```r
#Kaplan-Meier and Logrank test
library(ggplot2)
library(ggpubr)
library(survival)
library(survminer)
library(export)
A<-read.csv("d:\\R\\Survival analysis\\Survival analysis.csv")
sfitA<- survfit(Surv(DaysToEvent, status)~L, data=A)
AP<-ggsurvplot(sfitA, pval=TRUE,surv.scale="percent",
                legend=c("right"),
                legend.labs=c("A. catechu    c","A. sinensis    a","C. nucifera    ab","C.
oleifera   d","D. odorifera   c", "H. brasiliensis   b","Z. mays   a"),
                legend.title="",
                palette=c("green3","yellow3","skyblue3","pink3","brown4","orange3",
"aquamarine4"),
                xlab="Days to eclosion (days)",
                ylab="Survival rate (%)")
AP
survdiff(Surv(DaysToEvent, status==1)~L, data=A)

#leaf area
library(ggplot2)
library(Matrix)
library(lmerTest)
library(carData)
library(car)
library(RColorBrewer)
library(export)
library(ggthemes)
area<-read.csv("d:\\R\\Survival analysis\\area.csv")
area$group<- as.factor(area$group)
area$repetition<- as.factor(area$repetition)
area$group<- factor(area$group,levels = c("Z. mays","A. catechu","A. sinensis","C.
nucifera","C. oleifera","D. odorifera","H. brasiliensis"))
areap<-lmer(area~day*group+(1|repetition),data =area)
summary(areap)
Anova(areap,type="III")
B<-subset(area,group=="Z. mays"|group=="A. catechu")
areapB<-lmer(area~day*group+(1|repetition),data =B)
Anova(areapB,type="III")
C<-subset(area,group=="Z. mays"|group=="A. sinensis")
areapC<-lmer(area~day*group+(1|repetition),data =C)
Anova(areapC,type="III")
YZ<-subset(area,group=="Z. mays"|group=="C. nucifera")
```

```r
areapYZ<-lmer(area~day*group+(1|repetition),data =YZ)
Anova(areapYZ,type="III")
YC<-subset(area,group=="Z. mays"|group=="C. oleifera")
areapYC<-lmer(area~day*group+(1|repetition),data =YC)
Anova(areapYC,type="III")
H<-subset(area,group=="Z. mays"|group=="D. odorifera")
areapH<-lmer(area~day*group+(1|repetition),data =H)
Anova(areapH,type="III")
X<-subset(area,group=="Z. mays"|group=="H. brasiliensis")
areapX<-lmer(area~day*group+(1|repetition),data =X)
Anova(areapX,type="III")
B1<-subset(area,group=="A. catechu"|group=="A. sinensis")
areapB1<-lmer(area~day*group+(1|repetition),data =B1)
Anova(areapB1,type="III")
B2<-subset(area,group=="A. catechu"|group=="C. nucifera")
areapB2<-lmer(area~day*group+(1|repetition),data =B2)
Anova(areapB2,type="III")
B3<-subset(area,group=="A. catechu"|group=="C. oleifera")
areapB3<-lmer(area~day*group+(1|repetition),data =B3)
Anova(areapB3,type="III")
B4<-subset(area,group=="A. catechu"|group=="D. odorifera")
areapB4<-lmer(area~day*group+(1|repetition),data =B4)
Anova(areapB4,type="III")
B5<-subset(area,group=="A. catechu"|group=="H. brasiliensis")
areapB5<-lmer(area~day*group+(1|repetition),data =B5)
Anova(areapB5,type="III")
C1<-subset(area,group=="A. sinensis"|group=="C. nucifera")
areapC1<-lmer(area~day*group+(1|repetition),data =C1)
Anova(areapC1,type="III")
C2<-subset(area,group=="A. sinensis"|group=="C. oleifera")
areapC2<-lmer(area~day*group+(1|repetition),data =C2)
Anova(areapC2,type="III")
C3<-subset(area,group=="A. sinensis"|group=="D. odorifera")
areapC3<-lmer(area~day*group+(1|repetition),data =C3)
Anova(areapC3,type="III")
C4<-subset(area,group=="A. sinensis"|group=="H. brasiliensis")
areapC4<-lmer(area~day*group+(1|repetition),data =C4)
Anova(areapC4,type="III")
YZ1<-subset(area,group=="C. nucifera"|group=="C. oleifera")
areapYZ1<-lmer(area~day*group+(1|repetition),data =YZ1)
Anova(areapYZ1,type="III")
YZ2<-subset(area,group=="C. nucifera"|group=="D. odorifera")
areapYZ2<-lmer(area~day*group+(1|repetition),data =YZ2)
Anova(areapYZ2,type="III")
```

```
YZ3<-subset(area,group=="C. nucifera"|group=="H. brasiliensis")
areapYZ3<-lmer(area~day*group+(1|repetition),data =YZ3)
Anova(areapYZ3,type="III")
YC1<-subset(area,group=="C. oleifera"|group=="D. odorifera")
areapYC1<-lmer(area~day*group+(1|repetition),data =YC1)
Anova(areapYC1,type="III")
YC2<-subset(area,group=="C. oleifera"|group=="H. brasiliensis")
areapYC2<-lmer(area~day*group+(1|repetition),data =YC2)
Anova(areapYC2,type="III")
H1<-subset(area,group=="D. odorifera"|group=="H. brasiliensis")
areapH1<-lmer(area~day*group+(1|repetition),data =H1)
Anova(areapH1,type="III")
areap<-ggplot(data=area,aes(x=day,y=area,group=group,color=group))+
    geom_smooth(method = 'loess',size=1)+
    theme_classic()+
    labs(x="Time (days)",y="leaf area (mm2)")+
    scale_y_continuous(breaks = c(-200,0,200,400,600,800,1000,1200,1400))+
    theme(legend.title=element_blank())+

scale_color_manual(values=c("green3","yellow3","skyblue3","pink3","brown4","orange3",
"aquamarine4"),
                         labels = c("A. catechu    d","A. sinensis    b","C. nucifera    c","C.
oleifera    cd","D. odorifera    c", "H. brasiliensis    b","Z. mays    a"))
areap

library(tidyr)
library(dplyr)
library(export)
library(ggthemes)
library(tidyr)
library(DescTools)
library(ggplot2)
library(PMCMRplus)
library(rcompanion)
data<-read.csv("d:\\R\\Survival analysis\\Survival analysis.csv")
#pupae(ratio)
pu<-data[,c(12,5)]
pu[is.na(pu)]<-0
pu$check<-NA
pu$check<- ifelse(pu$pupae> 0, 1, 0)
putab<-table(pu$L,pu$check)
putab#1:pupae
chisq.test(putab)
pairwiseNominalIndependence(putab, fisher = T,gtest = FALSE, chisq = TRUE, method =
```

```
"fdr")

#pupae(days)
pup<-data[,c(12,5)]
pup<-na.omit(pup)
pup$L <- as.factor(pup$L)
kru<-kruskal.test(pup$pupae~pup$L,data)
kru
kw<-kwAllPairsDunnTest(pup$pupae~pup$L,data)
summary(kw)
meanpup<-aggregate(pup$pupae,by=list(trt=pup$L),FUN=mean)
sdpup<-aggregate(pup$pupae,by=list(trt=pup$L),FUN=sd)
sepup<-sdpup$x/sqrt(nrow(pup)/nrow(sdpup))
newpup<-data.frame(trt=meanpup$trt,mean=meanpup$x,sd=sdpup$x,sepup)
medianpup<-aggregate(pup$pup,by=list(trt=pup$L),FUN=median)
totalpup<-transform(newpup,label=c("ab","ab","a","b","c"))
totalpup

#eclosion
e<-data[,c(12,8)]
e[is.na(e)]<-0
e$check<-NA
e$check<- ifelse(e$sex> 0, 1, 0)
etab<-table(e$L,e$check)
etab#1:pupae
chisq.test(etab)
pairwiseNominalIndependence(etab, fisher = T,gtest = FALSE, chisq = TRUE, method =
"fdr")

#sex
sex<- subset(data,Group=="YM"|Group=="X"|Group=="C"|Group=="YZ")
sex<-sex[,c(12,8)]
sex<-na.omit(sex)
sextab<-table(sex$L,sex$sex)
sextab#1：male，2：female
chisq.test(sextab)
pairwiseNominalIndependence(sextab, fisher = T,gtest = FALSE, chisq = TRUE, method =
"fdr")

#length
len<-data[,c(12,6,11)]
len<-na.omit(len)
len$L <- as.factor(len$L)
aovl<-aov(Nlength~L,data=len)
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```r
summary(aovl)
PostHocTest(aovl, method = "duncan")
meanl<-aggregate(len$length,by=list(trt=len$L),FUN=mean)
sdl<-aggregate(len$length,by=list(trt=len$L),FUN=sd)
sel<-sdl$x/sqrt(nrow(len)/nrow(sdl))
newl<-data.frame(trt=meanl$trt,mean=meanl$x,sd=sdl$x,sel)
totall<-transform(newl,label=c("a","a","a","a","a"))
totall

#weight
w<-data[,c(12,7)]
w<-na.omit(w)
w$L <- as.factor(w$L)
aovw<-aov(weight~L,data=w)
summary(aovw)
TukeyHSD(aovw)
meanw<-aggregate(w$weight,by=list(trt=w$L),FUN=mean)
sdw<-aggregate(w$weight,by=list(trt=w$L),FUN=sd)
sew<-sdw$x/sqrt(nrow(w)/nrow(sdw))
neww<-data.frame(trt=meanw$trt,mean=meanw$x,sd=sdw$x,sew)
totalw<-transform(neww,label=c("b","a","b","a","a"))
totalw

#enzymatic activity
enz<-read.csv("d:\\R\\enzymatic activity\\enzymatic activity.csv")
#SOD
aovSOD<-aov(NSOD~sample,data=enz)
summary(aovSOD)
TukeyHSD(aovSOD)
meanSOD<-aggregate(enz$SOD,by=list(trt=enz$sample),FUN=mean)
sdSOD<-aggregate(enz$SOD,by=list(trt=enz$sample),FUN=sd)
seSOD<-sdSOD$x/sqrt(nrow(enz)/nrow(sdSOD))
medianSOD<-aggregate(enz$SOD,by=list(trt=enz$sample),FUN=median)
meanSOD
seSOD
medianSOD
newSOD<-data.frame(trt=meanSOD$trt,mean=meanSOD$x,sd=sdSOD$x,seSOD)
totalSOD<-transform(newSOD,label=c("a","b","b","b","b","b","c"))
totalSOD
totalSOD$trt<- factor(totalSOD$trt,levels = c("A. catechu","A. sinensis","C. nucifera",
                                              "C.    oleifera","D.    odorifera","H.
brasiliensis","Z. mays"))
SOD<-ggplot(totalSOD,aes(x=trt, y=mean))+
   geom_col(aes(fill=trt),color="black")+
```

```r
  geom_errorbar(aes(ymin=mean-seSOD,ymax=mean+seSOD),width=0.1)+
  geom_text(aes(y=mean+seSOD,label=label,vjust=-0.5,hjust="center"))+
  theme_classic() +
  theme(axis.text.x= element_text(face="italic"))+
  labs(x="",y="Concentration of SOD (U/mgprot)")+ylim(0,150)+
  scale_fill_manual(values=c("gray0","gray15","gray30",
'gray45','gray60',"gray75",'gray100'))+
  theme(legend.position = "none")
SOD

#POD
aovPOD<-aov(NPOD~sample,data=enz)
summary(aovPOD)
TukeyHSD(aovPOD)
meanPOD<-aggregate(enz$POD,by=list(trt=enz$sample),FUN=mean)
sdPOD<-aggregate(enz$POD,by=list(trt=enz$sample),FUN=sd)
sePOD<-sdPOD$x/sqrt(nrow(enz)/nrow(sdPOD))
medianPOD<-aggregate(enz$POD,by=list(trt=enz$sample),FUN=median)
meanPOD
sePOD
medianPOD
newPOD<-data.frame(trt=meanPOD$trt,mean=meanPOD$x,sd=sdPOD$x,sePOD)
totalPOD<-transform(newPOD,label=c("a","b","c","b","b","b","b"))
totalPOD
totalPOD$trt<- factor(totalPOD$trt,levels = c("A. catechu","A. sinensis","C. nucifera",
                                              "C.    oleifera","D.    odorifera","H.
brasiliensis","Z. mays"))
POD<-ggplot(totalPOD,aes(x=trt, y=mean))+
  geom_col(aes(fill=trt),color="black")+
  geom_errorbar(aes(ymin=mean-sePOD,ymax=mean+sePOD),width=0.1)+
  geom_text(aes(y=mean+sePOD,label=label,vjust=-0.5,hjust="center"))+
  theme_classic() +
  theme(axis.text.x= element_text(face="italic"))+
  labs(x="",y="Concentration of POD (U/mgprot)")+ylim(0,150)+
  scale_fill_manual(values=c("gray0","gray15","gray30",
'gray45','gray60',"gray75",'gray100'))+
  theme(legend.position = "none")
POD
cowplot::plot_grid(SOD,POD, ncol=2,nrow=1,labels = LETTERS[1:2])

#The preference index of third-instar S. frugiperda on six plant species
cho<-read.csv("d:\\R\\Survival analysis\\choose.csv")
cho<-na.omit(cho)
cho$sample<- as.factor(cho$sample)
```

```
aovc<-aov(area~sample,data=cho)
summary(aovc)
TukeyHSD(aovc)
mean<-aggregate(cho$Parea,by=list(trt=cho$sample),FUN=mean)
sd<-aggregate(cho$Parea,by=list(trt=cho$sample),FUN=sd)
se<-sd$x/sqrt(nrow(cho)/nrow(sd))
median<-aggregate(cho$Parea,by=list(trt=cho$sample),FUN=median)
mean
se
median
new<-data.frame(trt=mean$trt,mean=mean$x,sd=sd$x,se)
total<-transform(new,label=c("c","bc","b","c","c","a"))
total
total$trt<- factor(total$trt,levels = c("A. catechu","A. sinensis","C. nucifera",
                                         "C. oleifera","D. odorifera","H. brasiliensis"))
choosep<-ggplot(total,aes(x=trt, y=mean))+
  geom_col(aes(fill=trt),color="black")+
  geom_errorbar(aes(ymin=mean-se,ymax=mean+se),width=0.1)+
  geom_text(aes(y=mean,label=label,vjust=-2.5,hjust="center"))+
  theme_classic() +
  theme(axis.text.x= element_text(face="italic"))+
  labs(x="",y="Preference index (%)")+ylim(0,80)+
  scale_fill_manual(values=c("gray0","gray15","gray30", 'gray45','gray60',"gray75"))+
  theme(legend.position = "none")
choosep
```