylogeographical assessment of the *Acanthodactylus erythrurus* group (Reptilia: Lacertidae) based on phylogenetic analyses of mitochondrial and nuclear DNA. Mol Phylogenet Evol. 51(2):131-42
- Fonseca MM, Posada D, Harris DJ. 2008. Inverted replication of vertebrate mitochondria. Molecular Biology and Evolution 25: 805-808.