

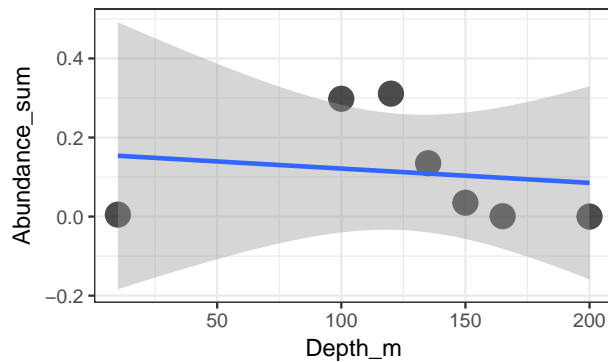
```

dfworkingQTaxa <- workingQTaxa %>% psmelt() %>% group_by(Sample) %>%
  summarize(Abundance_sum = sum(Abundance), Oxyzen = mean(O2_uM))
p4 <- ggplot(dfworkingQTaxa) + geom_point(aes(x = Oxyzen, y = Abundance_sum),
  size = 5, alpha = 0.7) + geom_smooth(method = "lm", aes(x = as.numeric(Oxyzen),
  y = Abundance_sum)) + labs(title = "Abundance of Plantomyces with respect to oxyzen concen

figureM <- annotate_figure(ggarrange(p1, p2, ncol = 2, nrow = 1,
  labels = c("(a)", "(b)")), bottom = text_grob("Mothur", color = "blue",
  face = "bold", size = 12))
figureQ <- annotate_figure(ggarrange(p3, p4, ncol = 2, nrow = 1,
  labels = c("(a)", "(b)")), bottom = text_grob("QIIME2", color = "blue",
  face = "bold", size = 12))
annotate_figure(ggarrange(figureM, figureQ, ncol = 1, nrow = 2),
  bottom = text_grob("Figure 6: Regression analysis of *Planctomyces* across depth",
  face = "bold", size = 12))

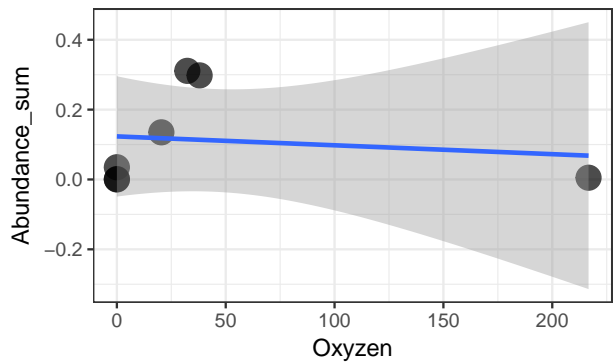
```

(a) Abundance of Plantomyces across depth

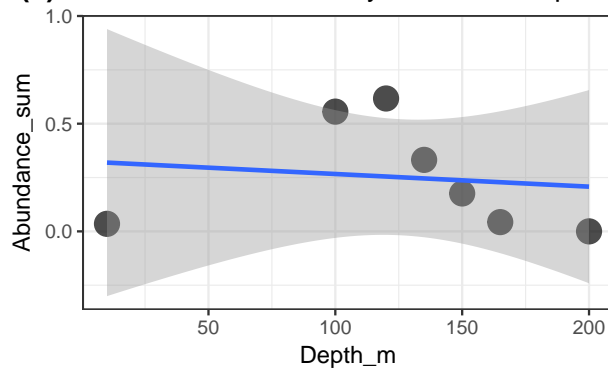


Mothur

(b) Abundance of Plantomyces with respect to



(a) Abundance of Plantomyces across depth



QIIME2

(b) Abundance of Plantomyces with respect to

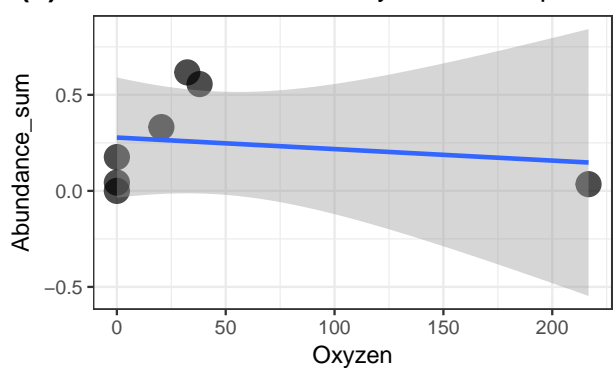


Figure 6: Regression analysis of *Planctomyces* across depth