```
> PA<-read.csv("Pest bird abundance.csv")
> # feral pigeon abundance
> PA$food.source<-relevel(PA$food.source,ref="fh")
> m1<-gamm(data=PA,abund.p~cb.phase*food.source+s(time),random=list(tc=~1),family="quasipoisson")

 Maximum number of PQL iterations:  20
iteration 1
iteration 2
iteration 3
> summary(m1$gam)


Family: quasipoisson
Link function: log

Formula:
abund.p ~ cb.phase * food.source + s(time)

Parametric coefficients:
                          Estimate Std. Error t value Pr(>|t|)
(Intercept)                 2.7181     0.1432  18.980  < 2e-16 ***
cb.phasep0                 -0.1866     0.1821  -1.025  0.30580
cb.phasep2                 -0.3089     0.1872  -1.650  0.09947 .
food.sourcebc              -0.7086     0.2171  -3.264  0.00117 **
food.sourcegs              -3.7965     0.8019  -4.735 2.78e-06 ***
food.sourcehc              -0.3527     0.1954  -1.805  0.07162 .
cb.phasep0:food.sourcebc    0.2827     0.3024   0.935  0.35019
cb.phasep2:food.sourcebc    0.1449     0.3192   0.454  0.65015
cb.phasep0:food.sourcegs    0.3136     1.1344   0.276  0.78230
cb.phasep2:food.sourcegs    1.0488     0.9964   1.053  0.29300
cb.phasep0:food.sourcehc   -0.2408     0.3035  -0.793  0.42791
cb.phasep2:food.sourcehc   -0.4290     0.3264  -1.314  0.18932
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


Approximate significance of smooth terms:
        edf Ref.df    F p-value
s(time)   1      1 6.52  0.0109 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


R-sq.(adj) =  0.157
  Scale est. = 11.654    n = 579
> ((exp(2.7181-0.1866)-exp(2.7181))/exp(2.7181))*100
[1] -17.02244
```

Decrease in feral pigeon abundance of -17%