

# Microbiome Analysis

## How does a gut reaction affect your research?



More  
thorough  
results

### Microbiome Analysis includes:

- DNA isolation from all bacteria
- Deep sequencing, up to 500 megabases
- Identifies ALL bacteria present
- Comparative analysis

## The role of the gut microbiome

The microbiome is becoming increasingly important to a wide variety of researchers and can be a variable that affects research findings. The microbiome can also be impacted by experimental treatments that could affect the physiology of the research animal.

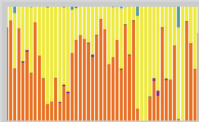
- Influences proliferation of gut epithelial and immune cells
- Modifies the host gene expression
- Increases propensity for disease

So it is important to easily determine the gut microbiome of research animals.

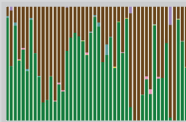
## Reduce your research variables

- An IDEXX BioResearch Microbiome Analysis allows you to easily determine the animal's gut microbiome
- By combining next-generation sequencing technology, along with metagenomics and bioinformatics tools in one place, an IDEXX BioResearch Microbiome Analysis provides a convenient, cost-effective and most importantly, a comprehensive picture of the animal's microbiome.
- Easy sample collection—just 2 frozen fecal pellets required for rodents
- Quick turnaround in just 4 weeks or less

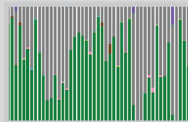
Phylum



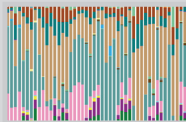
Class



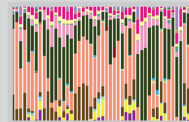
Order



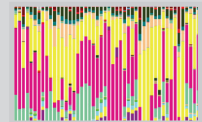
Family



Genus



Species



**IDEXX**

BioAnalytics

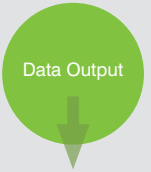
# Determining the animal's microbiome



- DNA is isolated from all bacteria present in sample
- Short genome fragments (400 bp) of V4 segment of 16S rRNA are amplified
- Data is generated: 200-500 megabases of sequence



- Bioinformatics are applied to assemble fragments
- We compare to known bacterial sequences: BLAST and/or Greengenes databases
- *Identifies all bacteria present and their relative abundance*



- Raw Data
- Graphic representation of data type and abundance of bacteria
- Rarefaction curves indicate the depth of sequence for each sample

**Microbiome Analysis**  
Data reports, interpretation,  
and consultation

# Sequencing Data

## Bar Chart

Each column in the bar chart represents the sequence data from one animal.

## Data Table

The table shows a small portion of the associated data indicating the abundance of each operational taxonomic unit detected in each sample. Separate bar charts are provided showing the microbes annotated at each successive taxonomic level.

Bar Chart



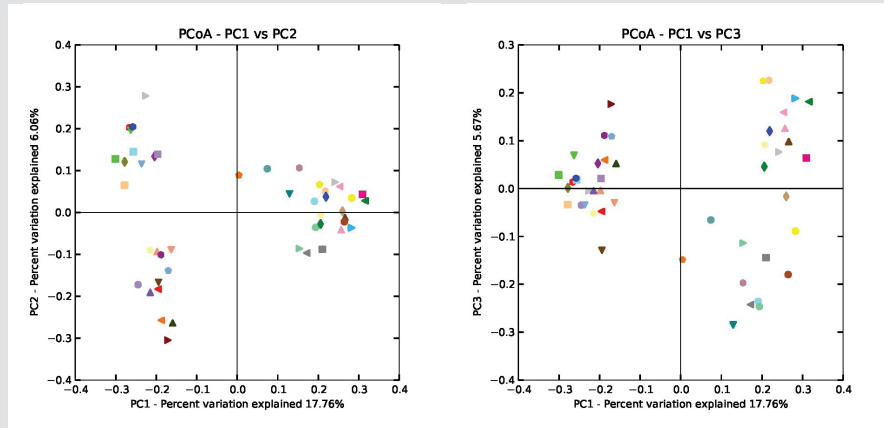
Table

Legend	Taxonomy	Total count	%	G1a.A1	G2a.A2	G3a.A3	G4a.A4	G5a.A5	G6a.J
	no blast	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	hit:Other:Other:Other:Other:Other:Other	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	k_Bacteria; p_Actinobacteria; c_Actinobacteriia; o_Bifidobacteriales; f_Bifidobacteriaceae; g_Bifidobacterium; s_	0	0.0%	0.1%	0.0%	0.1%	0.0%	0.0%	0.0%
	k_Bacteria; p_Actinobacteria; c_Coriobacteriia; o_Coriobacteriales; f_Coriobacteriaceae; g_S	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	k_Bacteria; p_Actinobacteria; c_Coriobacteriia; o_Coriobacteriales; f_Coriobacteriaceae; g_Adlercreutzia; s_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_	2	3.6%	0.0%	0.0%	0.0%	0.0%	9.9%	11.8%
	g_S	1	1.7%	0.0%	0.0%	0.0%	0.0%	1.9%	4.8%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae; g_Bacteroides; s_	2	4.1%	0.2%	0.2%	0.2%	0.2%	3.4%	3.6%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae; g_Bacteroides; s_acidifaciens	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae; g_Bacteroides; s_ovatus	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae; g_Bacteroides; s_uniformis	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.1%	0.2%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Porphyromonadaceae; g_Parabacteroides; s_	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.2%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Porphyromonadaceae; g_Parabacteroides; s_dissimilans	0	0.2%	0.0%	0.0%	0.0%	0.0%	1.3%	2.1%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Porphyromonadaceae; g_Parabacteroides; s_dissimilans	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Porphyromonadaceae; g_Parabacteroides; s_dissimilans	0	0.1%	0.0%	0.0%	0.0%	0.0%	0.3%	0.4%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Porphyromonadaceae; g_Parabacteroides; s_dissimilans	4	8.4%	11.9%	11.1%	8.4%	15.1%	2.9%	3.2%
	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Porphyromonadaceae; g_Parabacteroides; s_dissimilans	0	0.3%	0.0%	0.0%	0.0%	0.0%	0.1%	0.1%

# Principal Component Analysis (PCoA) of sequencing data

## PCoA

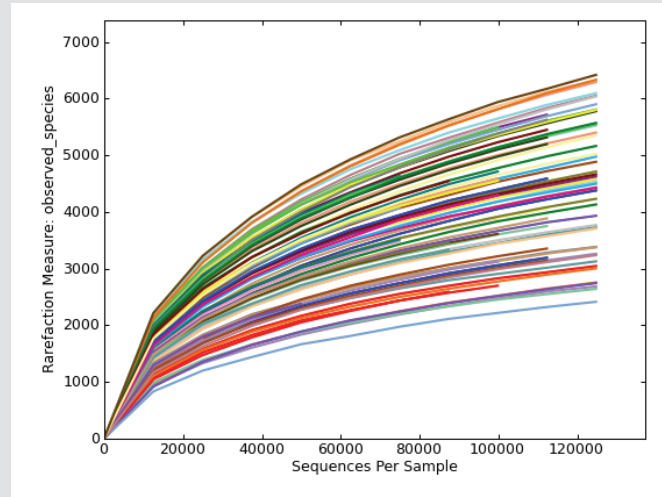
Each point represents one animal and distance between points indicates similarity between samples taking into account all operational taxonomic units (OTUs). Principal component 1 (PC1) and PC2 are shown on the left in the chart; PC1 and PC3 are shown at the right. These plots can be used to visualize clustering of similar samples, taking into account all OTUs detected.



# Sequencing Data Assessment

Rarefaction curves demonstrate the number of unique sequences detected when the data for each sample are repeatedly sub-sampled. Each line depicts the relationship between increased sequencing depth and the number of operational taxonomic units detected.

These plots can be used to visualize differences in microbial richness, and to assess whether the depth of sequencing is adequate for the samples tested.



# Resources

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**IDEXX**

**BioAnalytics**