

PCoA

Here we make beta diversity PCoA plots. Make any character vectors in to factors for plotting purposes.

```
metadata <- metadata %>%
  mutate(Ring = factor(Ring,
    levels = c("Ring_1",
      "Ring_3",
      "Ring_8",
      "Ring_4",
      "Ring_7",
      "Ring_12"),
    labels = c("Pen 1",
      "Pen 3",
      "Pen 8",
      "Pen 4",
      "Pen 7",
      "Pen 12")),
  Type = factor(Type),
  Shelter = factor(Shelter),
  Cycle = factor(Cycle))
```

Bray-curtis PCoA plot.

```
VFLA_bray_curtis$data$Vectors %>%
  select(SampleID,
    PC1, PC2) %>%
  left_join(metadata,
    by = c(SampleID = "SampleID")) %>%
  filter(Shelter1 !=
    "Growth") %>%
  ggplot(aes(x = PC1,
    y = PC2, color = Type)) +
  geom_point(alpha = 0.7) +
  theme_bw() + theme(legend.position = "bottom",
    legend.margin = margin(t = -10),
    panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(),
    panel.spacing = unit(0.8,
      "lines"), text = element_text(size = 13)) +
  scale_color_manual(values = c("purple2",
    "springgreen3",
    "deepskyblue1",
    "gold")) + facet_grid(Cycle ~
    Ring + Shelter1)

# ggsave('PCoA_VFLA_braycurtis_ringcycle_b_v5.tiff',
# dpi = 300)
```

Distance matrix created in R rather than Qiime2

```

VFLA_transposed <- t(VFLA_table)
VFLA_bray <- vegdist(VFLA_transposed,
  method = "bray")

metadata2 <- metadata

rownames(metadata2) <- metadata2$SampleID
metadata2$SampleID <- NULL

permanova_result <- adonis2(VFLA_bray ~
  Shelter1 + Cycle1 +
  Type1, data = metadata2,
  by = "terms", permutations = 10000)

print(permanova_result)

```