Bioflims: Microbial Ecology of Drinking Water Systems, experimental and bioinformatic approaches.

From 27/11/2017 till 08/12/2017

MODULE 1: Microbial Ecology of Drinking Water Systems

1. Microorganisms in drinking water systems

2. Biofilms in drinking water systems

    2.1 Introduction

    2.2 Processes that govern the formation and persistence of biofilms

    2.3 Problems and solutions

3. Methodological approaches for studying the microbial ecology of drinking water distribution systems

    3.1 Sampling water distribution systems
    3.2 Conventional and molecular microbiological techniques
    3.3 Application and integration of methods to inform management of drinking water distribution systems

4. Studies in DWDS: case studies: example "*Pipe Dreams"*

5. Operation and maintenance of water distribution systems

Practicals, examples (will be further defined in the future): Culture of microorganisms present in water, ability of biofilm formation, observation of viable and non-viable microorganisms, extraction of genomic and plasmidic DNA, purification of DNA, PCR and qPCR.

MODULE 2 Bioinformatics for the metagenomic study of microbial ecosystems

- **Data generation**

o Shotgun metagenome sequencing
o 16s rRNA sequencing
o mRNA sequencing (metatranscriptomics)

- **Basics**

o Linux
o Sequence databases
▪ GenBank
▪ RDP
▪ Greengenes
o Protein function resources

▪ COG
▪ KEGG orthologs
o basic computational tools
▪ BLAST
▪ BWA, bowtie2
▪ MUMmer
▪ Principal Component Analysis (PCA), principal coordinate analysis (PCoA)
▪ hierarchical clustering and heatmaps

● **Data analysis: sequence clean-up**

● **Data analysis: 16S**

o OTU picking strategies
o OTU picking softwares: uclust, espirit, uparse,
o OTU picking pipelines: LotuS, NINJA-OPS, uparse
o Softwares for 16S analysis: qiime, mothur, vegan (R), phyloseq (R), VAMPS
o Rarefaction curves: sequencing effort / sampling effort
o Calculating alpha and beta diversity
o Ordination
o Statistical analysis: STAMP, metagenomeSeq (R), qiime
o Other analysis: microbial source tracking, high-level phenotypes, oligotyping

● **Data analysis: whole genome shotgun**

o assembly
▪ soap, mira, spades o taxonomic profiling
▪ binning: reads (Metaprob), contigs (MaxBin, myCC)
▪ kraken, centrifuge, clark, metakallisto, metaphlan2
o genome retrieval (CheckM for completeness/contamination/heterogeneity)
o functional profiling
▪ FMAP
o web platforms
▪ MG-RAST
▪ IMG/M

Module 2 methodology:

This will be a hands-on course. Each student will have a desktop available with biolinux installed: http://environmentalomics.org/bio-linux/

Additional specific tools [to be determined] will also be pre-installed.

In each period the instructors will spend at most 30 minutes providing theoretical background or other information, and the rest of the time the students will actively work on datasets with the tools to be used in this course.

Profs.

Module 1: Isabel Douterelo, University of Sheffield

Module 2: João C. Setubal, University of San Pablo

Total hours: 80

Theoreticals: 30

Practicals: 50

Credits: 9 (Posgrad course of the Facultad de Química, application: http://www.fq.edu.uy/es/node/654)

Prospective students: Postgraduate students in chemistry, biology, bioinformatics.

Approval of the course:

Throughout the course, different evaluation instances will be carried out, including: presentation of results of the practical course (Module 1), evaluation of practical bioinformatics exercises (Module 2). Presentation and discussion of a scientific article (Workshop). A final written global assessment will be done.

Auspicia:

Apoyan: