

Calculate differential abundance across multiple groups

- Identify groups
- Perform ANOVA test and extract p-values
- Correct p-values for multiple hypothesis testing error

```
# e.g. define a vector with the sample names. You can extract it directly using names(my_data)
sample_names <- c("A01", "A02", "A03",
                  "B01", "B02", "B03",
                  "C01", "C02", "C03")

# Define a second vector with the group names, keeping the same order with above
group_names <- c("A", "A", "A",
                 "B", "B", "B",
                 "C", "C", "C")

# Merge both vectors in one dataframe in case that you need to exclude groups etc
sample_groups <- data.frame(samples = sample_names, groups = group_names)

# Calculate pvalues. No-pairwise comparison is performed. If there is significant difference
# it is across the complete set.
processed_data <- calc_aov_padj(x = my_data,
                               sample_names = sample_groups$samples,
                               group_names = sample_groups$groups,
                               pAdj = "BH") # see ?p.adjust for more options
```