### Shallow and mesophotic Temperature correlation

library("ggpubr")

library(ggplot2)

shapiro.test(CorrelationTem$Meso)

shapiro.test(CorrelationTem$Shallow)

res <- cor.test(CorrelationTem$Meso, CorrelationTem$Shallow,

method = "spearman",exact=FALSE)

res

### Survival probability

library("survival")

library("survminer")

SurvivalAllSp$Condition <- ordered (SurvivalAllSp$Condition,

levels = c ("~28 C", "~30 C", "~31 C"))

SurvivalAllSp$DepSp <- factor(SurvivalAllSp$DepSp, levels=c("A", "B", "C", "D", "E", "F",

"G", "H", "I", "J", "K", "L"),

labels=c("Acropora valida", "Galaxea fascicularis",

"Acropora cf.horrida", "Galaxea cf. astreata",

"Pachyseris speciosa1", "Porites sp.1",

"Pachyseris speciosa","Porites sp.",

"Porites cylindrica", "Turbinaria sp",

"Leptoseris papyracea", "Seriatopora hystrix"))

fit <- survfit(Surv(Day, censor) ~ Condition+DepSp, data = SurvivalAllSp)

print(fit)

# Summary of survival curves

summary(fit)

# Access to the sort summary table

summary(fit)$table

# To visualize all survival graph

ggsurvplot(fit, data = SurvivalAllSp, conf.int = TRUE,

legend.title = "Condition",

color = "Condition",

palette = c("#313695","#fdae61","#a50026")) %>%.$plot+facet\_wrap (.~DepSp, ncol=4)+ theme\_classic() +

scale\_x\_continuous(breaks = c(2,4,6,8,10,12,14))

######### Photosynthesis efficiency Fv/fm (GLM)

library(emmeans)

library(sjstats)

library(lme4)

library(lmerTest)

library(MuMIn)

###turn off scientfic notation

options(scipen = 999)

###Introduce factor

Totaldata$Condition<- factor(Totaldata$Condition)

model <- glm(FvFm ~ Species \* Condition \* Day, data = Totaldatatest, family = Gamma) ###linear model DV predicted by the IV (drink\*picture)

summary(model)

anova(model)

###show model as anova

effectsize::eta\_squared(model, partial = TRUE) ### partial eta sq

r.squaredGLMM(model) ### adjust R2 for the model as an alternative

marginal = lsmeans(model,

pairwise ~ Condition | Species |Day,

adjust="tukey")

marginal

###Post hocs for main effects

emmeans(model, pairwise~Species) ### post hoc for picture type, as its two level this isnt really

### Post hoc tests for the interaction this does pairwise comparisons for condition,

###separately for the species

emmeans(model, pairwise~Condition | Species)

########## Brightness

model <- glm(Brightness ~ Species \* Condition \* Day, data = Totaldatatest, family = Gamma) ###linear model DV predicted by the IV (drink\*picture)

summary(model)

anova(model) ###show model as anova

effectsize::eta\_squared(model, partial = TRUE) ### partial eta sq

r.squaredGLMM(model) ### adjust R2 for the model as an alternative

marginal = lsmeans(model,

pairwise ~ Condition | Species |Day,

adjust="tukey")

marginal

###Post hocs for main effects

emmeans(model, pairwise~Species) ### post hoc for picture type, as its two level this isnt really

### Post hoc tests for the interaction this does pairwise comparisons for condition,

###separately for the species

emmeans(model, pairwise~Condition | Species)

### Generalized linear model (GLM) Symbiont density

library(multcompView)

library(lsmeans)

### Normality test

shapiro.test(Symdensity$CellCm2)

model2 <- glm(CellCm2 ~ Condition \* Species + Day, data = Symdensity)

###show model as anova

effectsize::eta\_squared(model2, partial = TRUE) ### partial eta sq

r.squaredGLMM(model2) ### adjust R2 for the model as an alternative

###Post hocs for main effects

emmeans(model2, pairwise~ Condition|Species)

### post hoc for picture type, as its two level this isnt really

marginal = lsmeans(model2,

pairwise ~Condition|Species|Day,

adjust="sidak")

marginal

### Post hoc tests for the interaction this does pairwise comparisons for conditions,

###separately for the species

emmeans(model2, pairwise~Condition | Species)

### Generalized linear model (GLM) total chlorophyll per cm

### Normality test

shapiro.test(Symdensity$TotalChlCm)

model1 <- glm(TotalChlCm ~ Condition \* Species +Day, data = Symdensity)

anova(model1)

#show model as anova

effectsize::eta\_squared(model2, partial = TRUE) ### partial eta sq

r.squaredGLMM(model2) ### adjust R2 for the model as an alternative

marginal = lsmeans(model2,

pairwise ~Condition|Species,

adjust="sidak")

marginal

### Post hoc tests for the interaction this does pairwise comparisons for conditions,

emmeans(model2, pairwise~Condition | Species)

#### Meta analysis

library(meta)

library(forestplot)

#### SMDs of brightness data

m1 <- metacont(D0, M0, S0, D14, M14, S14,

data=HighBrightSMD, sm = "SMD")

m1

forest(m1)

m2 <- metacont(D0, M0, S0, D14, M14, S14,

data=MediumBrightSMD, sm = "SMD")

m2

forest(m2)

###### SMD of Fv/Fm data

m3 <- metacont(D0, M0, S0, D14, M14, S14,

data=HighFvFmSMD, sm = "SMD")

m3

forest(m3)

m4 <- metacont(D0, M0, S0, D14, M14, S14,

data=MediumFvFmSMD, sm = "SMD")

m4

forest(m4)

forest (m4, layout = "JAMA")

m5 <- metacont(D0, M0, S0, D14, M14, S14,

data=HighCellSMD, sm = "SMD")

m5

forest(m5)

m6 <- metacont(D0, M0, S0, D14, M14, S14,

data=mediumCellSMD, sm = "SMD")

m6

forest(m6)

m7 <- metacont(D0, M0, S0, D14, M14, S14,

data=HighchlSMD, sm = "SMD")

m7

forest(m7)

m8 <- metacont(D0, M0, S0, D14, M14, S14,

data=mediumchlSMD, sm = "SMD")

m8

forest(m8)

############ Forest plot

library(magrittr)

library(ggplot2)

library(plotrix)

FvFmSMD$No <- factor(FvFmSMD$No , levels=c("12", "11", "10", "9", "8", "7",

"6", "5", "4", "3", "2", "1"),

labels=c("Leptoseris papyracea","Seriatopora hystrix", "Porites sp MS", "Pachyseris speciosa MS", "Galaxea cf astreata",

"Acropora sp", "Turbinaria mesentarina", "Porites cylindrica", "Porites sp SH", "Pachyseris speciosa SH",

"Galaxea facicularis", "Acropora valida"))

"#fdae61","#a50026"

dotCOLS = c("#f1b6da","#fee090")

barCOLS = c("#8e0152","#fdae61")

p <- ggplot(FvFmSMD, aes(x=No, y=OR, ymin=LL, ymax=UL, col=Lable,fill=Lable)) +

scale\_x\_discrete(limits = c("Leptoseris papyracea","Seriatopora hystrix", "Porites sp MS", "Pachyseris speciosa MS", "Galaxea cf astreata",

"Acropora sp", "Turbinaria mesentarina", "Porites cylindrica", "Porites sp SH", "Pachyseris speciosa SH",

"Galaxea facicularis", "Acropora valida"))+

geom\_linerange (size=3,position=position\_dodge(width = 0.3)) +

geom\_hline(yintercept=1, lty=2) +

geom\_point(size=3, shape=21, colour="white", stroke = 0.3,position=position\_dodge(width = 0.3)) +

scale\_fill\_manual(values=barCOLS)+

scale\_color\_manual(values=dotCOLS)+

scale\_x\_discrete (name="Species")+

coord\_flip() +

theme\_classic()\_meta+ facet\_grid(~Parameter)

p

SymChlSMD$No <- factor(SymChlSMD$No , levels=c("12", "11", "10", "9", "8", "7",

"6", "5", "4", "3", "2", "1"),

labels=c("Leptoseris papyracea","Seriatopora hystrix", "Porites sp MS", "Pachyseris speciosa MS", "Galaxea cf astreata",

"Acropora sp", "Turbinaria mesentarina", "Porites cylindrica", "Porites sp SH", "Pachyseris speciosa SH",

"Galaxea facicularis", "Acropora valida"))

p1 <- ggplot(SymChlSMD, aes(x=No, y=OR, ymin=LL, ymax=UL, col=Lable,fill=Lable)) +

scale\_x\_discrete(limits = c("Leptoseris papyracea","Seriatopora hystrix", "Porites sp MS", "Pachyseris speciosa MS", "Galaxea cf astreata",

"Acropora sp", "Turbinaria mesentarina", "Porites cylindrica", "Porites sp SH", "Pachyseris speciosa SH",

"Galaxea facicularis", "Acropora valida"))+

geom\_linerange (size=3,position=position\_dodge(width = 0.3)) +

geom\_hline(yintercept=1, lty=2) +

geom\_point(size=3, shape=21, colour="white", stroke = 0.3,position=position\_dodge(width = 0.3)) +

scale\_fill\_manual(values=barCOLS)+

scale\_color\_manual(values=dotCOLS)+

scale\_x\_discrete (name="Species")+

coord\_flip() +

theme\_classic()\_meta+ facet\_grid(~Parameter)

p1