Alpha and Beta Diversity Analysis Tutorial PART 2

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Introduction

This tutorial demonstrates how to directly modify the functions.R script to match the output of the Alpha and Beta diversity analysis with your desired analysis.

1) Performing Alpha and Beta diversity on the species level :

If you desire performing your analysis on the `species` level, replace the following line of the process_data function:

```
ps_s_genus <- tax_glom(ps_s, "Genus", NArm = FALSE)
```

with:

```
ps_s_genus <- tax_glom(ps_s, "Species", NArm = FALSE)
```

2) Changing the measure method used to perform and plot the alpha diversity :

For the alpha diversity function `process_data`, replace:

```
alpha_div <- estimate_richness(ps_s_genus, measures = "Shannon")
```

with:

```
alpha_div <- estimate_richness(ps_s_genus, measures = "Observed") ## Or any other type of
mesure you desire to use/test.
```

3) Assigning categories for the sample names when plotting the boxplots of the alpha diversity:

If you want to categorize your samples when plotting the alpha diversity results using the `generate_alpha_diversity_boxplo` replace :

```
nouveau_tableau$Category[str_detect(nouveau_tableau$Sample_name, "^BPDAC")] <- "pancreas_microdissec"
nouveau_tableau$Category[str_detect(nouveau_tableau$Sample_name, "^X")] <- "pancreas_microdissec"
```

with: (For example if you are working on Melanoma samples that start with TRZ in their name)

```
nouveau_tableau$Category[str_detect(nouveau_tableau$Sample_name, "^TRZ")] <- "Melanoma"
```

4) Changing the distance calculation method when performing Beta diversity analysis:

The function `generate_beta_diversity_boxplot` uses by default `jaccard` method to calculate the beta diversity distances, if you want to change it, replace:

```
bray_dist <- distance(ps_s_genus, method = "jaccard", binary = TRUE)
```

with:

```
bray_dist <- distance(ps_s_genus, method = "bray", binary = TRUE) ## or any other method
that you desire to use/test.
```

Also, by default PcoA (Principal Coordinate Analysis) is performed on the beta diversity distances. By replacing this line of the code:

```
pcoa_result <- ordinate(ps_s_genus, method = "PCoA", distance = bray_dist)
```

with:

```
pcoa_result <- ordinate(ps_s_genus, method = "MDS", distance = bray_dist) ##or any other
method that you desire to use/test. Here are the available methods for this function
("DCA", "CCA", "RDA", "CAP", "DPCoA", "NMDS", "MDS", "PCoA")
```

Moreover, changing the label that colors the dots on the Beta plot requires replacing the following line in the `generate_beta_diversity_boxplot` function:

```
pcoa_df$histological_aspect <- ps_s_genus@sam_data$histological_aspect
```

with:

```
pcoa_df$sous_type_visuel <- ps_s_genus@sam_data$sous_type_visuel ## Or any other label
that you want to use/test.
```

Finally, if you want to test different combinations of beta axis. Change the following line of the code:

```
beta_plot <- ggplot(pcoa_df_filtered, aes(x = Axis.1, y = Axis.2, color = histological_aspect))
+     geom_point() +     labs(title = "Beta Diversity Plot based on histological aspect")
+     theme(plot.title = element_text(hjust = 0.5))
```

with: (Based on the axis that you want to plot)

```
beta_plot <- ggplot(pcoa_df_filtered, aes(x = Axis.1, y = Axis.3, color = histological_aspect))
+     geom_point() +     labs(title = "Beta Diversity Plot based on histological aspect")
+     theme(plot.title = element_text(hjust = 0.5))
```