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    psmelt() %>% lm(Abundance ~ Depth_m, .) %>% summary()
lmQTaxa2 <- workingQTaxa %>% tax_glom(taxrank = "Genus") %>%
    psmelt() %>% lm(Abundance ~ O2_uM, .) %>% summary()

otu_stats <- rbind(otu_stats, lmMTaxa1$coefficients["Depth_m",
])
otu_stats <- rbind(otu_stats, lmMTaxa2$coefficients["O2_uM",
])
otu_stats <- rbind(otu_stats, lmQTaxa1$coefficients["Depth_m",
])
otu_stats <- rbind(otu_stats, lmQTaxa2$coefficients["O2_uM",
])
tmpNames <- c("Depth (mothur)", "O2_uM (mothur)", "Depth (QIIME2)",
    "O2_uM (QIIME2)")
otu_stats <- cbind(tmpNames, otu_stats)
colnames(otu_stats) <- c("Covariates", "Estimate", "Std. Error",
    "t-value", "Pr(>|t|)")
kable(otu_stats, caption = "Table 2: Correlation data of OTUs within *Planctomyces* genus across

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Table 2: Table 2: Correlation data of OTUs within *Planctomyces* genus across depth and oxyzen concentration from Mothur and QIIME2

Covariates	Estimate	Std. Error	t-value	Pr(> t)
Depth (mothur)	-0.0003609	0.0010227	-0.3528908	0.7385598
O2_uM (mothur)	-0.0002544	0.0007941	-0.3203956	0.7616253
Depth (QIIME2)	-0.0005878	0.0018774	-0.3130933	0.7668485
O2_uM (QIIME2)	-0.0005997	0.0014441	-0.4152436	0.6951812

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dfworkingMTaxa <- workingMTaxa %>% psmelt() %>% group_by(Sample) %>%
    summarize(Abundance_sum = sum(Abundance), Depth_m = mean(Depth_m))
p1 <- ggplot(dfworkingMTaxa) + 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")

dfworkingMTaxa <- workingMTaxa %>% psmelt() %>% group_by(Sample) %>%
    summarize(Abundance_sum = sum(Abundance), Oxyzen = mean(O2_uM))
p2 <- ggplot(dfworkingMTaxa) + 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

dfworkingQTaxa <- workingQTaxa %>% psmelt() %>% group_by(Sample) %>%
    summarize(Abundance_sum = sum(Abundance), Depth_m = mean(Depth_m))
p3 <- ggplot(dfworkingQTaxa) + 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")

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