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