



Microbiome profiling provides a highly sensitive, cost effective way to sample the microbiota composition of a clinical, environmental or food sample. NIZO offers microbiome profiling services as a one stop shop, from sample prep to advanced multivariate statistical analyses.

## WHY NIZO

- Over 10 years of experience in *in silico*, *in vitro* and *in vivo* microbiological research: strong focus on GI tract, skin and food.
- NIZO acts as one-stop-shop with its partners hereby guaranteeing high quality experimental designs, execution, project management and NIZO reporting, no need to interact with multiple service providers.
- Proven track record in microbiota analyses and bioinformatics interpretation using dedicated metagenomics based pipeline (16S & Shotgun) for profiling the gut and skin microbiota in health and disease.

## DELIVERABLES

- Proven track record in microbiota analyses and bioinformatics interpretation using dedicated metagenomics based pipeline
- Overview of the microbiome composition in relevant visualizations
- Overview of the main contrast differences and the relationship of the meta data and the microbiota composition using multivariate statistics (PCA, RDA)

At the end of the project a telcon will be organized to go over the main results and discuss potential follow-up in the form of in depth interpretation.

## OUR APPROACH

### 1. Experimental set-up

#### A. Sample registration & processing

Samples will be shipped to NIZO at cost of the customer. As soon as the samples arrive they will be processed for DNA isolation. The 16S gene will be amplified from the isolated DNA using specific 16S primers (V3-V4). Quality and quantity of the material will be checked before sequencing. DNA samples (PCR products) will be sequenced using Illumina technology (Miseq, 300bp PE reads).

#### B. 16S-based microbiome profiling

Raw sequencing data will be evaluated using our in-house developed (Qiime-based) analysis platform.

#### Analyses include:

- General QC (number of reads, read quality/length)
- Removal of low quality reads (QC or chimera sequences)
- Read mapping to different taxonomic levels
- Functional assessment of the main contrast in the study
- Mapping of the different metadata information of the study to the microbiome differences.

### 2. Reporting and Project Management

All results including a brief description of the method used will be communicated to you in the form of a confidential, written report. Overall project management includes regular communication on the progress of the data.