library(brglm)

data=read.csv(file.choose(),sep='\t')

data$pH=factor(data$pH) *# pH was coded as a factor (control vs. acidified)*

glm1=brglm(cbind(Alive,Dead)~pH,family=binomial, data=data) *# testing the effect of pH treatment on the mortality of individuals*

summary(glm1) *# obtain the summary statistics # confidence intervals of estimates were calculated by hand using the formula +/- standard error\*1.96*