

[Title]

Module 3: Project 1 by Team 5

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Abstract

This is the abstract. It consists of two paragraphs.

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1 Introduction

2 Problem Formulation

3 Materials and Experimental Configuration

3.1 Experimental Protocols

Here:

P1. Analysis of microbial community structure along with depth and oxygen concentration (see Section 4.1).

P2. Analysis of abundance information of [OTU****] along with depth and/or oxygen concentration (see Section 4.2).

P3. Estimate richness (number of OTUs/ASVs) for [OTU****] (see Section 4.3).

P4. Interpretation of abundance information of OTUs/ASVs of [OTU****] along with depth and/or oxygen concentration (see Section 4.4).

3.2 Dataset

3.3 Parameters Configuration

```
## try http:// if https:// URLs are not supported
source("https://bioconductor.org/biocLite.R")
biocLite("phyloseq")
library("tidyverse")
library("gridExtra")
library("magrittr")
```

3.4 Data Preprocessing

We use saanich inlet datasets that are propocessed using mothur and QIIME2

```
load("data/mothur_phyloseq.RData")
load("data/qiime2_phyloseq.RData")
```

Samples are then rarefied/normalized to 100,000 sequences per sample to facilitate comparisons between samples. A random seed was set to ensure reproducibility.

```
set.seed(4832)
rarefied = rarefy_even_depth(mothur, sample.size=100000)
```

Rarefied counts were converted to relative abundance percentages.

```
rarefiedPer = transform_sample_counts(rarefied, function(x) 100 * x/sum(x))
```

Next, we perform a series of filterings according to three rules: i)- exclude OTUs that are not observed for more than 4 samples; ii)- prune samples and OTUs with unknown values, such as unclassified value; and iii)- any phylum fail to have more than 5 OTUs should be trimmed. The codes used for applying the three rules are:

```
# First rule
firstTaxa = filter_taxa(rarefiedPer, function(x) sum(x == 0) <= 4, TRUE)

# Second rule
basedOnGenus <- as.data.frame(tax_table(firstTaxa)) %>%
  filter(!str_detect(Genus, 'uncultured'), !str_detect(Genus, 'unclassified'))
secondTaxa = subset_taxa(firstTaxa, Genus %in% basedOnGenus$Genus)

# Third rule
basedOnPhylums <- as.data.frame(tax_table(secondTaxa)) %>%
  group_by(Phylum) %>%
  count() %>%
  filter(n > 5)
## In contrary we can run the following:
# thirdTaxa <- prune_taxa(taxa_sums(secondTaxa) > 5, secondTaxa)
thirdTaxa <- subset_taxa(secondTaxa, Phylum %in% basedOnPhylums$Phylum)
```

4 Results

4.1 Analysis of microbial community structure along with depth and oxygen concentration

We first estimate the overall taxa diversity using Shannon's diversity index.

```
rarefiedRich <- estimate_richness(rarefied, measures = "Shannon")
rarefiedRichAlpha <- full_join(rownames_to_column(rarefiedRich),
                              rownames_to_column(data.frame(sample_data(rarefiedPer))),
                              by = "rowname")

p1 <- rarefiedRichAlpha %>% 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 <- rarefiedRichAlpha %>% ggplot() +
  geom_point(aes(x=O2_uM, y=Shannon), size=4, alpha=0.7) +
  labs(title="Alpha-diversity across oxygen",
       y="Shannon's diversity index", x="Oxygen (uM)")
```

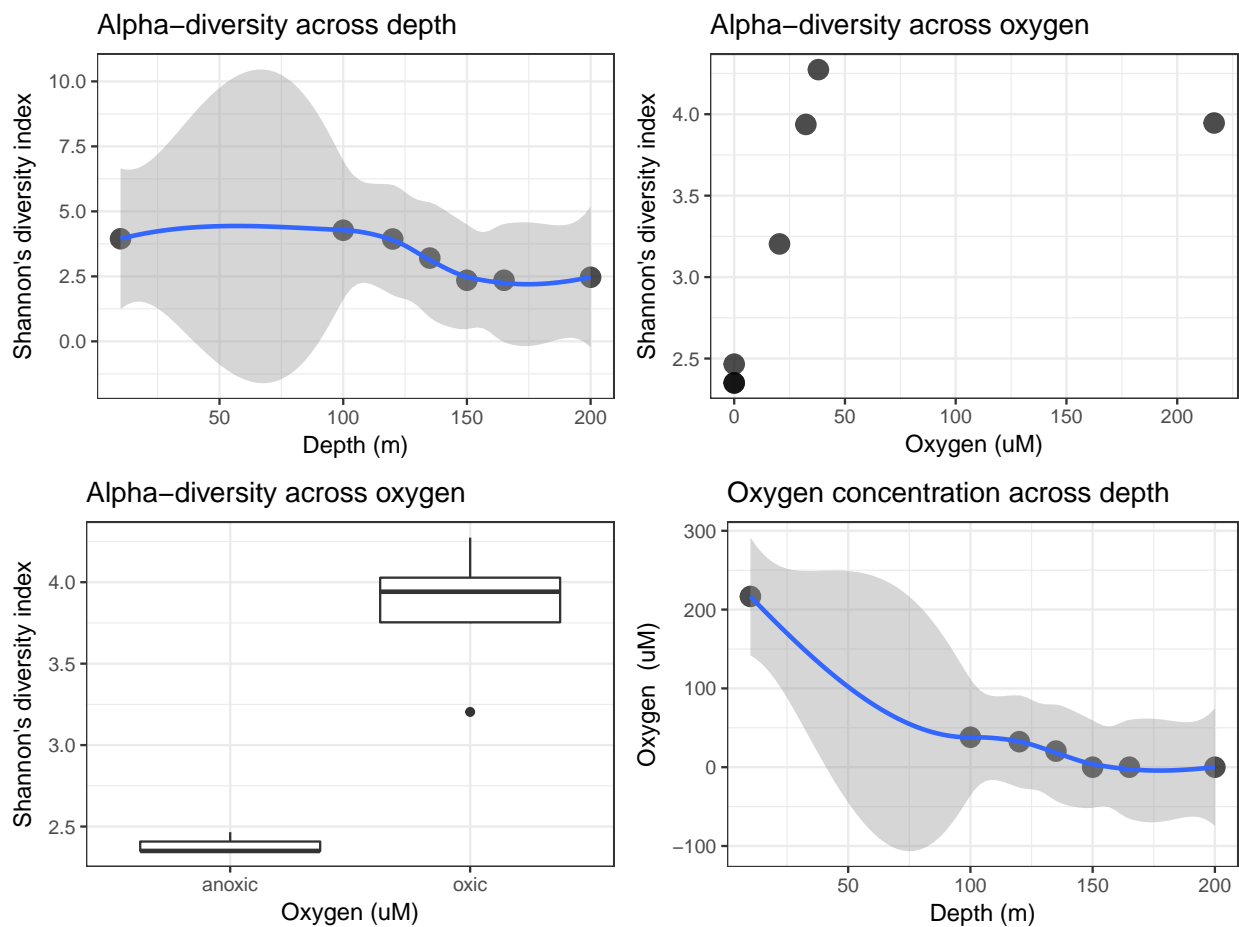
```

p3 <- rarefiedRichAlpha %>%
  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 <- rarefiedRichAlpha %>% 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)")

grid.arrange(p1, p2, p3, p4, ncol=2)

```



The following function will assist us to understand the unique Phylum rank:

```

get_taxa_unique(physeq = thirdTaxa, taxonomic.rank = "Phylum")

```

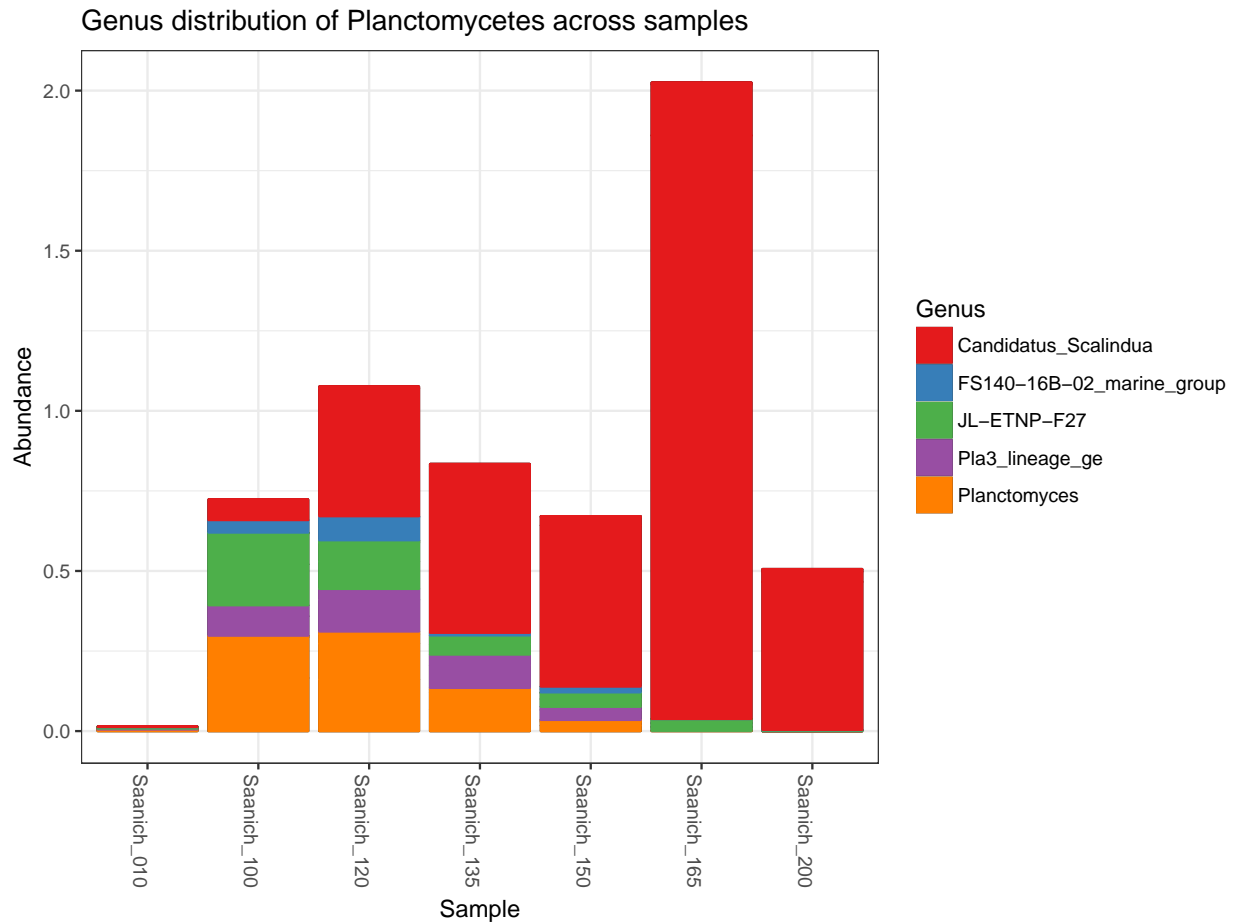
```

## [1] "Proteobacteria"          "Bacteroidetes"
## [3] "Thaumarchaeota"         "Actinobacteria"
## [5] "Marinimicrobia_(SAR406_clade)" "Planctomycetes"
## [7] "Verrucomicrobia"

```

We choose the *Planctomycetes* phylum, and explored the distribution of genera of this phylum.

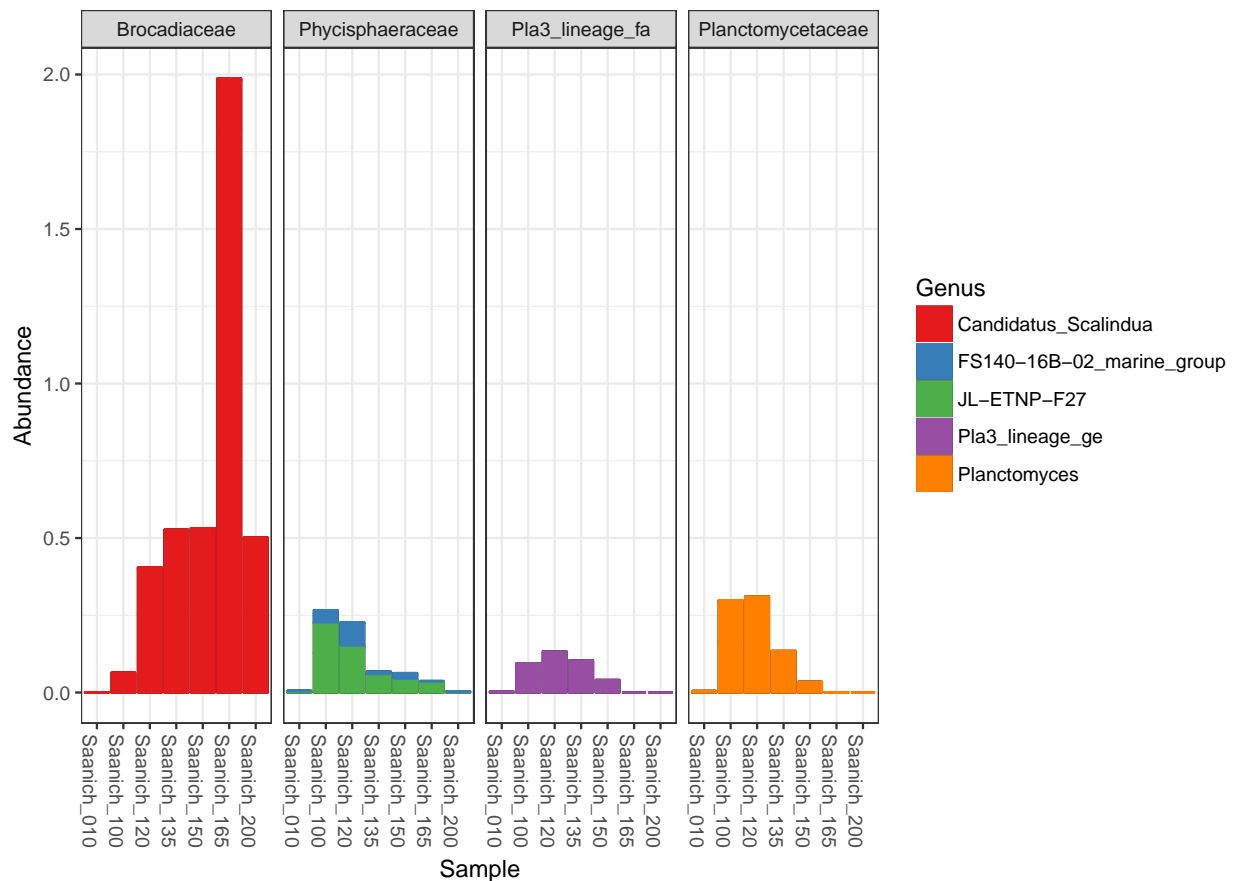
```
subTaxa = subset_taxa(thirdTaxa, Phylum == "Planctomycetes")
plot_bar(subTaxa, fill="Genus") +
  geom_bar(aes(color = Genus, fill = Genus), stat = 'identity',
    position = 'stack') +
  labs(title="Genus distribution of Planctomycetes across samples")
```



We further investigated the genus distribution of this phylum across samples grouped by family level.

```
plot_bar(subTaxa, fill="Genus", facet_grid=~Family) +
  geom_bar(aes(color = Genus, fill = Genus), stat = 'identity',
    position = 'stack') +
  labs(title="Genus distribution of Planctomycetes across samples grouped by family level")
```

Genus distribution of Planctomycetes across samples grouped by family level



Finally, we settled on performing experimental analysis at *Planctomyces* genus level and it's associated OTUs.

```
workingTaxa = subset_taxa(thirdTaxa, Genus == "Planctomyces")
(suggestedOTUs <- colnames(otu_table(workingTaxa)))
```

```
## [1] "0tu0125" "0tu0144" "0tu0401" "0tu0592"
```

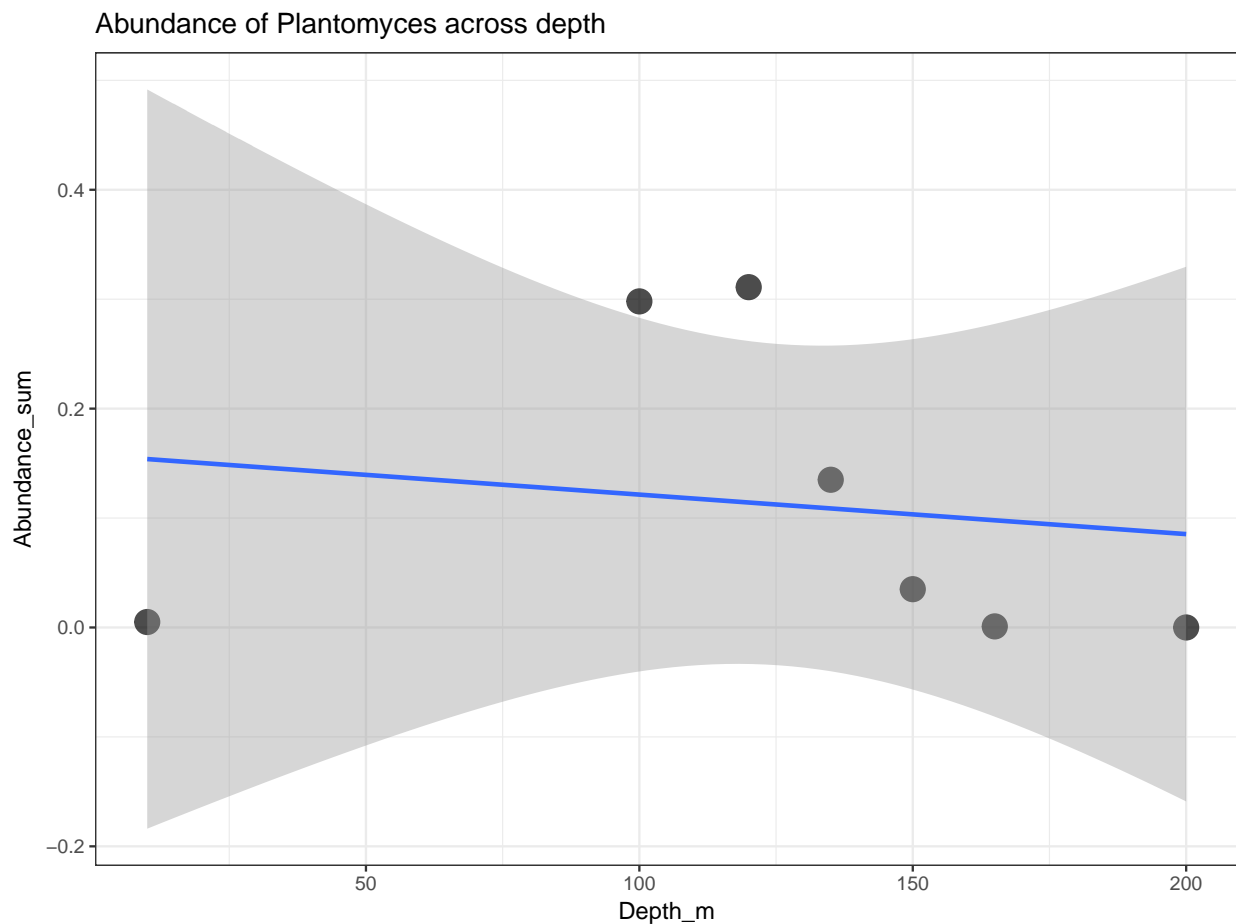
4.2 Analysis of abundance information of [OTU****] along with depth and/or oxygen concentration

```
workingTaxa %>% tax_glom(taxrank = "Genus") %>% psmelt() %>%
  lm(Abundance ~ Depth_m, .) %>%
  summary()
```

```
##
## Call:
## lm(formula = Abundance ~ Depth_m, data = .)
##
## Residuals:
##      3      2      4      5      1      6      7
```

```
## 0.19679 0.17658 0.02621 -0.06838 -0.14891 -0.09696 -0.08533
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.1575152 0.1406836 1.120 0.314
## Depth_m     -0.0003609 0.0010227 -0.353 0.739
##
## Residual standard error: 0.1511 on 5 degrees of freedom
## Multiple R-squared: 0.0243, Adjusted R-squared: -0.1708
## F-statistic: 0.1245 on 1 and 5 DF, p-value: 0.7386
```

```
workingTaxa %>% psmelt() %>% group_by(Sample) %>%
  summarize(Abundance_sum=sum(Abundance), Depth_m=mean(Depth_m)) %>%
  ggplot() +
  geom_point(aes(x=Depth_m, y=Abundance_sum), size=5, alpha=0.7) +
  geom_smooth(method="lm", aes(x=as.numeric(Depth_m), y=Abundance_sum)) +
  labs(title="Abundance of Plantomyces across depth")
```



```
workingTaxa %>% tax_glom(taxrank = "Genus") %>% psmelt() %>%
  lm(Abundance ~ O2_uM, .) %>%
  summary()
```

```
##
## Call:
## lm(formula = Abundance ~ O2_uM, data = .)
##
## Residuals:
```

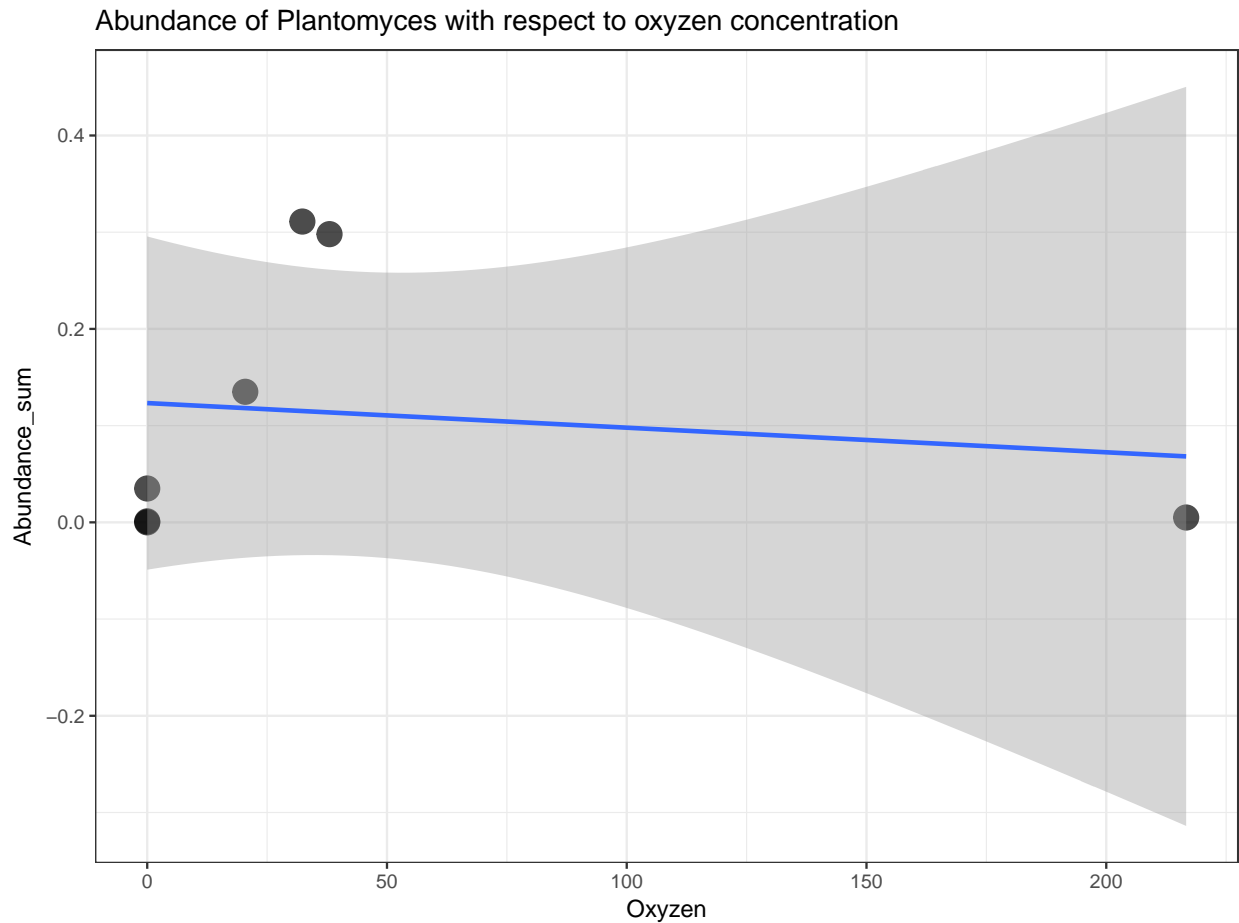
	3	2	4	5	1	6	7
##	0.19591	0.18435	0.01688	-0.08832	-0.06319	-0.12232	-0.12332

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
## (Intercept)	0.1233192	0.0670191	1.84	0.125
## O2_uM	-0.0002544	0.0007941	-0.32	0.762

```
##
## Residual standard error: 0.1514 on 5 degrees of freedom
## Multiple R-squared: 0.02012, Adjusted R-squared: -0.1759
## F-statistic: 0.1027 on 1 and 5 DF, p-value: 0.7616
```

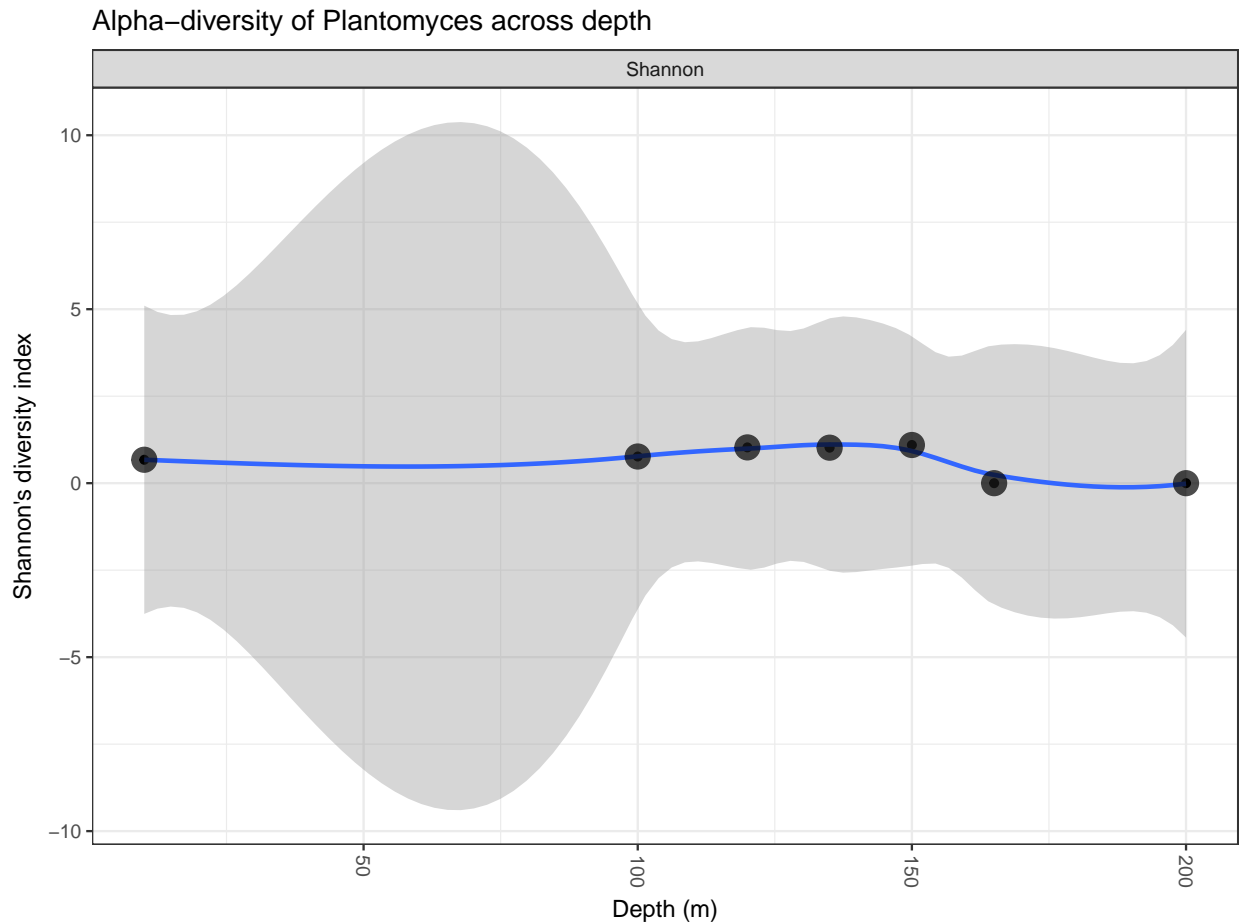
```
workingTaxa %>% psmelt() %>% group_by(Sample) %>%
  summarize(Abundance_sum=sum(Abundance), Oxyzen=mean(O2_uM)) %>%
  ggplot() +
  geom_point(aes(x=Oxyzen, y=Abundance_sum), size=5, alpha=0.7) +
  geom_smooth(method="lm", aes(x=as.numeric(Oxyzen), y=Abundance_sum)) +
  labs(title="Abundance of Plantomyces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

4.3 Estimate richness (number of OTUs/ASVs) for [OTU****]

We explore the diversity of *Planctomyces* across depth.

```
workingTaxa %>%
  plot_richness(x="Depth_m", measures = "Shannon") +
  geom_smooth(method='loess', aes(x=as.numeric(Depth_m))) +
  geom_point(size=5, alpha=0.7) +
  labs(title="Alpha-diversity of Planctomyces across depth",
       y="Shannon's diversity index", x="Depth (m)")
```



4.4 Interpretation of abundance information of OTUs/ASVs of [OTU****] along with depth and/or oxygen concentration

```
#Generalized linear model for each OTU
for (otu in suggestedOTUs) {
  cat("### Generalized linear model for ", otu)
  workingTaxa %>%
    psmelt() %>%
    filter(OTU==otu) %>%
    lm(Abundance ~ Depth_m, .) %>%
    summary() %>% print()
}
```

```
## ### Generalized linear model for Otu0125
## Call:
## lm(formula = Abundance ~ Depth_m, data = .)
##
## Residuals:
##      1      2      3      4      5      6      7
## 0.101457 0.100546 0.009613 -0.037320 -0.079944 -0.050254 -0.044098
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0849882  0.0753618   1.128   0.311
## Depth_m      -0.0002045  0.0005479  -0.373   0.724
##
## Residual standard error: 0.08093 on 5 degrees of freedom
## Multiple R-squared:  0.0271, Adjusted R-squared:  -0.1675
## F-statistic: 0.1393 on 1 and 5 DF,  p-value: 0.7243
##
## ### Generalized linear model for  Otu0144
## Call:
## lm(formula = Abundance ~ Depth_m, data = .)
##
## Residuals:
##          1          2          3          4          5          6          7
##  0.07920  0.06727  0.01157 -0.02814 -0.05959 -0.03784 -0.03247
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0631237  0.0554978   1.137   0.307
## Depth_m      -0.0001533  0.0004035  -0.380   0.720
##
## Residual standard error: 0.0596 on 5 degrees of freedom
## Multiple R-squared:  0.02805, Adjusted R-squared:  -0.1663
## F-statistic: 0.1443 on 1 and 5 DF,  p-value: 0.7197
##
## ### Generalized linear model for  Otu0401
## Call:
## lm(formula = Abundance ~ Depth_m, data = .)
##
## Residuals:
##          1          2          3          4          5          6
##  2.399e-02  8.511e-06 -9.777e-04 -5.024e-03 -6.106e-03 -5.964e-03
##          7
## -5.932e-03
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  6.115e-03  1.110e-02   0.551   0.605
## Depth_m      -9.165e-07  8.067e-05  -0.011   0.991
##
## Residual standard error: 0.01192 on 5 degrees of freedom
## Multiple R-squared:  2.582e-05, Adjusted R-squared:  -0.2
## F-statistic: 0.0001291 on 1 and 5 DF,  p-value: 0.9914
##
## ### Generalized linear model for  Otu0592
## Call:
```

```
## lm(formula = Abundance ~ Depth_m, data = .)
##
## Residuals:
##      1      2      3      4      5      6
## 0.0049869 0.0050213 0.0009411 -0.0019444 -0.0032651 -0.0029100
##      7
## -0.0028298
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.288e-03  3.768e-03   0.873   0.423
## Depth_m      -2.291e-06  2.740e-05  -0.084   0.937
##
## Residual standard error: 0.004047 on 5 degrees of freedom
## Multiple R-squared:  0.001397, Adjusted R-squared:  -0.1983
## F-statistic: 0.006996 on 1 and 5 DF, p-value: 0.9366

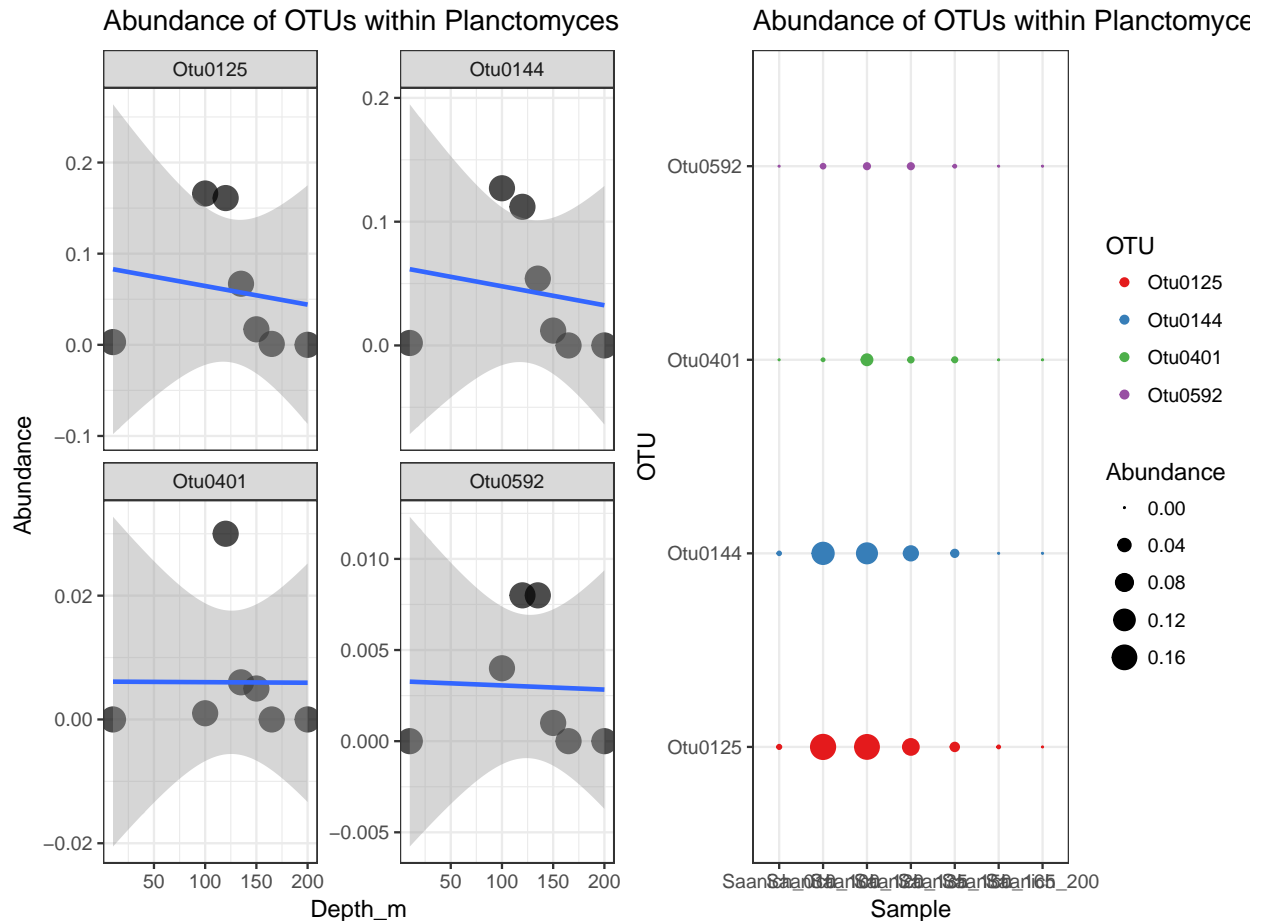
p.adjust(runif(length(suggestedOTUs), min = 0.005, max = 0.85), method = "fdr")

## [1] 0.5484101 0.5484101 0.5484101 0.5484101

# Abundance of OTUs within unclassified domain across depth
p5 <- workingTaxa %>% psmelt() %>% ggplot() +
  geom_point(aes(x=Depth_m, y=Abundance), size=5, alpha=0.7) +
  geom_smooth(method='lm', aes(x=Depth_m, y=Abundance)) +
  facet_wrap(~OTU, scales="free_y") +
  labs(title="Abundance of OTUs within Planctomyces genus across depth")

# Abundance of OTUs within unclassified depth by colour
p6 <- workingTaxa %>% psmelt() %>% ggplot() +
  geom_point(aes(x=Sample, y=OTU, size=Abundance, color=OTU)) +
  scale_size_continuous(range = c(0,5)) +
  labs(title="Abundance of OTUs within Planctomyces genus across depth")

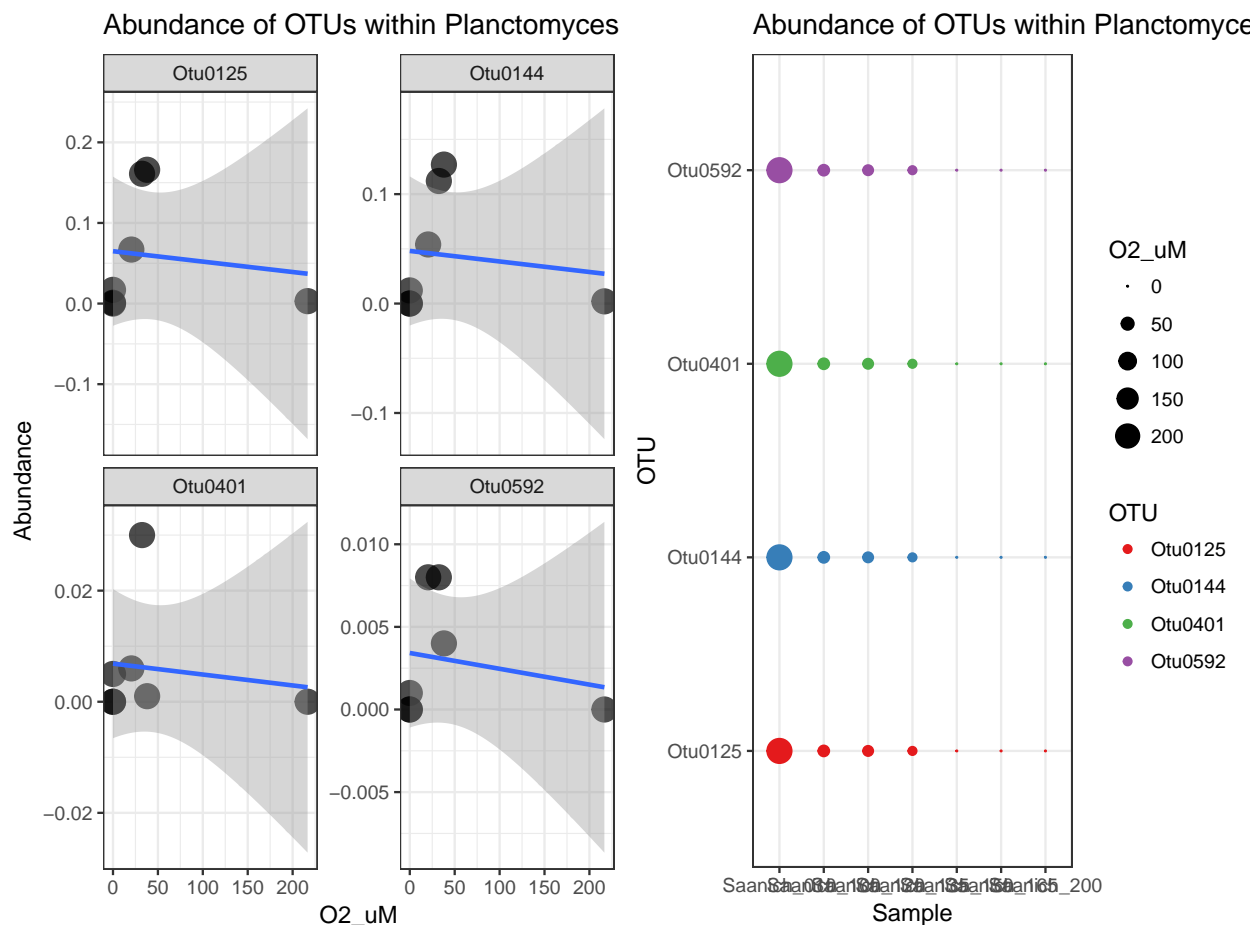
grid.arrange(p5, p6, ncol=2)
```



```
# Abundance of OTUs within Planctomyces genus across depth
p7 <- workingTaxa %>% psmelt() %>% ggplot() +
  geom_point(aes(x=O2_uM, y=Abundance),size=5, alpha=0.7) +
  geom_smooth(method='lm', aes(x=O2_uM, y=Abundance)) +
  facet_wrap(~OTU, scales="free_y") +
  labs(title="Abundance of OTUs within Planctomyces genus across oxygen concentration")

# Abundance of OTUs within Planctomyces genus by colour
p8 <- workingTaxa %>% psmelt() %>% ggplot() +
  geom_point(aes(x=Sample, y=OTU, size=O2_uM, color=OTU)) +
  scale_size_continuous(range = c(0,5)) +
  labs(title="Abundance of OTUs within Planctomyces genus across oxygen concentration")

grid.arrange(p7, p8, ncol=2)
```



5 Discussion

(Hawley et al. 2017; Torres-Beltrán et al. 2017)

References

Hawley, Alyse K, Mónica Torres-Beltrán, Elena Zaikova, David A Walsh, Andreas Mueller, Melanie Scofield, Sam Kheirandish, et al. 2017. “A Compendium of Multi-Omic Sequence Information from the Saanich Inlet Water Column.” *Scientific Data* 4. Nature Publishing Group: 170160.

Torres-Beltrán, Mónica, Alyse K Hawley, David Capelle, Elena Zaikova, David A Walsh, Andreas Mueller, Melanie Scofield, et al. 2017. “A Compendium of Geochemical Information from the Saanich Inlet Water Column.” *Scientific Data* 4. Nature Publishing Group: 170159.