

PiGutNet Training School - February 13th-17th 2017

COST Action FA1401

Analysis of porcine metagenomic datasets - INRA Jouy-en-Josas

The objective of the training school is to provide a global overview of the analysis of pig gut metagenomic datasets, from the bioinformatics analysis of NGS datasets to the advanced biostatistical approaches necessary for data interpretation.

The training school will combine theoretical and practical courses. The training school will aim at i) sharing expertise and knowhow with the attendees in order for them to acquire necessary knowledge to analyze 16S data, and ii) introducing the attendees to whole shot-gun metagenome sequencing using the pig gut gene catalogue.

Global organisation:

- Day 1 – Overview of 16S data production and quality control on NGS datasets
- Day 2 – OTU calling and summary statistics
- Days 3 & 4 – Diversity and ordination analyses on 16S datasets, differential abundance analyses on OTU.
- Day 4- Functional analyses based on 16S datasets
- Day 5 – Advanced analyses for biomarker discovery and network inference. Introduction to the pig gut microbiome gene catalogue.

Courses pre-requisites:

- Attendees are expected to have basic knowledge on R software and Linux command line, no specific lessons will be provided on this during the training school.
- Attendees are expected to bring their own laptops with R (www.r-project.org) and Qiime virtual box (http://qiime.org/install/virtual_box.html) already installed and ready to use.

Location and access:

- INRA, Jouy-en-Josas research center
Access: <http://www.jouy.inra.fr/en/Center-Research/About-us/Getting-to-Jouy-en-Josas>

Housing recommendations:

- Several hotels and residences are available at Versailles and Massy close to the RER-C train line (Versailles-Chantiers station and Massy-Palaiseau stations), with direct access to Jouy-en-Josas. In addition, Paris has an extensive hotel offer, but it is recommended to check the time necessary to arrive to Jouy-en-Josas with public transportation (<http://www.ratp.fr/en/>).

Course programme

	Monday Feb 13	Tuesday Feb 14	Wednesday Feb 15	Thursday Feb 16	Friday Feb 17
9h00-10h30	General outline of the course and introduction on pig metagenomics	OTU calling: Identification of Operational Taxonomic Units from 16S sequencing data	Diversity analysis and ordination of 16S datasets	Differential abundance analysis on metagenomic datasets	Advanced analyses: an introduction to biomarker discovery in 16S datasets
<i>Coffee break</i>					
11h00-12h30	Overview of NGS technologies and data analysis pipelines (16S data)	Hands on data: OTU calling in Qiime	Hands on data: PhyloSeq and Vegan R packages	Hands on data: metagenomeSeq R package	Advanced analysis: network inference and enterotype prediction from 16S datasets
<i>Lunch break</i>					
14h00-15h30	NGS sequencing and quality control of fastq files	BIOM format for the storage of OTU datasets	Linking global microbiome composition to co-factors and co-variables	Prediction of metagenome functions from 16S datasets: PICRUSt	An introduction to whole metagenome sequencing
<i>Coffee break</i>					
16h00-17h30	Hands on data: Quality control of MiSeq datasets in Qiime	Hands on data: summary statistics of 16S datasets files with BIOM and Qiime	Hands on data: PhyloSeq and Vegan R packages	Hands on data: differential abundance analysis of PICRUSt functions with DESeq2 R package	Hands on data: exploration of the porcine microbiome catalogue datasets