Programme détaillé de la formation metabarcoding

Du 14 au 18 mai 2018
à la Station biologique de Roscoff

Programme *(détail des exposés en fin de document)*

Lundi 14 mai :
1/ Introduction à l'analyse de données metabarcoding
2/ Introduction à FROGS

13h30-14H	accueil et introduction
14H-16h30	**Exposé de Lucie Zinger -** *Environmental DNA to study biodiversity in space and time*
17H-18H30	**Introduction à FROGS par Anne-Laure Abraham et Mahendra Mariadassou** *Tour de table, introduction aux analyses amplicon, chargement des données dans Galaxy.*
19H	repas au Gulf Stream

Mardi 15 mai :
Formation à FROGS

9H-12H	**Formation à FROGS par Anne-Laure Abraham et Mahendra Mariadassou** **Analyses** Présentation et mise en application avec la suite FROGS : nettoyage des données, clustering, détection de chimères.
12H15-13H15	repas au Gulf Stream
13H30-18H30	**Formation à FROGS par Anne-Laure Abraham et Mahendra Mariadassou** **Analyses** Mise en application avec la suite FROGS : filtres, assignation taxonomique, arbre phylogénétique, étapes annexes, conclusion et limites des méthodes
19H	repas au Gulf Stream

Mercredi 16 mai :

  Formation à FROGS

9H-12H	**Formation à FROGS par Anne-Laure Abraham et Mahendra Mariadassou** **Statistiques** *Présentation de phyloseq et de ses différentes fonctionnalités, descriptions des objets, import des données et premiers graphiques descriptifs (composition)*
12H15-13H15	repas au Gulf Stream
13H30-18H30	**Formation à FROGS par Anne-Laure Abraham et Mahendra Mariadassou** **Statistiques** *Notions de diversité alpha et beta (présentation théorique et calcul). Construction et exploitation des matrices de distances : (i) clustering, (ii) ordination des échantillons, (iii) test d'effet d'une covariable par ANOVA multivarié (adonis). Visualisation de la matrice de comptage des OTUs.*
19H	repas au Gulf Stream

Jeudi 17 mai :
  1/ Formation à FROGS
  2/ retour d'expériences

9H-12H	**Formation à FROGS par Anne-Laure Abraham et Mahendra Mariadassou** **Statistiques** *Détection d'OTUs différentiellement abondants (en fonction du temps). Mise en œuvre par les stagiaires sur des jeux de données exemples.*
12H15-13H15	repas au Gulf Stream
13h30-15h30	**Exposé de Frédéric Mahé -** *Progress and limitations of bioinformatics tools for metabarcoding data*
16h-18h30	**Exposé de Laurent Toffin -** *Diversity and biogeography of microbial communities in methane marine sediments of the Mozambique Channel*
19H	repas au Gulf Stream

Vendredi 18 mai :

   Tutoriaux : (1) Mothur et (2) visualisation sous R

9h-10h30	**Exposé d'Angélique Gobet - Introduction to Mothur, an open-source software to clean and analyze metabarcoding data**
10H30-12H	**Exposé de Daniel Vaulot - Visualization and Analysis metabarcoding data with the R Phyloseq package**
12h15-13h30	repas Gulf Stream (Optionel)
13H30	Fin

Résumés des interventions :

Lucie Zinger (Institut de Biologie de l'ENS, Paris) - " Environmental DNA to study biodiversity in space and time " : *DNA metabarcoding is revolutionising ecological and environmental sciences by bypassing the limitations of classical biodiversity census methods. The genomic information contained in sediments can now be used to retrieve past communities. Sampling of organisms body parts can reveal ecological interactions such as those between plants and their pollinators or between hosts and their microbiota. More generally, it is now possible to expand our understanding of how multi-trophique assemblages are distributed in the environment. During this lecture, I will illustrate different applications of DNA metabarcoding and address the challenges of this approach, their consequences on ecological inferences, and possible avenues for improvement.*

Frédéric Mahé (Cirad, Montpellier) - " Progress and limitations of bioinformatics tools for metabarcoding data " : *DNA amplification and DNA sequencing are noisy processes. This accumulation of erroneous and contaminant sequences slows down and hinders metabarcoding's capacity to describe molecular communities. During this lecture, we will go down the rabbit hole and have a look at the inner working of popular metabarcoding algorithms, revealing the art and tricks used to reduce in vitro noise (denoising, clustering, chimera checking) and in silico noise (fastq paired-read merging).*

Laurent Toffin (Ifremer, Brest) - " Diversity and biogeography of microbial communities in methane marine sediments of the Mozambique Channel " : *Abstract. Microbial community diversity and distribution as well as the crucial environmental factors shaping the communities distribution were studied and compared among four pockmarks sites on Mozambique and Madagascar continental margins. The samling strategy provides a spatial resolution depending on the depth (centimetric and metric scales below the seafloor) and on the distance to the physical pockmark center. Archaea and Bacteria diversity was analyzed by 16S rRNA (V3-V4 region) high throughput sequencing and analyses with FROGS pipeline implemented on Sigenae Galaxy instance. In order to provide a graphic representation of the potential relationships between microbial taxa, a co-occurrence network analysis was performed.*

Angélique Gobet (Cnrs, Roscoff) - " Introduction to Mothur, an open-source software to clean and analyze metabarcoding data " : *During this tutorial, we will follow the different steps (e.g. reducing errors, removing chimeras, OTU clustering) needed to curate bacterial 16S rRNA gene sequences generated using an Illumina MiSeq's platform. The software will be explained by using a metabarcoding dataset from the gut microbiota of a generalist marine herbivore, the European abalone, as a model.*

Daniel Vaulot (Cnrs, Roscoff) - " Visualization and Analysis metabarcoding data with the R Phyloseq package " : *During this tutorial we will demonstrate how to import data generated by using the create.database command of mothur in order to create a phyloseq object. Using this object we will show how to select specific taxonomic groups, generate bargraphs, heatmaps, compute alpha-diversity indexes, make multivariate and network analysis. We will take as example a dataset of 18S rRNA V4 metabarcodes generated on flow cytometry sorted samples from the CARBOM cruise that took place of Brazil in 2013.*