



Figure 1: Mothur

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rarefiedQRich <- estimate_richness(rarefiedQ, measures = "Shannon")
rarefiedQRichAlpha <- full_join(rownames_to_column(rarefiedQRich),
  rownames_to_column(data.frame(sample_data(rarefiedQPer))),
  by = "rowname")
p1 <- rarefiedQRichAlpha %>% ggplot() + geom_point(aes(x = Depth_m,
  y = Shannon), size = 4, alpha = 0.7) + geom_smooth(method = "loess",
  aes(x = as.numeric(Depth_m), y = Shannon)) + labs(title = "Alpha-diversity across depth",
  y = "Shannon's diversity index", x = "Depth (m)")
p2 <- rarefiedQRichAlpha %>% ggplot() + geom_point(aes(x = O2_uM,
  y = Shannon), size = 4, alpha = 0.7) + geom_smooth(method = "loess",
  aes(x = as.numeric(O2_uM), y = Shannon)) + labs(title = "Alpha-diversity across oxygen",
  y = "Shannon's diversity index", x = "Oxygen (uM)")
p3 <- rarefiedQRichAlpha %>% mutate(O2_group = ifelse(O2_uM ==
  0, "anoxic", "oxic")) %>% ggplot() + geom_boxplot(aes(x = O2_group,
  y = Shannon)) + labs(title = "Alpha-diversity across oxygen",
  y = "Shannon's diversity index", x = "Oxygen (uM)")
p4 <- rarefiedQRichAlpha %>% ggplot() + geom_point(aes(x = Depth_m,
  y = O2_uM), size = 4, alpha = 0.7) + geom_smooth(method = "loess",
  aes(x = as.numeric(Depth_m), y = O2_uM)) + labs(title = "Oxygen concentration across depth",
  y = "Oxygen (uM)", x = "Depth (m)")
```