GAMM Trials

Molly Wilson

1/6/2018

Contents

```r
library(rmarkdown)
library(dplyr)
library(nlme)
library(pls)
library(mgcv)
library(ggsignif)
```

```r
setwd("~/github/Scarid-Behavior/data")
data <- read.csv("data2.csv", stringsAsFactors=FALSE)
vir<-data%>%filter(Species.Code=="stop")
vet<-data%>%filter(Species.Code=="qup")
auro<-data%>%filter(Species.Code=="rbp")
vetvir<-data%>%filter(Species.Code!="rbp")
```
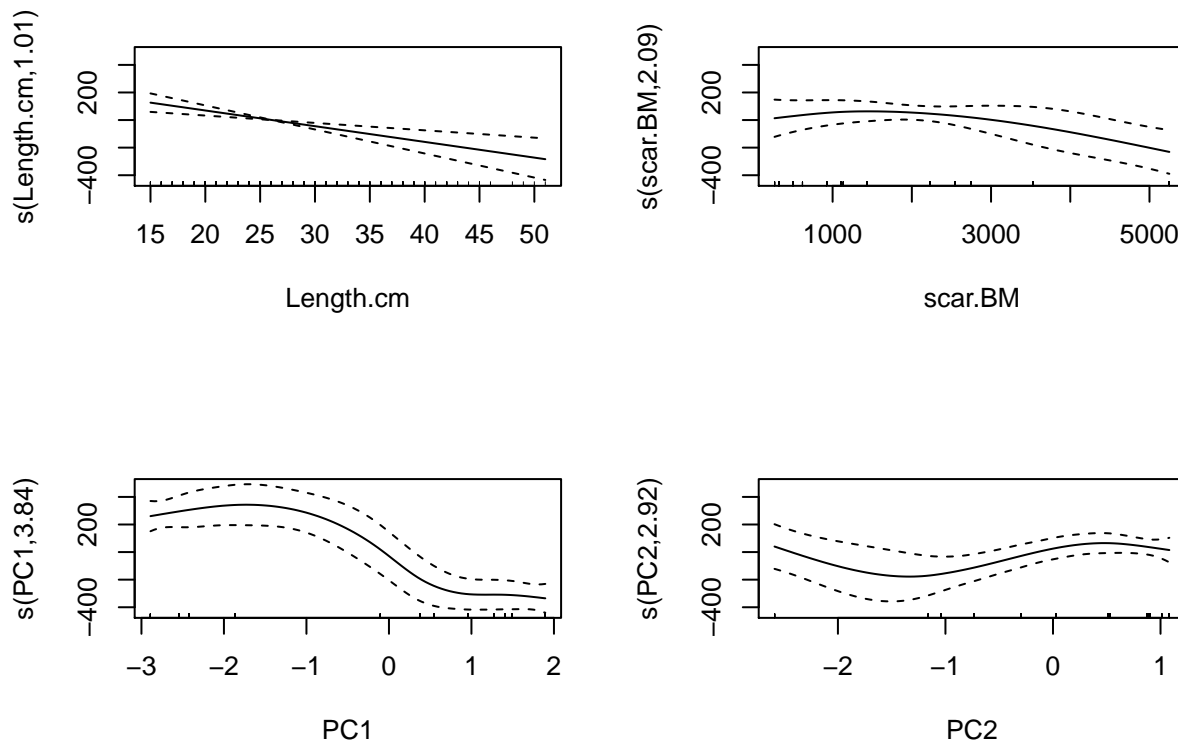
GAMs

All species

```r
gam<-gam(FR~Species+Phase+s(Length.cm)+s(scar.BM)+s(PC1)+s(PC2), family=gaussian(link=identity),data=da
summary(gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## FR ~ Species + Phase + s(Length.cm) + s(scar.BM) + s(PC1) + s(PC2)
##
## Parametric coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 1085.85      27.51  39.468  < 2e-16 ***
## SpeciesSparisoma aurofrenatum  -494.24      49.48  -9.989  < 2e-16 ***
## SpeciesSparisoma viride       -612.35      33.27 -18.405  < 2e-16 ***
```

```
## Phaset                           -124.73      39.00  -3.198  0.00144 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                edf Ref.df      F  p-value
## s(Length.cm) 1.005  1.010 14.119 0.000179 ***
## s(scar.BM)   2.092  2.271  6.565 0.002184 **
## s(PC1)       3.842  4.366 15.107 3.86e-11 ***
## s(PC2)       2.922  3.198  2.945 0.062738 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.511   Deviance explained = 51.9%
## -REML = 5818.5  Scale est. = 1.6266e+05  n = 788
```
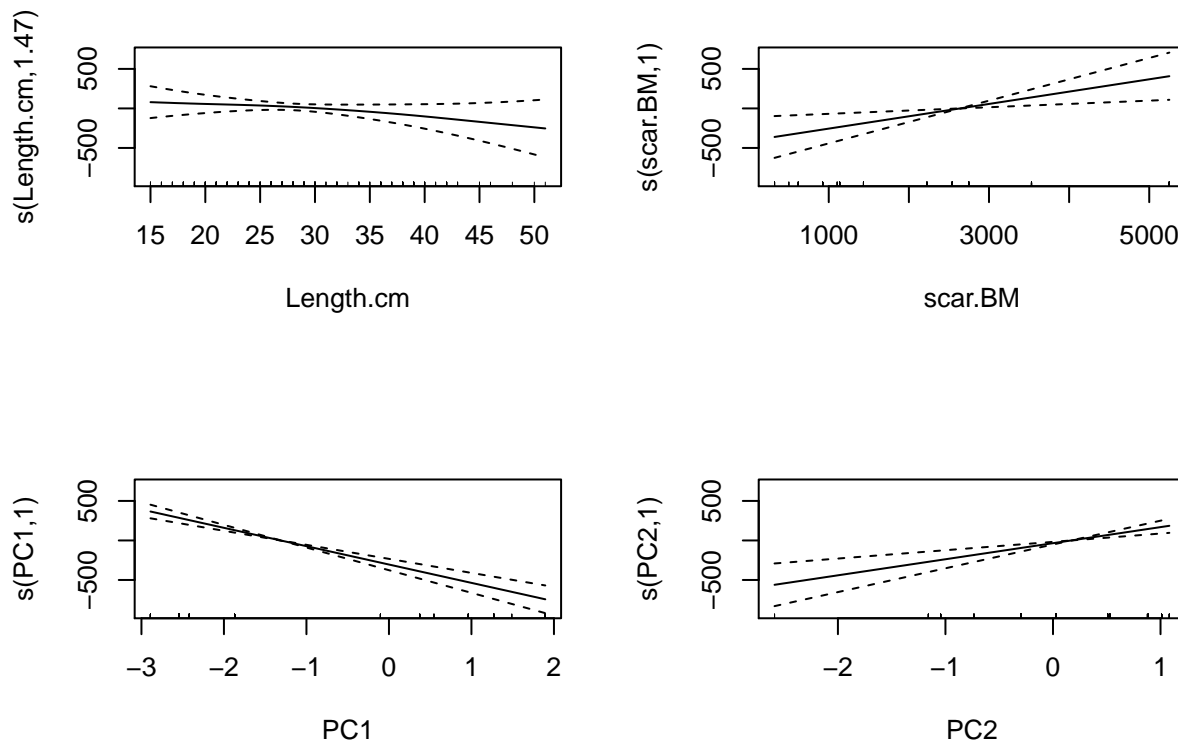
```
plot(gam,pages=1)
```


Scarus vetula

```
gamvet<-gam(FR~Phase+s(Length.cm)+s(scar.BM)+(carn.BM)+s(PC1)+s(PC2), family=gaussian(link=identity),da
summary(gamvet)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## FR ~ Phase + s(Length.cm) + s(scar.BM) + (carn.BM) + s(PC1) +
##     s(PC2)
```

```
## 
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1666.7344   113.3283  14.707  < 2e-16 ***
## Phaset      -333.2738   100.6780  -3.310 0.001055 **
## carn.BM       -0.3274     0.0833  -3.931 0.000107 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Approximate significance of smooth terms:
##               edf Ref.df      F  p-value
## s(Length.cm) 1.473  1.816   1.314  0.34404
## s(scar.BM)   1.001  1.002   7.451  0.00673 **
## s(PC1)       1.000  1.000 72.280 6.42e-16 ***
## s(PC2)       1.000  1.000 17.281 4.26e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## R-sq.(adj) =  0.363   Deviance explained = 37.8%
## -REML = 2170.7  Scale est. = 2.973e+05  n = 285
```

```
plot(gamvet,pages=1)
```


Sparisoma viride

```
vir<-data %>% filter(Species.Code=="stop" & Site!="Snapper Point")
gamvir<-gam(FR~Phase+s(Length.cm)+s(scar.BM)+s(PC1)+s(PC2), family=gaussian(link=identity),data=vir,met
summary(gamvir)
```

```
## 
```

```
## Family: gaussian
## Link function: identity
##
## Formula:
## FR ~ Phase + s(Length.cm) + s(scar.BM) + s(PC1) + s(PC2)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   472.29      19.78   23.87   <2e-16 ***
## Phaset        -61.48      38.42   -1.60    0.111
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                edf Ref.df     F  p-value
## s(Length.cm) 2.935  3.697 5.173 0.000759 ***
## s(scar.BM)   2.932  3.266 5.451 0.030570 *
## s(PC1)       4.166  4.747 2.895 0.039222 *
## s(PC2)       1.121  1.172 2.681 0.135997
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.278   Deviance explained = 30.5%
## -REML = 2222.8  Scale est. = 64342     n = 322
```
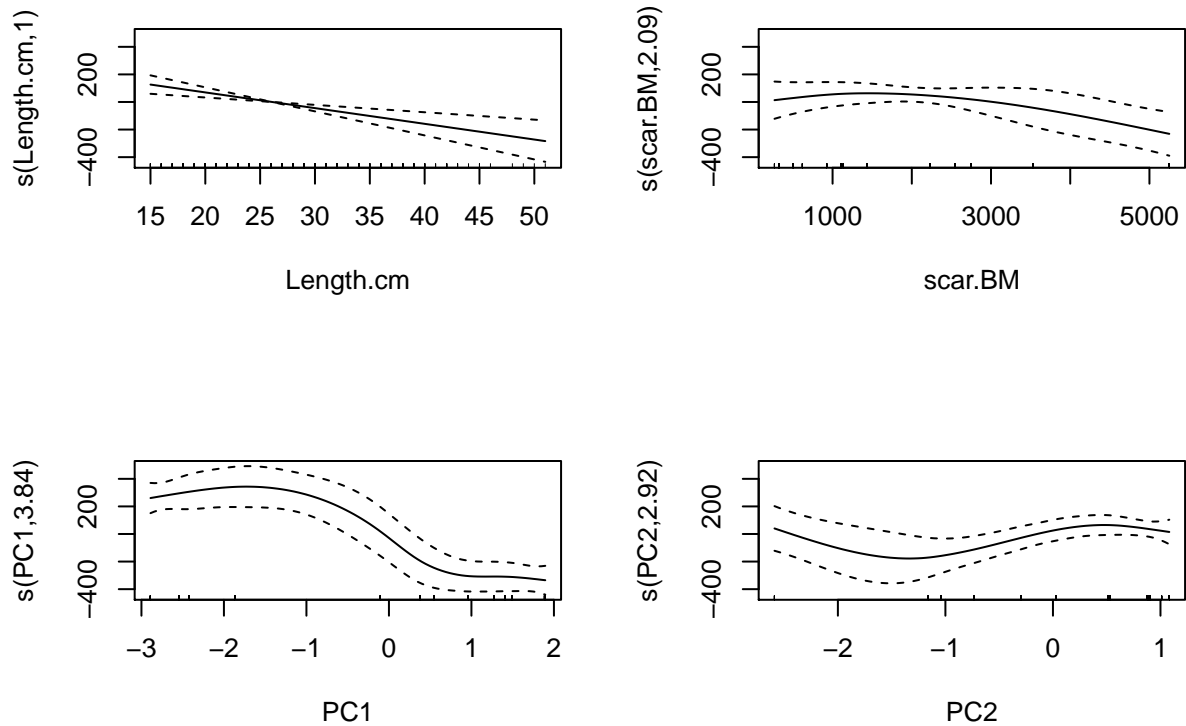
```
plot(gamvir,pages=1)
```
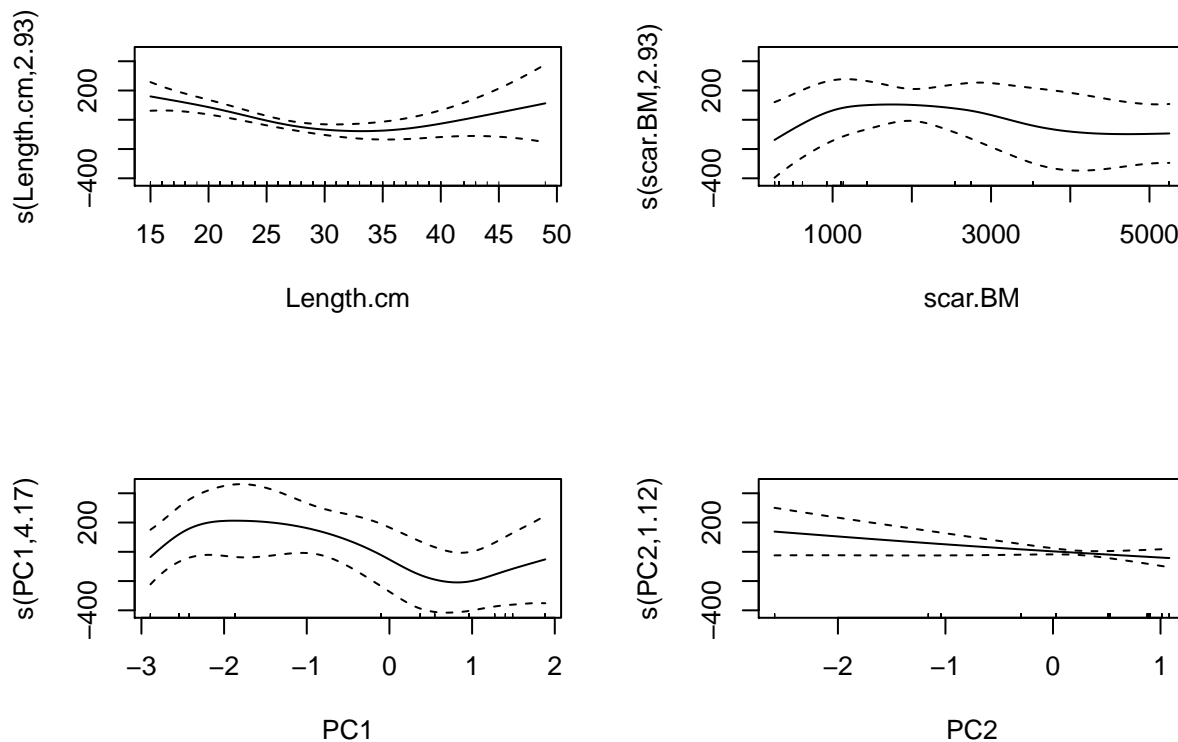
GAMMs

All species

```
gamm<-gamm(FR~Species+Phase+s(Length.cm)+s(scar.BM)+s(PC1)+s(PC2), family=gaussian(link=identity),data=
summary(gamm$gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## FR ~ Species + Phase + s(Length.cm) + s(scar.BM) + s(PC1) + s(PC2)
##
## Parametric coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  1085.85      27.51  39.467  < 2e-16 ***
## SpeciesSparisoma aurofrenatum -494.24      49.48  -9.989  < 2e-16 ***
## SpeciesSparisoma viride       -612.35      33.27 -18.405  < 2e-16 ***
## Phaset                        -124.73      39.00  -3.198  0.00144 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                edf Ref.df      F  p-value
## s(Length.cm) 1.000  1.000 14.248 0.000172 ***
## s(scar.BM)   2.092  2.092  6.883 0.001541 **
## s(PC1)       3.842  3.842 15.189 2.05e-11 ***
## s(PC2)       2.922  2.922  2.750 0.058675 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.511
##   Scale est. = 1.6266e+05  n = 788
```
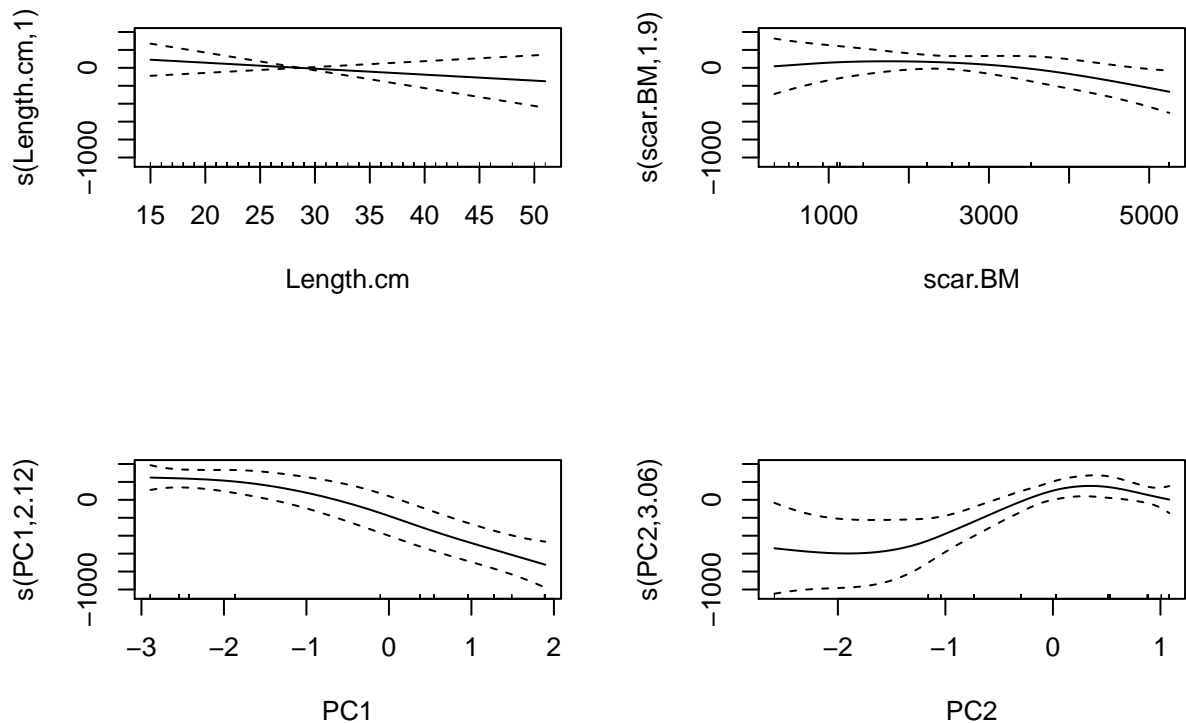
```
plot(gamm$gam,pages=1)
```

Scarus vetula

```
gamm<-gamm(FR~Phase+s(Length.cm)+s(scar.BM)+s(PC1)+s(PC2), family=gaussian(link=identity),data=vet, rand
summary(gamm$gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## FR ~ Phase + s(Length.cm) + s(scar.BM) + s(PC1) + s(PC2)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1266.71      49.27  25.707  < 2e-16 ***
## Phaset       -376.25     100.65  -3.738 0.000226 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                edf Ref.df      F  p-value
## s(Length.cm) 1.000  1.000  1.020 0.313375
## s(scar.BM)   1.901  1.901  3.566 0.053298 .
## s(PC1)       2.116  2.116 15.345 8.58e-07 ***
## s(PC2)       3.064  3.064  5.861 0.000637 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.373
```

```
##    Scale est. = 2.9258e+05  n = 285
```

```
plot(gamm$gam,pages=1)
```


Sparisoma viride

```
gamm<-gamm(FR~Phase+s(Length.cm)+s(scar.BM)+s(PC1)+s(PC2), family=gaussian(link=identity),data=vir, ran
summary(gamm$gam)
```

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## FR ~ Phase + s(Length.cm) + s(scar.BM) + s(PC1) + s(PC2)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   472.29      19.79   23.87   <2e-16 ***
## Phaset        -61.48      38.42   -1.60    0.111
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##                edf Ref.df     F  p-value
## s(Length.cm) 2.935  2.935 6.153 0.000364 ***
## s(scar.BM)   2.932  2.932 4.035 0.017765 *
## s(PC1)       4.166  4.166 2.065 0.166163
## s(PC2)       1.120  1.120 2.722 0.128824
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.278
##   Scale est. = 64342     n = 322
```

```
plot(gamm$gam,pages=1)
```