



# 1st BASE Amplicon Metagenomics Sequencing Service

*A Powerful Tool for Human, Animal & Environmental Microbiome Studies of any Scale*

Amplicon sequencing is a form of NGS that uses oligonucleotide probes design to target and capture regions of interest. It is useful for the discovery of biological diversity in environment samples. This is also especially useful amongst discovery of fungal and bacterial communities within a host organism or environmental samples.



**SCAN QR Code  
to Watch Video**

# Why Partner with 1st BASE?



## Fast Turnaround Time

As fast as 4 weeks with Bioinformatics report.



## High Quality Report

More than 20 years of expertise in molecular services, enabling us to produce high quality sequencing and reports.



## Prompt Technical Support

Post-sequencing technical support from our Bioinformatics team.



# Applications offered by 1st BASE



## 16s rDNA Amplicon Sequencing

The 16S rRNA amplicon sequencing technique is a microbiome analysis to uncover and study the diversity of Bacteria within a given sample. Choose between the 16s region of V1 – V9 for better resolution in your data, or simply choose region V3-V4 for uncovering general diversity in your samples.



## ITS Amplicon Sequencing

The ITS amplicon sequencing is a sensitive method for Fungal diversity analysis in your environmental samples. Choose between region ITS 1 or ITS 2 depending on the nature of Fungi within your environmental samples.



## Custom Metagenomics Sequencing

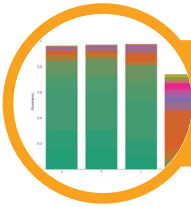
This is a service where preparation of custom metagenomic amplicon libraries targeting diverse population of pathogens of any specific gene, Archaea, and Cyanobacteria regions are being sequence. Just provide us your Primer sequence of interest to get started.

# Bioinformatics Deliverables



- 1** Data QC and trimming
- 2** ASV table generation and Taxonomic characterisation
- 3** ASV Analysis and Species Annotation, including KRONA results, Heatmap, Taxonomic Abundance and up to 5 Venn diagrams\*
- 4** Alpha-diversity Analysis, including Alpha Indices table with ANOVA, Rarefaction curve, Rank abundance curve
- 5** Beta-diversity Analysis, including Ordination (CCA, RDA, DPCoA, NMDS, MDS, PCoA), Unifrac distance analysis, UPGMA (Unweighted Pair-group Method with Arithmetic Means)
- 6** Phylogenetic Trees, including ASV co-occurrence networks & Metacoder
- 7** Statistics Between Groups: DESeq2, ANOSIM, LEfSE
- 8** Metagenome Functional Prediction using Picrust2 (only applicable for 16s)

# Key Diagrams



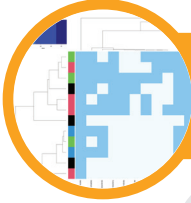
## Taxa Barplot

This graphs depicts the Taxonomy overview across



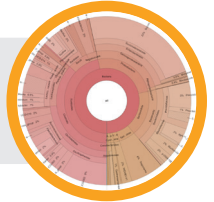
## Top 10 Taxa (Boxplot)

A box plot of the top **10 OTUs/ ASV** by group. For each sample type, the median and range of abundances of the most abundant OTUs/ASV are plotted.



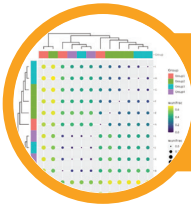
## Heatmap

Heatmap exhibits the relative abundances of taxa (phyla) using shades of colour. The higher a value is, the darker the represented colour



## Krona Chart

Krona allows visualization of hierarchical data through a zoomable pie chart. It presents the abundances of taxa across multiple levels of the phylogenetic hierarchy simultaneously



## Distant Matrix

UniFrac measures the phylogenetic distance between sets of taxa in a phylogenetic tree as the fraction of the branch length of the tree that leads to descendants from either one environment or the other, but not both.



## UPGMA

UniFrac measures the phylogenetic distance between sets of taxa in a phylogenetic tree as the fraction of the branch length of the tree that leads to descendants from either one environment or the other, but not both.



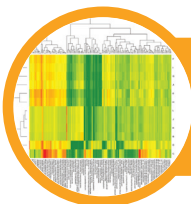
## Alpha Diversity

In ecology, alpha diversity is the mean species diversity in sites at a local scale, whereas beta diversity refers to the ratio between regional and local species diversity.



## Venn Diagram

A Venn diagram is an illustration of the relationships between and among sets, groups of samples with their own unique OTU/ ASVs and those that share OTU /ASVs in common.



## Picrust

Picrust2 predict2 metagenome functional content based on the microbiome composition. Complete Picrust2 prediction results based on KO, Metacyc and EC and be found in the Picrusts2 folder (only applicable for 16s Amplicon sequencing)

## What Our Customers Are Saying

### “ Great service, molecular work can't happen without it ”

The samples are sent very easily and the results are always given on time. The service has been integral part of my research during my doctorate.

Muhammad Moman Khan, Institute for Biotechnology,  
BTU Cottbus-Senftenberg (June 2022)

### “ Bioinformatic support has been very helpful! ”

Apical Scientific has provided excellent support from sample preparation to amplicon data analysis. The analysis report was comprehensive and the figures provided were attractive and neatly organised. More importantly, the local bioinformatic support has been very helpful where we have had interactive discussion and received professional advice to ensure our research is properly designed and correctly analysed. Thank you Apical Scientific for such a great assistance and help throughout our research journey at UPM!

Dr. Amalia Mohd. Hashim  
Biotech Faculty, UPM (September 2022)