

From: Soledad De Esteban-Trivigno
Subject: Course: Metagenomics and Barcoding in Crete, March 19-23

Dear colleagues,

Registration is open for the course AN INTRODUCTION TO METAGENOMICS AND METABARCODING.

Dates: March 19-23, 2018.

Place: Heraklion (Crete, Greece).

Instructor: Dr. M. Lisandra Zepeda-Mendoza (Chr. Hansen – Bacterial Physiology & Improvement, Denmark).

Metagenomics is the **study of the collection of genomes in an environment**. Environments as diverse as Antarctic lakes, hot springs, or the human gut can be biologically characterized by extracting and sequencing DNA from samples taken from them. A characteristic of many of these samples is their complexity, posing difficulties to their analysis and characterization. However, metagenomics allows **the taxonomic and functional characterization** of samples. These two kinds of characterizations also enable the comparison of different habitats for **biodiversity assessment**.

In this course students will be introduced to the command line environment used to analyze **high-throughput sequencing** data (HTS). The initial cleaning steps that must be performed on every HTS dataset will be described and we will use the processed data for proper functional and taxonomical characterization of a metagenomic dataset. We will use methods such as **mapping to whole genome databases, de novo assembly, gene annotation, building of non-redundant gene catalogue, and metagenomic species concept identification**. Due to the wide usage of **metabarcoding** for the taxonomic characterization of an environment, we will also discuss **amplicon sequencing** strategies and data analysis. The course will be based on both **theory and hands-on exercises**.

More information: <http://www.transmittingscience.org/courses/genetics-and-genomics/introduction-metagenomics-metabarcoding/> or writing to courses.crete@transmittingscience.org

This course is organized by Transmitting Science.

Best regards

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