

IMAGINE Microbiome Profile

Surette Laboratory

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Importing background data

```
## phyloseq-class experiment-level object
## otu_table() OTU Table: [ 5951 taxa and 105 samples ]
## sample_data() Sample Data: [ 105 samples by 2 sample variables ]
## tax_table() Taxonomy Table: [ 5951 taxa by 8 taxonomic ranks ]
```

Clean the data

```
summary(taxa_sums(ps))
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      1.0      8.0     42.0  1063.7   178.5 349592.0
```

```
summary(sample_sums(ps))
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      9389  41749   59464   60288   75470  123766
```

```
# Remove host sequences
ps = prop_tax_down(ps, indic = FALSE)
```

```
## Joining with 'by = join_by(X, Kingdom, Phylum, Class, Order, Family, Genus)'
```

```
ps
```

```
## phyloseq-class experiment-level object
## otu_table() OTU Table: [ 5951 taxa and 105 samples ]
## sample_data() Sample Data: [ 105 samples by 2 sample variables ]
## tax_table() Taxonomy Table: [ 5951 taxa by 9 taxonomic ranks ]
```

```
ps = subset_taxa(ps, Kingdom %in% c('Bacteria', 'Archaea') &
                  !(Phylum %in% Kingdom) &
                  (Family != 'Mitochondria'))
ps
```

```
## phyloseq-class experiment-level object
## otu_table() OTU Table: [ 5940 taxa and 105 samples ]
## sample_data() Sample Data: [ 105 samples by 2 sample variables ]
## tax_table() Taxonomy Table: [ 5940 taxa by 9 taxonomic ranks ]
```

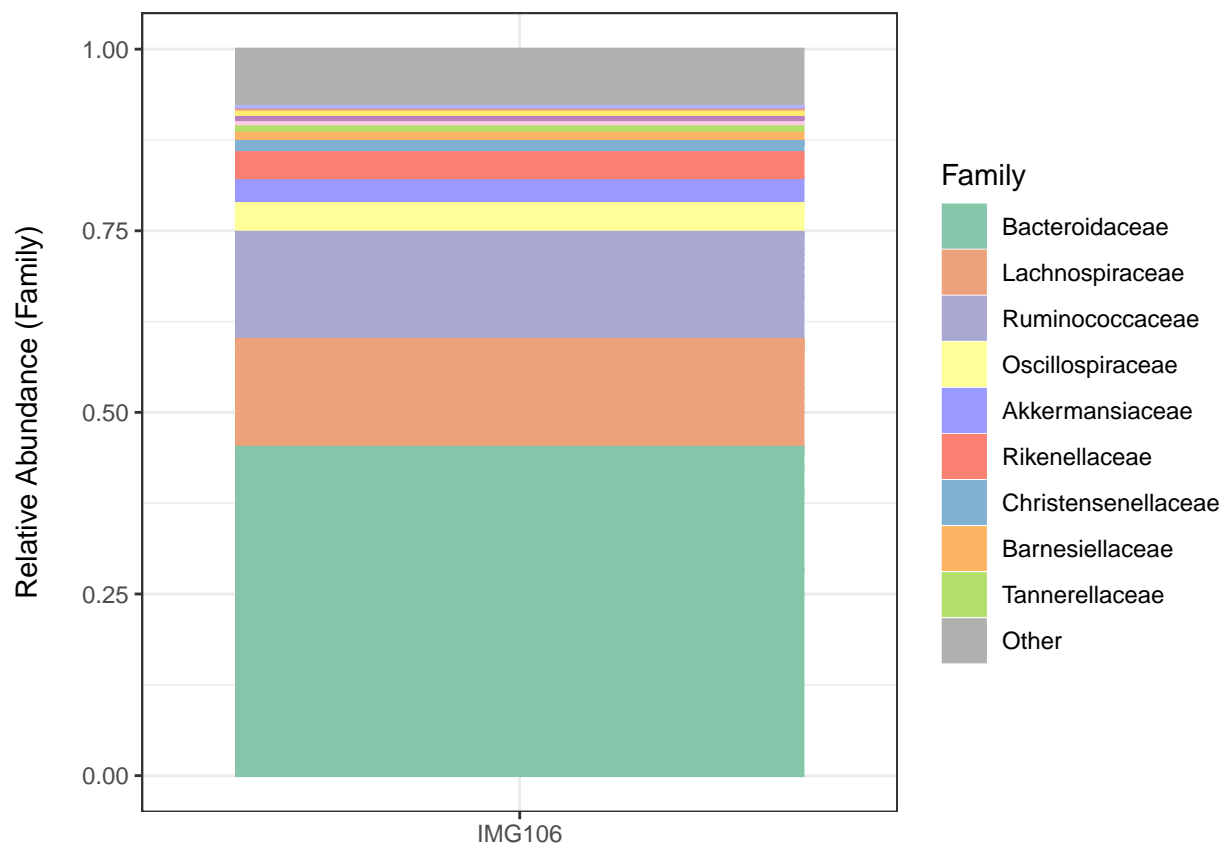
```
# Take relative abundance before any abundance filtering
ps_rel = transform_sample_counts(ps, function(x) x/sum(x))
ps_rel
```

```
## phyloseq-class experiment-level object
## otu_table() OTU Table: [ 5940 taxa and 105 samples ]
## sample_data() Sample Data: [ 105 samples by 2 sample variables ]
## tax_table() Taxonomy Table: [ 5940 taxa by 9 taxonomic ranks ]
```

```
# Remove low-abundance taxa
keep = filter_taxa(ps, function(x) mean(x) > 10)
ps_rel_filt = prune_taxa(keep, ps_rel)
ps_filt = prune_taxa(keep, ps)
```

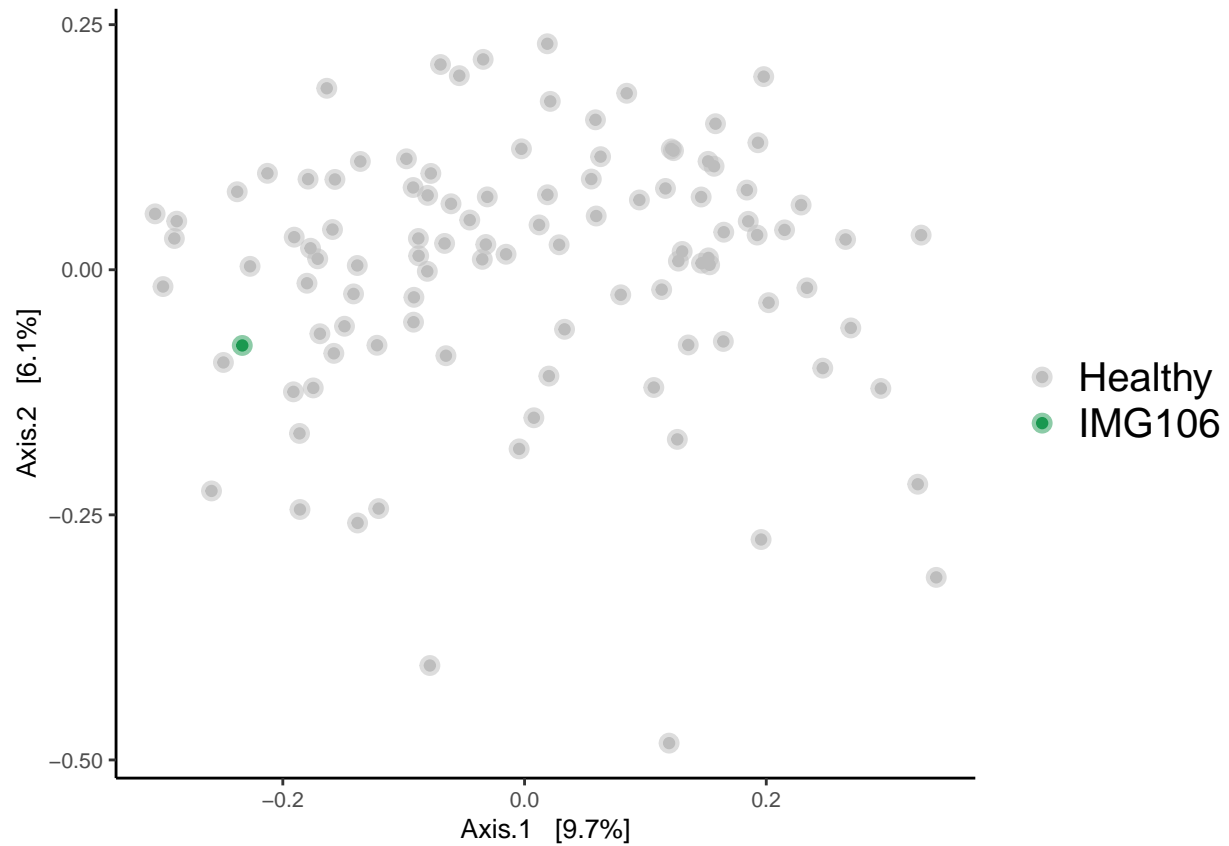
Microbial Composition

Here, you can see relative abundance of your gut bacteria



Microbiome diversity

This figure shows the diversity of microbiome in healthy individual. Each dot shows one IMAGINE participant and your microbiome profile is shown in green.



Inset

Inset the bar plot onto the