```
library(DESeq2)
library(phyloseq)

# Make sure your phyloseq object `ps` is loaded
# Ensure your sample data has a column "When" with values "Early" and "Late"
sample_data(ps)$When <- factor(sample_data(ps)$When, levels = c("Early", "Late"))

# Step 1: Create a DESeqDataSet
# The DESeqDataSet requires the OTU counts as a matrix, so we will extract the OTU table as an integer matrix
dds <- phyloseq_to_deseq2(ps, ~ When)  # "When" is the condition (Early vs Late)

# Step 2: Run DESeq2 analysis
dds <- DESeq(dds)

# Step 3: Extract results
# Get the differential abundance results (early vs late comparison)
res <- results(dds)

# Step 4: Filter results and visualize
# Filter out taxa with low counts (adjust p-value threshold as necessary)
res_filtered <- res[!is.na(res$padj) & res$padj < 0.05, ]

# You can also sort the results by the log2 fold change (adjust threshold as necessary)
res_sorted <- res_filtered[order(res_filtered$log2FoldChange, decreasing = TRUE), ]
```

```
# Step 5: Visualize results
# Plot MA plot
plotMA(res, main = "DESeq2 MA plot", ylim = c(-5, 5))

# Step 6: Create a summary table
# Prepare the result table for easy viewing
res_table <- data.frame(
  Taxa = rownames(res_sorted),
  Log2FoldChange = res_sorted$log2FoldChange,
  pvalue = res_sorted$pvalue,
  adjusted_pvalue = res_sorted$padj
)

# Print the table
library(knitr)
kable(res_table, caption = "Differential Abundance of Early vs Late Taxa Using DESeq2")
```