

Supporting Information S1. R code for *a priori* comparisons of fungal hyphal growth and brine shrimp survivorship in response to plant extracts.

```
# Generalized linear mixed models of hyphal fungal growth with normally distributed errors
m1 =lmer(FusariumHyphalGrowth~Extract + (1|Dish.Nu))
m2 =lmer(PhomaHyphalGrowth~Extract + (1|Dish.Nu))

# Generalized linear mixed model of brine shrimp survivorship with binomially distributed errors
m3=lmer(cbind(Artemia.alive,Artemia.dead)~Extract+(1|Plate.Nu),family=binomial)

betahat <- fixef(m1) # Estimates of fixed effects from model
sebetahat <- sqrt(diag(vcov(m1))) # Standard errors of estimates
tval <- betahat/sebetahat # t-value
pval <- 2*pnorm(-abs(tval)) # p-value

betahat <- data.frame(betahat)

# Function for analysis of a priori contrasts
comparePairs=function(m,which,trmt){
  b<-fixef(m)
  s<-vcov(m)
  con<-rep(0,length(b))
  if(missing(which)){
    which<-expand.grid(1:length(b),1:length(b))
    which<-which[which[,1]!=which[,2],]
  }
  contrast<-se<-tval<-trmt1<-trmt2<-t1<-t2<-rep(0,dim(which)[1])

  for(j in 1:dim(which)[1]){
    c1<-con
    trmt1[j]=as.character(trmt[trmt[,2]==which[j,1],1])
    trmt2[j]=as.character(trmt[trmt[,2]==which[j,2],1])
    t1[j]<-which[j,1]
    t2[j]<-which[j,2]
    c1[as.numeric(which[j,])]<-c(1,-1)
    contrast[j]<-c1%*%b
    se[j]<-sqrt(c1%*%as.matrix(s)%*%c1)
  }

  data.frame(Trt1=trmt1,Trt1.nu=t1,Trt2=trmt2,Trt2.nu=t2,contrast,se,tval=tval<-contrast/se,pval=2*pnorm(-abs(tval)))
}

pwcomp=comparePairs(m1, w, apriori) # m1 is summary of model, w is a matrix of the contrasts, apriori is dataframe of treatments
```