

# Alpha diversity

Plots and statistics for alpha-diversity.

Joint data frame for metadata and alpha diversity.

```
VFLA_alpha_data <- metadata %>%
  left_join(VFLA_shannon,
    by = c(SampleID = "SampleID")) %>%
  left_join(VFLA_faith_pd,
    by = c(SampleID = "SampleID")) %>%
  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,
    levels = c("Plastic",
      "Seaweed",
      "Skin",
      "Gills"))) %>%
  filter(Shelter !=
    "Growth")
```

Alpha diversity split by cages and sample type with facet on shelter type

```
faith_pd_plot <- ggplot(VFLA_alpha_data,
  aes(x = Ring, y = faith_pd,
    fill = Type)) +
  geom_boxplot() +
  xlab("Pen number") +
  ylab("Faith's PD") +
  scale_fill_brewer(palette = "Paired") +
  facet_wrap(~Shelter1,
    scales = "free_x",
    dir = "h", ncol = 2) +
  theme_classic() +
  theme(text = element_text(size = 13))

shannon_plot <- ggplot(VFLA_alpha_data,
  aes(x = Ring, y = shannon_entropy,
    fill = Type)) +
```

```

geom_boxplot() +
xlab("Pen number") +
ylab("Shannon") +
scale_fill_brewer(palette = "Paired") +
facet_wrap(~Shelter1,
  scales = "free_x") +
theme_classic() +
theme(text = element_text(size = 13))

```

Alpha diversity split by sample type and sampling time point with facet on shelter type

```

shannon_all <- ggplot(VFLA_alpha_data,
  aes(x = Type1, y = shannon_entropy,
    fill = Cycle)) +
  geom_boxplot() +
  facet_grid(Shelter1 ~
    .) + scale_fill_brewer(palette = "OrRd") +
  labs(x = "Type",
    y = "Shannon",
    fill = "Sampling point") +
  theme_classic() +
  theme(text = element_text(size = 13))

```

```

pd_all <- ggplot(VFLA_alpha_data,
  aes(x = Type1, y = faith_pd,
    fill = Cycle)) +
  geom_boxplot() +
  facet_grid(Shelter1 ~
    .) + scale_fill_brewer(palette = "OrRd") +
  labs(x = "Type",
    y = "Faith's PD",
    fill = "Sampling point") +
  theme_classic() +
  theme(text = element_text(size = 13))

```

```

ggarrange(shannon_plot,
  faith_pd_plot, shannon_all,
  pd_all, nrow = 2,
  ncol = 2, labels = c("a)",
    "b)", "c)", "d)"))
ggsave("alpha_diversity_plots.tiff",
  dpi = 300)

```

Comparisons of sample types. Relevel is used to get a different base level, so that all comparisons can be made

```

VFLA_alpha_data$Type <- relevel(factor(VFLA_alpha_data$Type),
  ref = "Gills")
VFLA_type_faithmod <- lmer(faith_pd ~
  Type + (1 | Ring),
  data = VFLA_alpha_data)
summary(VFLA_type_faithmod)

VFLA_type_shannonmod <- lmer(shannon_entropy ~
  Type + (1 | Ring),

```

```
data = VFLA_alpha_data)
summary(VFLA_type_shannonmod)
```

Gills and Skin in plastic and seaweed shelters

```
VFLA_alpha_data$Shelter1 <- relevel(factor(VFLA_alpha_data$Shelter1),
  ref = "Seaweed")
```

```
VFLA_faithmod_shelter_gills <- lmer(faith_pd ~
  Shelter1 + (1 | Ring),
  data = subset(VFLA_alpha_data,
    Type == "Gills"))
summary(VFLA_faithmod_shelter_gills)
```

```
VFLA_shannonmod_shelter_gills <- lmer(shannon_entropy ~
  Shelter1 + (1 | Ring),
  data = subset(VFLA_alpha_data,
    Type == "Gills"))
summary(VFLA_shannonmod_shelter_gills)
```

```
VFLA_faithmod_shelter_skin <- lmer(faith_pd ~
  Shelter1 + (1 | Ring),
  data = subset(VFLA_alpha_data,
    Type == "Skin"))
summary(VFLA_faithmod_shelter_skin)
```

```
VFLA_shannonmod_shelter_skin <- lmer(shannon_entropy ~
  Shelter1 + (1 | Ring),
  data = subset(VFLA_alpha_data,
    Type == "Skin"))
summary(VFLA_shannonmod_shelter_skin)
```

Change over time

```
VFLA_alpha_data$Cycle <- relevel(factor(VFLA_alpha_data$Cycle),
  ref = "A")
```

```
VFLA_faithmod_time <- lmer(faith_pd ~
  Cycle + (1 | Type),
  data = VFLA_alpha_data)
summary(VFLA_faithmod_time)
```

```
VFLA_shannonmod_time <- lmer(shannon_entropy ~
  Cycle + (1 | Type),
  data = VFLA_alpha_data)
summary(VFLA_shannonmod_time)
```