library(vegan)

morf<-read.table("Emollis.csv", head = T, sep = ",")

head(morf)

str(morf)

morf1<-read.table("pscutatum.csv", head = T, sep = ",")

head(morf1)

str(morf1)

morf2<-read.table("ptrichoides.csv", head = T, sep = ",")

head(morf2)

str(morf2)

morf3<-read.table("pfimbriatum.csv", head = T, sep = ",")

head(morf3)

str(morf3)

clima <- read.table("medclima.csv", head = T, sep = ",")

head(clima)

str(clima)

medclima <- read.table("medclima.csv", head = T, sep = ",")

tabela\_merge <- merge(morf, medclima, by = "ano")

modelo\_anova <- lm( ~ , data = morf)

anova(modelo\_anova)

library(ggplot2)

jpeg(filename = " .jpeg ",width = 15, height = 8,

units = "cm",pointsize = 12, "lzw",res = 1200)

ggplot(data = morf1, mapping = aes(x = , y = )) + geom\_smooth(method = lm, formula = y ~x, fill = "black", color = "black") +

labs(x = " " , y = " ")

dev.off()