Příloha 23 – Skript R

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rm(list = ls()) # clean the R environment
install.packages(c("ggplot2", "Matrix", "expss", "sjPlot", "vegan", "multcomp", "lme4", "remotes", "strengejacke"))
library(ggplot2)
library(lme4)
library(multcomp)
library(vegan)
library(expss)
library(sjPlot)

data <- read.csv2("data/food4.csv", sep=",", header = TRUE, stringsAsFactors = FALSE, na.strings = "NA" )
data$navnada <- as.factor(data$navnada)
data$lokalita <- as.factor(data$lokalita)
data$rok <- as.factor(data$rok)
data$biotop <- as.factor(data$biotop)

data <- data[data$biotop=="pole"]
str(data)
data$total <- rowSums(data[,1:40])

data$total[data$total <1 ] <- NA
data <- data [complete.cases(data),]
install.packages("plyr")
library(plyr)
brillouin <- function(x) {
  N <- sum(x)
  (log(factorial(N)) - sum(log(factorial(x))))/N
}
apply(data[1:40],1,brillouin)
data$brillouin <- apply(data[1:40],1,brillouin)
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mod_div <- lm(brillouin~navnada, data=data)
summary(mod_div)
plot_model(mod_div,
        type = "pred",
        terms = c("navnada"),
        show.data=TRUE,
        colors=c("#EC3F4A", "#1E90FF"),
        #colors = "black",
        title = "Diverzita (Brillouin)",
        axis.title=c("Návnada"," Brillouin index"),
        show.legend = T)
ggsave("outputs/brillouin_diversita.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/brillouin_diversita.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")
#species number as a function of a bait
str(data)
data$total.spec <- count_row_if(gt(0), data[1:40])
mod_spec <- glm(total.spec~navnada, data=data, family = poisson())
exp(0.1781)
summary(mod_spec)
plot_model(mod_spec,
        type = "pred",
        terms = c("navnada"),
        show.data=TRUE,
        colors=c("#EC3F4A", "#1E90FF"),
        # colors = "black",
        title = "Diverzita (Druhy)",
        axis.title=c("Návnada"," Počet druhů"),
        show.legend = T)
ggsave("outputs/druhova_diversita.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/druhova_diversita.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")
```

```
str(data)


#POSTHOC - mod2
post.hoc <- glht(mod_spec, alternative = "greater", linfct = mcp(navnada = "Tukey"))
par(mfrow=c(1,1))
jpeg('outputs/posthoc_vsechnydruhy.jpg')
plot(glht(mod_spec, alternative = "greater", linfct = mcp(navnada = "Tukey")))
dev.off()
summary(post.hoc)
#ANALYSIS of Necrobiont species
data_necrophagous <- data[1:19]
navnada <- data$navnada
data_necrophagous <- cbind(data_necrophagous, navnada)


str(data_necrophagous)
data_necrophagous$total.spec <- count_row_if(gt(0), data_necrophagous)
mod_spec_necr <- glm(total.spec~navnada, data=data_necrophagous, family = poisson())
summary(mod_spec_necr)


#POSTHOC - mod2
post.hoc <- glht(mod_spec_necr, alternative = "greater", linfct = mcp(navnada = "Tukey"))
par(mfrow=c(1,1))
jpeg('outputs/posthoc_nekrofagove.jpg')
plot(glht(mod_spec_necr, alternative = "greater", linfct = mcp(navnada = "Tukey")))
dev.off()
summary(post.hoc)


plot_model(mod_spec_necr,
    type = "pred",
    terms = c("navnada"),
    show.data=TRUE,
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        colors=c("#EC3F4A", "#1E90FF"),
        # colors = "black",
        title = "Počet nekrofágních druhů",
        axis.title=c("Návnada"," Počet druhů"),
        show.legend = T)

ggsave("outputs/druhova_diversita_nekrofagove.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/druhova_diversita_nekrofagove.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")

#ANALYSIS of Not necrobiont species
data_notnecrophagous <- data[20:40]
navnada <- data$navnada
data_notnecrophagous <- cbind(data_notnecrophagous, navnada)

str(data_notnecrophagous)
data_notnecrophagous$total.spec <- count_row_if(gt(0), data_notnecrophagous)
mod_spec_notnecr <- glm(total.spec~navnada, data=data_notnecrophagous, family = poisson())
summary(mod_spec_notnecr)

#POSTHOC - mod2
post.hoc <- glht(mod_spec_notnecr, alternative = "greater", linfct = mcp(navnada = "Tukey"))
par(mfrow=c(1,1))
jpeg('outputs/posthoc_notnekrofagove.jpg')
plot(glht(mod_spec_notnecr, alternative = "greater", linfct = mcp(navnada = "Tukey")))
dev.off()
summary(post.hoc)

plot_model(mod_spec_notnecr,
        type = "pred",
        terms = c("navnada"),
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        show.data=TRUE,
        colors=c("#EC3F4A", "#1E90FF"),
        # colors = "black",
        title = "Počet ostatních druhů (mimo nekrofágní)",
        axis.title=c("Návnada"," Počet druhů"),
        show.legend = T)

ggsave("outputs/druhova_diversita_notnekrofagove.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/druhova_diversita_notnekrofagove.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")
#ANALYSIS of Silphidae
data_silp <- data[1:6]
data_silp <- cbind(data_silp, navnada)

str(data_silp)
summary(data_silp)
data_silp$total.spec <- count_row_if(gt(0), data_silp)
data_silp$abund <- rowSums(data_silp[,1:6])
mod_spec_silp <- lm(total.spec~navnada, data=data_silp)
mod_spec_silp2 <- lm(abund~navnada, data=data_silp)
summary(mod_spec_silp)
summary(mod_spec_silp2)
data_silp$abund[data_silp$navnada=="blank"]
plot_model(mod_spec_silp2,
        type = "pred",
        terms = c("navnada"),
        show.data=TRUE,
        colors=c("#EC3F4A", "#1E90FF"),
        # colors = "black",
        title = "Abundance Silphidae",
        axis.title=c("Návnada"," Počet jedinců"),
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        show.legend = T)

ggsave("outputs/abund_silphidae.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/abund_silphidae.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")
#POSTHOC - mod2
post.hoc2 <- glht(mod_spec_silp2, alternative = "greater", linfct = mcp(navnada = "Tukey"))
par(mfrow=c(1,1))
jpeg('outputs/posthoc_abund_silphidae.jpg')
plot(glht(mod_spec_silp2, alternative = "greater", linfct = mcp(navnada = "Tukey")))
dev.off()
summary(post.hoc2)

plot_model(mod_spec_silp,
        type = "pred",
        terms = c("navnada"),
        show.data=TRUE,
        colors=c("#EC3F4A", "#1E90FF"),
        # colors = "black",
        title = "Počet druhů Silphidae",
        axis.title=c("Návnada"," Počet druhů"),
        show.legend = T)

ggsave("outputs/druhova_diversita_silphidae.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/druhova_diversita_silphidae.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")
#POSTHOC - mod2
post.hoc1 <- glht(mod_spec_silp, alternative = "greater", linfct = mcp(navnada = "Tukey"))
par(mfrow=c(1,1))
jpeg('outputs/posthoc_silphidae.jpg')
plot(glht(mod_spec_silp, alternative = "greater", linfct = mcp(navnada = "Tukey")))
```

```
dev.off()
summary(post.hoc1)

#modeling for each species
str(data)
mod1 <- glm(Thanatophilus.sinuatus~navnada+lokalita, family = poisson(), data = data)
summary(mod1)

mod2 <- glm(Thanatophilus.rugosus~navnada+lokalita, family = poisson(), data = data)
summary(mod2)

mod3 <- glm(Nicrophorus.vespillo~navnada+lokalita, family = poisson(), data = data)
summary(mod3)

mod4 <- glm(Nicrophorus.investigator~navnada+lokalita, family = poisson(), data = data)
summary(mod4)

mod5 <- glm(Nicrophorus.sepultor~navnada+lokalita, family = poisson(), data = data)
summary(mod5)

mod6 <- glm(Nicrophorus.interruptus~navnada+lokalita, family = poisson(), data = data)
summary(mod6)

mod10 <- glm(Glischrochilus.quadrisignatus~navnada, family = poisson(), data = data)
summary(mod10)
post.hoc1 <- glht(mod10, alternative = "greater", linfct = mcp(navnada = "Tukey"))
par(mfrow=c(1,1))
jpeg('outputs/posthoc_glischrochilus.jpg')
plot(glht(mod10, alternative = "greater", linfct = mcp(navnada = "Tukey")))
summary(post.hoc1)
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mod_specgq <- glm(Glischrochilus.quadrisignatus~navnada, data=data, family = poisson())
exp(0.1781)
plot_model(mod_specgq,
        type = "pred",
        terms = c("navnada"),
        show.data=TRUE,
        colors=c("#EC3F4A", "#1E90FF"),
        # colors = "black",
        title = "Abundance Glischrochilus quadrisignatus",
        axis.title=c("Návnada"," Počet jedinců"),
        show.legend = T)
ggsave("outputs/gq_diversita.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/gq_diversita.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")
str(data)

mod11 <- glm(Poecilus.cupreus~navnada+lokalita, family = poisson(), data = data)
summary(mod11)
post.hoc1 <- glht(mod11, alternative = "greater", linfct = mcp(navnada = "Tukey"))
par(mfrow=c(1,1))
jpeg('outputs/poecilus_cupreus.jpg')
plot(glht(mod11, alternative = "greater", linfct = mcp(navnada = "Tukey")))
summary(post.hoc1)

mod_specpc <- glm(Poecilus.cupreus~navnada, data=data, family = poisson())
exp(0.1781)
plot_model(mod_specpc,
        type = "pred",
        terms = c("navnada"),
        show.data=TRUE,
        colors=c("#EC3F4A", "#1E90FF"),
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        # colors = "black",
        title = "Abundance Poecilus cupreus",
        axis.title=c("Návnada"," Počet jedinců"),
        show.legend = T)
ggsave("outputs/pc_diversita.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/pc_diversita.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")
str(data)

mod12 <- glm(Pterostichus.melanarius~navnada+lokalita, family = poisson(), data = data)
summary(mod12)
post.hoc2 <- glht(mod12, alternative = "greater", linfct = mcp(navnada = "Tukey"))
par(mfrow=c(1,1))
jpeg('outputs/Pterostichus_melanarius.jpg')
plot(glht(mod12, alternative = "greater", linfct = mcp(navnada = "Tukey")))
summary(post.hoc2)

mod_specpm <- glm(Pterostichus.melanarius~navnada, data=data, family = poisson())
exp(0.1781)
plot_model(mod_specpm,
        type = "pred",
        terms = c("navnada"),
        show.data=TRUE,
        colors=c("#EC3F4A", "#1E90FF"),
        # colors = "black",
        title = "Abundance Pterostichus melanarius",
        axis.title=c("Návnada"," Počet jedinců"),
        show.legend = T)
ggsave("outputs/pm_diversita.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/pm_diversita.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")
str(data)
```

```
mod13 <- glm(Saprinus.semistriatus~navnada+lokalita, family = poisson(), data = data)
summary(mod13)
post.hoc3 <- glht(mod13, alternative = "greater", linfct = mcp(navnada = "Tukey"))
par(mfrow=c(1,1))
jpeg('outputs/Saprinus_semistriatus.jpg')
plot(glht(mod13, alternative = "greater", linfct = mcp(navnada = "Tukey")))
summary(post.hoc3)

mod_specss <- glm(Saprinus.semistriatus~navnada, data=data, family = poisson())
exp(0.1781)
plot_model(mod_mod13,
        type = "pred",
        terms = c("navnada"),
        show.data=TRUE,
        colors=c("#EC3F4A", "#1E90FF"),
        # colors = "black",
        title = "Abundance Saprinus semistriatus",
        axis.title=c("Návnada"," Počet jedinců"),
        show.legend = T)
ggsave("outputs/ss_diversita.tiff", dpi = 600,compression = "lzw",width = 15, height = 10, units="cm")
ggsave("outputs/ss_diversita.tiff.jpeg", dpi = 600,width = 15, height = 10, units="cm")
str(data)
```