Biomechanical properties of a buzz-pollinated flower

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loading data information

```
lab.data<-read.csv2(file="labels.csv", header=T, dec=",")
head(lab.data)
```

loading libraries

```
library(viridis)
library(seewave)
require(lme4)
require(lmerTest)
library(AICcmodavg)
library(lmtest)
library(sjPlot)
library(ggplot2)
```

creating labels for files

```
temp<-list.files(pattern=".txt") #extracting .txt names
temp2<-gsub("\\..*", "", temp) #extracting .txt names
crow<-which(as.character(lab.data$File) == temp2)
lab.plot<-paste("Vel. = ", lab.data[crow,12], ";", "Str. = ",
lab.data[crow,14], ";", "Axis = " , lab.data[crow,15],";",  "Fl.
accession =", lab.data[crow,8],  sep=" ")
```

defining parameters and empty objects

```
mycol<-viridis(3)
sel<-c(11760:15360)
pdat<- vector("list", length(lab.plot))
spec <- vector("list", length(lab.plot))
xx <- vector("list", length(lab.plot))
yy <- vector("list", length(lab.plot))
d.freq<- vector("list", length(lab.plot))
rms <- vector("numeric", length(lab.plot))
```

loop to plot all oscillograms and spectograms

```
pdf(file = "oscillo-spec_II.pdf",
    width = 10, # The width of the plot in inches
    height = 15) # The height of the plot in inches

par(mfrow=c(3,2))
```

```
for(i in 1:length(lab.plot)) {

  pdat[[i]] <-
read.table(file=paste("C:/Users/vinic/OneDrive/Documentos/Colaborações/Pr
ofessores/Mario Vallejo-Marin/flower vibrations/analysis_II/", temp[i],
sep=""), skip=5)

  #Oscillogram
plot(pdat[[i]][,1],pdat[[i]][,2]*1000, type="n", xlab="Time (s)", ylab=
"Velocity (mm/s)", main= lab.plot[i], cex.main=0.95)
lines(x=pdat[[i]][c(1:min(sel)-1),1], y= pdat[[i]][c(1:min(sel)-
1),2]*1000, col="gray")
lines(x=pdat[[i]][c(min(sel):max(sel)),1], y=
pdat[[i]][c(min(sel):max(sel)),2]*1000, col=mycol[1])

  #Spectrum (B)
spec[[i]]<-spec(pdat[[i]][2]*1000, from= 0.98, to=1.28, f=12000,
flim=c(0.09,5), wn= "hamming", wl=512, ovlp=70, cex.lab=1.5,
alab="Relative amplitude", plot=TRUE, PSD=TRUE)
xx[[i]]<-c(spec[[i]], rev(spec[[i]][,1]))
yy[[i]] <- c(rep(0, length(spec[[i]])), rev(spec[[i]][,2]))
par(las=1)
polygon(xx[[i]],yy[[i]], col=mycol[1])
axis(2)
text(2.1,0.97, "", cex=2)
}

dev.off()
```

loop to plot domintant frequencies

```
pdf(file = "d.freq.pdf",
    width = 10, # The width of the plot in inches
    height = 15) # The height of the plot in inches

par(mfrow=c(3,2))

for(i in 1:length(lab.plot)) {
  pdat[[i]] <-
read.table(file=paste("C:/Users/vinic/OneDrive/Documentos/Colaborações/Pr
ofessores/Mario Vallejo-Marin/flower vibrations/analysis_II/", temp[i],
sep=""), skip=5)
  d.freq[[i]]<- dfreq(pdat[[i]][c(min(sel):max(sel)),2], f=12000, channel
= 1, wl = 512, wn = "hanning", ovlp = 70, main= lab.plot[i])
}

dev.off()
```

loop to calculate Vrms

```
for(i in 1:length(lab.plot)) {
  pdat[[i]] <-
read.table(file=paste("C:/Users/vinic/OneDrive/Documentos/Colaborações/Pr
ofessores/Mario Vallejo-Marin/flower vibrations/analysis_II/", temp[i],
sep=""), skip=5)
  rms[[i]]<- rms(pdat[[i]][c(min(sel):max(sel)),2])
}
```

plotting oscillograms and spectra for Fig. 2

```
pdf(file = "freq-oscillo.pdf",
    width = 8.27, # The width of the plot in inches
    height = 6.25) # The height of the plot in inches

par(mar=c(5.1,4.5,4.1,2.1))
par(mfrow = c(2, 3))  # Set up a 2 x 2 plotting space

plot((pdat[[263]][14760:15360,1]-1.229917)*1000,
pdat[[263]][14760:15360,2]*1000, type="l", col="#440154FF", lwd=2,
ylim=c(-400,400), ylab=  expression('V' [PEAK] *' (mm s'^-1*')'),
xlab="Time (ms)", las=1)
abline(h=0, col="gray", lty=2)

plot((pdat[[261]][14760:15360,1]-1.229917)*1000,
pdat[[261]][14760:15360,2]*1000, type="l",col="#31688EFF", lwd=2,
ylim=c(-400,400), ylab=  expression('V' [PEAK] *' (mm s'^-1*')'),
xlab="Time (ms)", las=1)
abline(h=0, col="gray", lty=2)

plot((pdat[[259]][14760:15360,1]-1.229917)*1000,
pdat[[259]][14760:15360,2]*1000, type="l", col="#35B779FF", lwd=2,
ylim=c(-400,400), ylab=  expression('V' [PEAK] *' (mm s'^-1*')'),
xlab="Time (ms)", las=1)
abline(h=0, col="gray", lty=2)

plot(spec[[263]][,1], spec[[263]][,2], type="l", col="#440154FF", lwd=2,
ylab=  expression("Relative amplitude"), xlab="Frequency (KHz)",
xlim=c(0,5), las=1)

plot(spec[[261]][,1], spec[[261]][,2], type="l", col="#31688EFF", lwd=2,
ylab=  expression("Relative amplitude"), xlab="Frequency (KHz)",
xlim=c(0,5), las=1)

plot(spec[[259]][,1], spec[[259]][,2], type="l", col="#35B779FF", lwd=2,
ylab=  expression("Relative amplitude"), xlab="Frequency (KHz)",
xlim=c(0,5), las=1)

dev.off()
```

analysis amplitude

```
summary(lab.data)
lab.data$new.rms_mm <- rms*1000

data_str <- as.data.frame(lab.data[lab.data$File!="190801-
268",][seq(1,539,2),]) #removing "receptacle" without match

data_str$new.rms_rec<-lab.data$new.rms_mm[lab.data$File!="190801-
268"][seq(2,540,2)] #removing "receptacle" without match
head(data_str)
```

model selection

```
A_B_C_AB_AC_CB_ABC <- lmer(new.rms_mm ~ labels*axis*new.rms_rec +
(1|flower_accession), data=data_str, REML=F)

A_B_C_AB_AC_CB <- lmer(new.rms_mm ~ labels + axis + new.rms_rec +
labels*axis + labels*new.rms_rec + axis*new.rms_rec +
(1|flower_accession), data=data_str, REML=F)

A_B_C_AB_AC <- lmer(new.rms_mm ~ labels + axis + new.rms_rec +
labels*axis + labels*new.rms_rec +  (1|flower_accession), data=data_str,
REML=F)

A_B_C_AB_CB <- lmer(new.rms_mm ~ labels + axis + new.rms_rec +
labels*axis + axis*new.rms_rec + (1|flower_accession), data=data_str,
REML=F)

A_B_C_AC_CB <- lmer(new.rms_mm ~ labels + axis + new.rms_rec +
labels*new.rms_rec + axis*new.rms_rec + (1|flower_accession),
data=data_str, REML=F)

A_B_C_AB <- lmer(new.rms_mm ~ labels + axis + new.rms_rec + labels*axis +
(1|flower_accession), data=data_str, REML=F)

A_B_C_AC <- lmer(new.rms_mm ~ labels + axis + new.rms_rec +
labels*new.rms_rec + (1|flower_accession), data=data_str, REML=F)

A_B_C_CB <- lmer(new.rms_mm ~ labels + axis + new.rms_rec +
axis*new.rms_rec + (1|flower_accession), data=data_str, REML=F)

A_B_C <- lmer(new.rms_mm ~ labels + axis + new.rms_rec  +
(1|flower_accession), data=data_str, REML=F)

null <- lmer(new.rms_mm ~ (1|flower_accession), data=data_str, REML=F)
```

aci_tab method

```
cand.mod.names <- c("A_B_C_AB_AC_CB_ABC", "A_B_C_AB_AC_CB",
"A_B_C_AB_AC", "A_B_C_AB_CB", "A_B_C_AC_CB", "A_B_C_AB", "A_B_C_AC",
"A_B_C_CB", "A_B_C", "null")
```

```
cand.mods <- list( )

for(i in 1:length(cand.mod.names)) {
  cand.mods[[i]] <- get(cand.mod.names[i]) }

print(aictab(cand.set = cand.mods,
             modnames = cand.mod.names))

anova(A_B_C_AB_AC_CB)

summary(A_B_C_AB_AC_CB)
```

plot model

```
pdf(file = "plot_model_II.pdf",
    width = 10, # The width of the plot in inches
    height = 3.3) # The height of the plot in inches

par(mfrow=c(1,3))


mycol<-viridis(4)
mycol<-mycol[1:3]

p <- plot_model(A_B_C_AB_AC_CB, type="pred", terms=c("new.rms_rec",
"labels", "axis"), show.data = FALSE,
                colors=mycol, line.size = 1.3, title="",
axis.title=c(expression('Input V' [RMS] * ' (mm/s)') ,
expression('Measured V' [RMS] * ' (mm/s)')))

p + theme_bw() + theme(panel.grid.major = element_blank(),
panel.grid.minor = element_blank(),
                       panel.background = element_blank(), axis.line =
element_line(colour = "black"))+
  geom_abline(slope=1, intercept=0, lty=2, col="darkgray", lwd=1.2)

dev.off()
```