```
library(phyloseq)
library(knitr)

# Assuming your phyloseq object is called `ps`
sample_data <- sample_data(ps)

# Check the sample data
print(head(sample_data))

# Calculate early and late abundances
early_samples <- sample_data$When == "Early"
late_samples <- sample_data$When == "Late"

# Sum the OTU table for early and late samples
early_abundance <- rowSums(otu_table(ps)[, early_samples, drop = FALSE], na.rm = TRUE)
late_abundance <- rowSums(otu_table(ps)[, late_samples, drop = FALSE], na.rm = TRUE)

# Check the calculated abundances
print(head(early_abundance))
print(head(late_abundance))

# Create a data frame for both early and late abundances
abundance_df <- data.frame(
  Taxa = taxa_names(ps),
  Early = early_abundance[match(taxa_names(ps), names(early_abundance))],
  Late = late_abundance[match(taxa_names(ps), names(late_abundance))]
```

```
)

# Replace NA with 0 for taxa not present in early or late samples
abundance_df[is.na(abundance_df)] <- 0

# Remove any taxa with zero abundance in both groups
abundance_df <- abundance_df[rowSums(abundance_df[, c("Early", "Late")]) > 0, ]

# Display the table
print(kable(abundance_df, caption = "Abundance of Early vs. Late Taxa"))
```