16S rRNA Barcoding Metagenomics

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Small things that matter.

Taxonomic profile and diversity analysis service for **bacteria and archaea** in all sample types.

The ***16S rRNA*** is a gene **exclusive** to **prokaryotic** organisms, mitochondria and chloroplasts, with a highly conserved nucleotide sequence, but with some hypervariable regions with virtually **unique** sequences for each **phylogenetic group**. Selective sequencing of these hypervariable regions of DNA extracted from the sample allows analysis of the diversity and taxonomy present in the samples. Bacteria and archaea are identified by comparing the obtained sequences against reference databases.

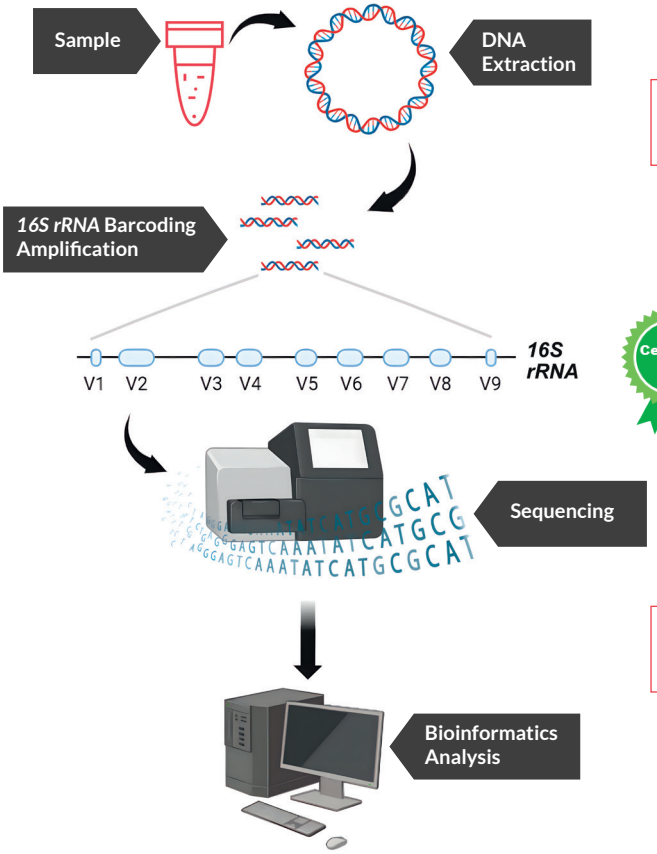
Consultancy and Study Design

Personalized scientific-technical consulting by our metagenomics experts for:

- Experimental Desing
- Sampling
- Project Tracking
- Results Delivery Meeting
- Drafting or Reviewing Publications

Molecular Biology Laboratory

A highly qualified team with extensive experience in metagenomics will carry out:



Sample quality control

Certified Cleanroom

Library Quality Control

Sample reception

- Biological sample reception 250 µl / 500 g*
  *According to the microbial load of the sample
- ADN up to 800 ng
  - Minimal volume = 40 µl
  - Minimal concentration = 20 ng/µl
  - Purity: OD260/280 = 1.8–2.0
    OD260/230 = 2.0

DNA extraction

- In anti-contamination **certified cleanroom**
- Experience with >50 different matrices
- Specific purification protocol

Amplification

- Hypervariable V3-V4 regions of *16S rRNA*
- Possibility to customize primers
- **Use of positive and negative controls to monitor contamination**

Sequencing

- Illumina MiSeq 2x300 pb
- 60.000 guaranteed reads per analysis

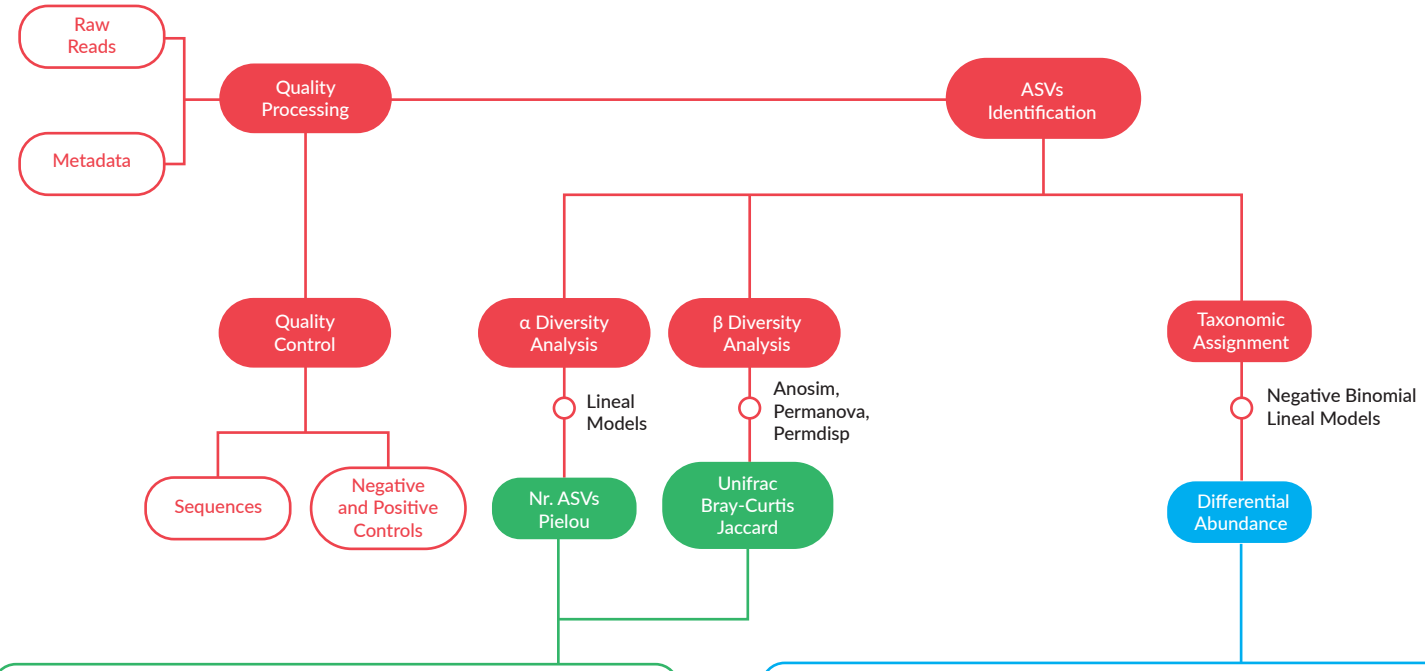
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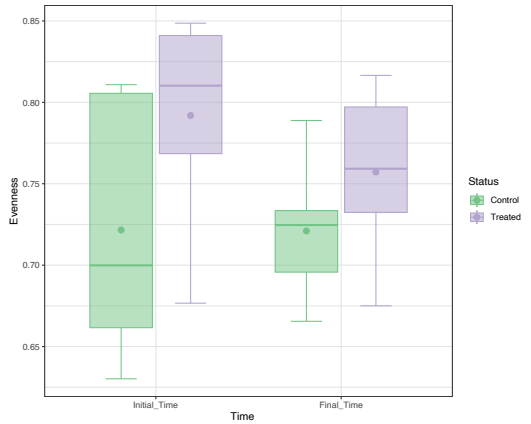
Bioinformatic and Statistical Analysis

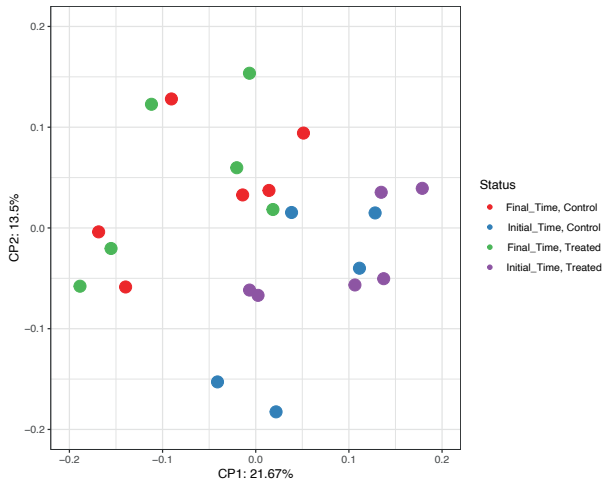
Our Bioinformatics Department has **pipelines designed to customize each analysis** according to the study's needs, addressing:



Diversity Analysis

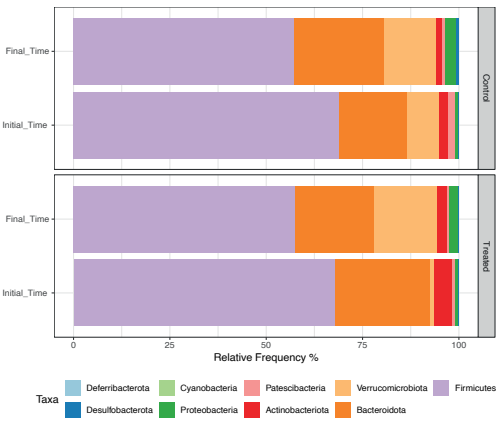
Study of the microbial ecological diversity present in each sample (α) and among samples (β).





Taxonomic Assignment

Identification of prokaryotes present in the sample with **high taxonomic resolution** down to the **genus level**. Adapted approach for some species.



Association or correlation studies with qualitative or quantitative variables.

Complementary services

Customized bioinformatics analysis: bioinformatics analysis consulting service, **which includes 2 hours of post-delivery analysis in any complete study.**

Express service: possibility of reducing the turnaround time for the complete analysis.

Functional inference: indirect analysis of metabolic pathway or gene enrichment.

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