GAMM Trials

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 library(rmarkdown)
library(dplyr)
library(nlme)
library(pls)
library(mgcv)
library(ggsignif)
setwd("~/github/Scarid-Behavior/data")
data <- read.csv("data2.csv", stringsAsFactors=FALSE)</pre>
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

##

(Intercept)

SpeciesSparisoma viride

SpeciesSparisoma aurofrenatum -494.24

```
All species
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
##
## FR ~ Species + Phase + s(Length.cm) + s(scar.BM) + s(PC1) + s(PC2)
## Parametric coefficients:
```

Estimate Std. Error t value Pr(>|t|)

27.51 39.468 < 2e-16 ***

49.48 -9.989 < 2e-16 *** 33.27 -18.405 < 2e-16 ***

1085.85

-612.35

```
-124.73
## Phaset
                                                  39.00 -3.198 0.00144 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Approximate significance of smooth terms:
                   edf Ref.df
##
## s(Length.cm) 1.005 1.010 14.119 0.000179 ***
                 2.092 2.271 6.565 0.002184 **
## s(scar.BM)
## 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 '**' 0.05 '.' 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)
s(Length.cm, 1.01)
                                                s(scar.BM,2.09)
    200
                                                     200
                                                     -400
    -400
                                                             1000
                  25
                      30
                          35
                              40
                                   45 50
                                                                          3000
                                                                                      5000
                     Length.cm
                                                                       scar.BM
s(PC1,3.84)
                                                s(PC2,2.92)
                                                     200
    200
    -400
                                                               -2
         -3
               -2
                            0
                                                                                0
                                                                                        1
                        PC1
                                                                        PC2
```

Scarus vetula

```
##
## 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 '**' 0.05 '.' 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 '**' 0.05 '.' 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)
s(Length.cm, 1.47)
                                                    500
     500
                                               s(scar.BM,1)
     -500
                                                            1000
                                                                        3000
                                                                                    5000
             20
                 25
                     30
                          35
                              40
                                  45
                     Length.cm
                                                                     scar.BM
     500
                                                    500
s(PC1,1)
                                               s(PC2,1)
     -500
                                                    -500
                                         2
         -3
               -2
                            0
                                                              -2
                                                                               0
                                                                                       1
                        PC1
                                                                       PC2
```

Sparisoma viride

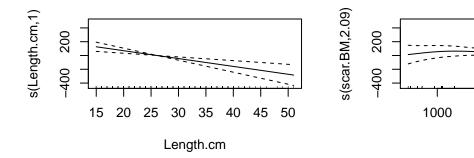
```
vir<-data %>% filter(Species.Code=="stop" & Site!="Snapper Point")
gamvir<-gam(FR~Phase+s(Length.cm)+s(scar.BM)+s(PC1)+s(PC2), family=gaussian(link=identity),data=vir,mets
summary(gamvir)</pre>
```

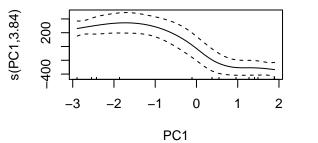
```
## Family: gaussian
## Link function: identity
##
## Formula:
## FR \sim Phase + s(Length.cm) + s(scar.BM) + s(PC1) + s(PC2)
##
## Parametric coefficients:
                Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                  472.29
                               19.78
                                        23.87
                                                <2e-16 ***
## Phaset
                  -61.48
                               38.42
                                        -1.60
                                                 0.111
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 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 *
                 4.166 4.747 2.895 0.039222 *
## s(PC1)
                 1.121 1.172 2.681 0.135997
## s(PC2)
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
                          Deviance explained = 30.5%
## R-sq.(adj) = 0.278
## -REML = 2222.8 Scale est. = 64342
plot(gamvir,pages=1)
s(Length.cm, 2.93)
                                                s(scar.BM,2.93)
                                                    200
     -400
                                                     -400
              20
                  25
                       30
                           35
                                40
                                    45
                                        50
                                                             1000
                                                                         3000
                                                                                     5000
                     Length.cm
                                                                      scar.BM
s(PC1,4.17)
                                                    200
     200
     -400
                                         2
                                                              -2
         -3
               -2
                      -1
                            0
                                   1
                                                                               0
                                                                                        1
                                                                       -1
                        PC1
                                                                        PC2
```

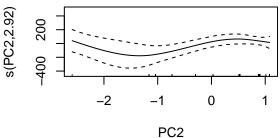
GAMMs

All species

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







3000

scar.BM

5000

Scarus vetula

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

```
##
## Family: gaussian
## Link function: identity
##
## FR \sim 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 '**' 0.05 '.' 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
                      1.901 3.566 0.053298 .
## s(scar.BM)
               1.901
## 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 '**' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) = 0.373
```

```
Scale est. = 2.9258e+05 n = 285
plot(gamm$gam,pages=1)
s(Length.cm,1)
                                                                  s(scar.BM, 1.9)
                                                                         0
                                                                         -1000
       -1000
                        25
                                                                                    1000
                                                                                                     3000
                                                                                                                      5000
                   20
                               30
                                    35
                                          40
                                                45
                                                      50
                             Length.cm
                                                                                                 scar.BM
s(PC1,2.12)
                                                                  s(PC2,3.06)
       0
                                                                         0
                                                                         -1000
      -1000
            -3
                     -2
                                       0
                                                1
                                                         2
                                                                                       -2
                                                                                                              0
                                                                                                                          1
```

PC2

Sparisoma viride

PC1

```
gamm<-gamm(FR~Phase+s(Length.cm)+s(scar.BM)+s(PC1)+s(PC2), family=gaussian(link=identity),data=vir, rank
summary(gamm$gam)
##
## Family: gaussian
## Link function: identity
## Formula:
## FR \sim 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:
                                 F p-value
                  edf Ref.df
## 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
## ---
```

