Complementary services

1. **Customized bioinformatics analysis:** bioinformatics analysis consulting service, **which includes 2 hours of post-delivery analysis in any complete study.**
2. **Additional microbiome fractions:** simultaneous analysis of various microbiome fractions (eukaryotes, viruses) within a single bioinformatics pipeline.
3. **Phagome analysis:** detailed analysis of the bacteriophages present in a sample and annotation of virus-bacterial host relationships.
4. **Metagenome-assembled genomes (MAGs):** recovery of parts of microbial genomes to increase taxonomic resolution (to species or sequentotype level) and/or to annotate the genes of each (functional analysis).
5. **Specific genetic profiling:** identification of genes belonging to specific functional groups, such as those related to resistance, pathogenicity, virulence or circulating proteins, amongst others.
6. **Detection of taxonomic patterns:** analysis of the co-presence, co-absence or presence/absence events of bacterial taxa using Dirichlet clustering algorithms for biomarker discovery.

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Shotgun Metagenomics

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The analysis service provides information about the taxonomic, functional and diversity profiles of bacteria, archaea, fungi and/or viruses present in all types of samples.

Shotgun *sequencing* is a method of DNA sequencing. It allows you to get reads from almost **all the gene fragments** present in a sample. Analysing these fragments enables us to identify the species present in the sample and study their diversity. Having all the DNA from the sample enables us to identify the genes present and carry out an enrichment analysis to check for the presence of certain metabolic pathways and whether they are more prevalent under specific conditions.

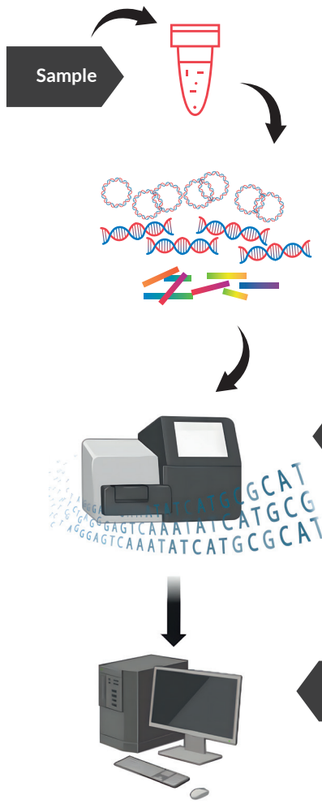
Consultancy and Study Design

Personalized scientific-technical consulting by our metagenomics experts for:

- Experimental desing
- Sampling
- Project Monitoring
- 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

Sample reception

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

Certified Cleanroom

DNA extraction

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

Library Quality Control

Amplification

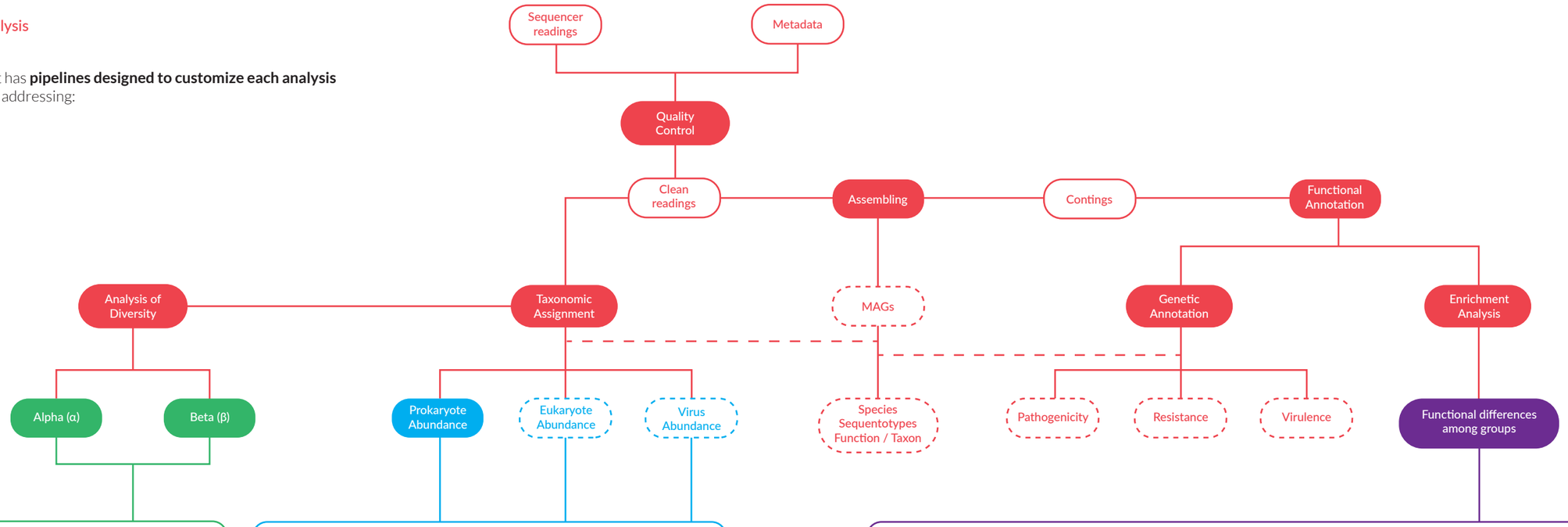
- Using random primers to amplify the entire genetic content

Sequencing

- Illumina NovaSeq 2x150 pb
- 40 million (20M paired-end) guaranteed reads per analysis.

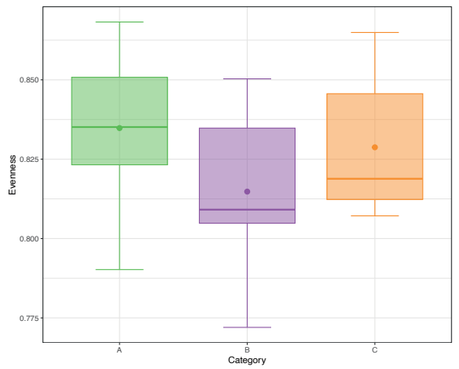
Bioinformatic analysis

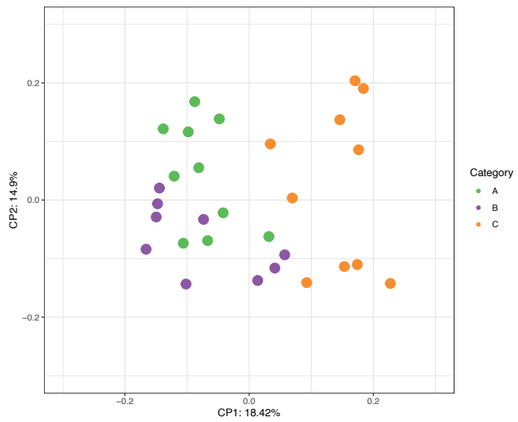
Our Bioinformatic Department has **pipelines designed to customize each analysis** according to the study's needs, addressing:



Diversity Analysis

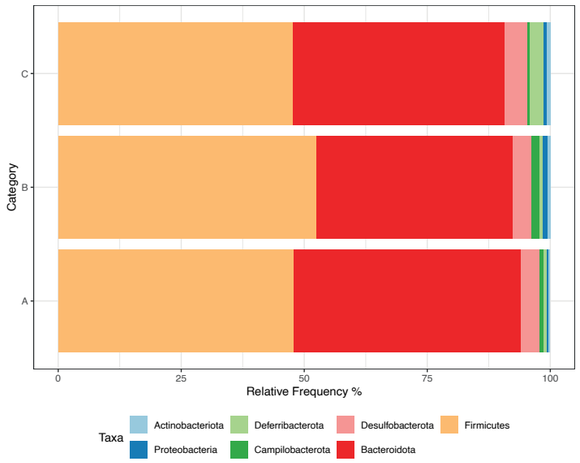
Study of the microbial ecological diversity present in each sample (**α**) and among samples (**β**).





Taxonomic Assignment

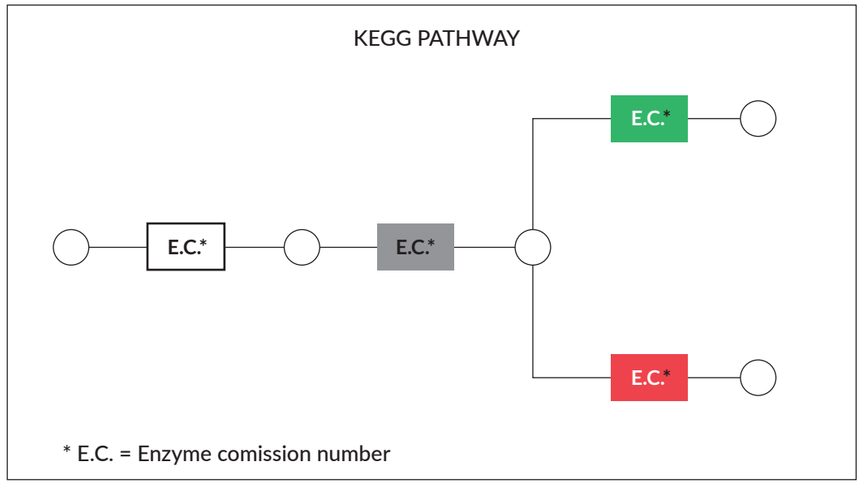
Identification of one of the microbiome components (bacteriome, fungome, eukaryote microbiome or virome) present in the samples, at species level resolution.



Association or correlation studies involving qualitative or quantitative variables.

Functional enrichment analysis

A differential study of the presence of genes or functional groups across the study groups.



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