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Article:

Brooks, ME, Mugabo, M, Rodgers, GM et al. (2 more authors) (2016) How well can body size represent effects of the environment on demographic rates? Disentangling correlated explanatory variables. Journal of Animal Ecology, 85. pp. 318-328. ISSN 0021-8790

https://doi.org/10.1111/1365-2656.12465

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Appendix S5: Full Model Predictions and Splines

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August 25, 2015

Contents

1 Description

In this appendix, we present the full models and their predictions and splines. These predictions closely resemble those of the best model chosen by AICc. We look at the full models to examine the past environment splines while controlling for the known effects of body size and the current environment. Not all splines are significantly different from 0 according to Wood's test (Table 2 main text), but the declining and fluctuating treatments were significant for several demographic rates. So we would like to examine these.

Readers may skip over chunks of R code to examine the figures. However, we also provide the code for repeatability.

2 Preliminaries

```
library(reshape)
library(ggplot2)
library(mgcv)
library(bbmle)
library(plyr)
```

```
load("../Individual soil mite data.Rdata")
Indiv$food.s=scale(Indiv$food)
newdata=ddply(Indiv, .(pop.ID, day, stage), summarize,
                        trt=trt[1],
                        density.s=density.s[1],
                        supply.s= supply.s[1],
                        food.s=food.s[1],
                        l0.s=quantile(l0.s,.5, na.rm=TRUE))
```

```
ke=10 #environment
kd=10 #days
kl=5 #length
```

3 Growth

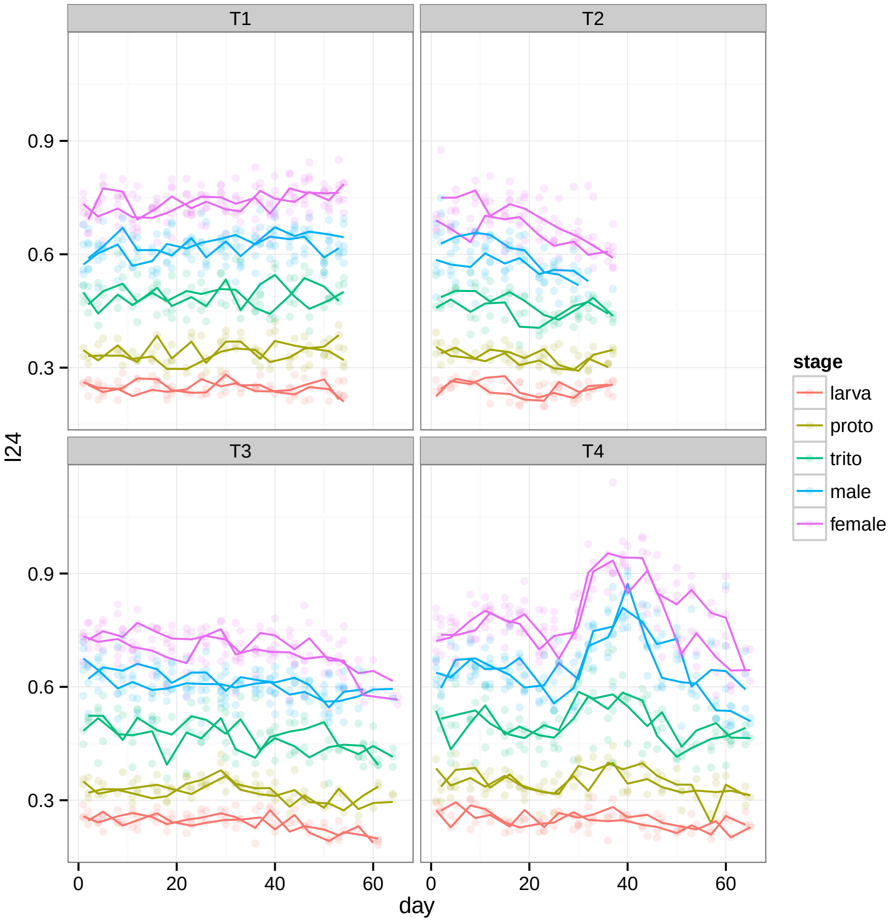
```
temp=na.omit(subset(Indiv, stage!="egg")[
        ,c("l0.s", "l24", "density.s", "supply.s", "day", "trt", "l0", "stage")])
```

```
gm_full=gam(l24~s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd),
        data=temp)
```

3.1 Predictions

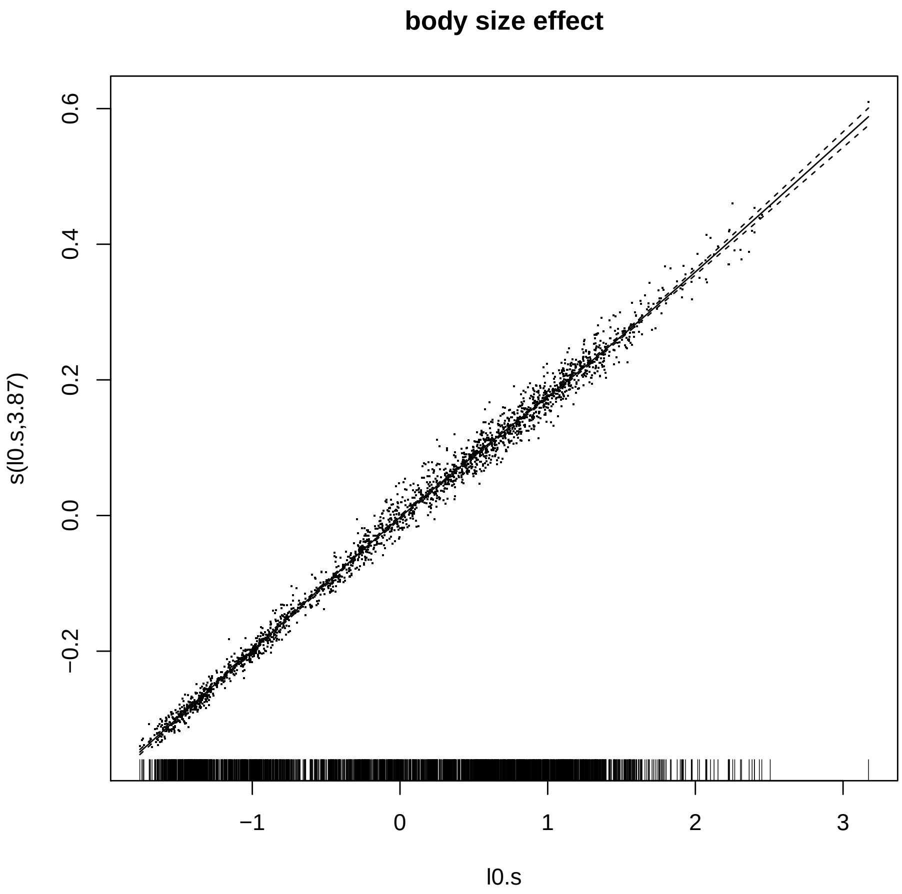
```
gn=newdata
gn$l24=predict(gm_full, gn)
p1=ggplot(gn, aes(x=day, y=l24))+
        geom_line(aes(colour=stage, group=pop.ID:stage))+
        facet_wrap(~trt)
p1+geom_point(data=temp,aes(colour=stage), alpha=.15)+theme_bw()

## Warning:  Removed 1 rows containing missing values (geom_path).
```

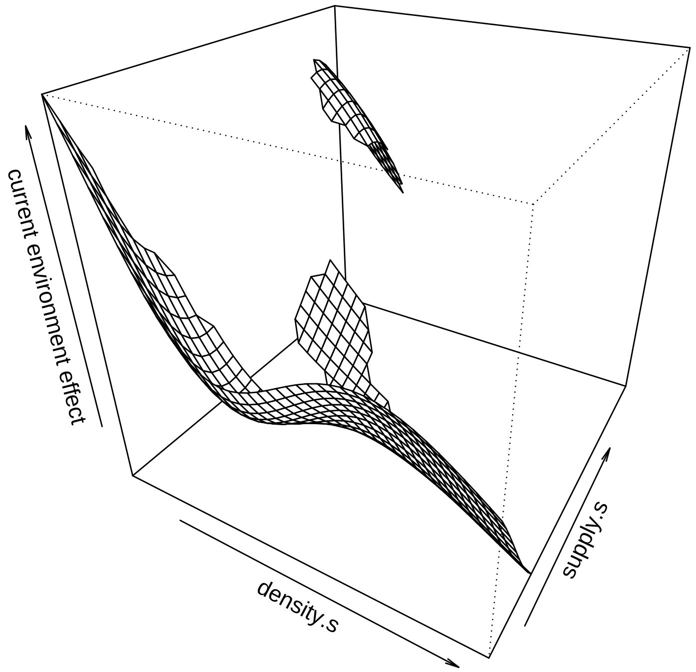


3.2 Explanatory Variable Effects

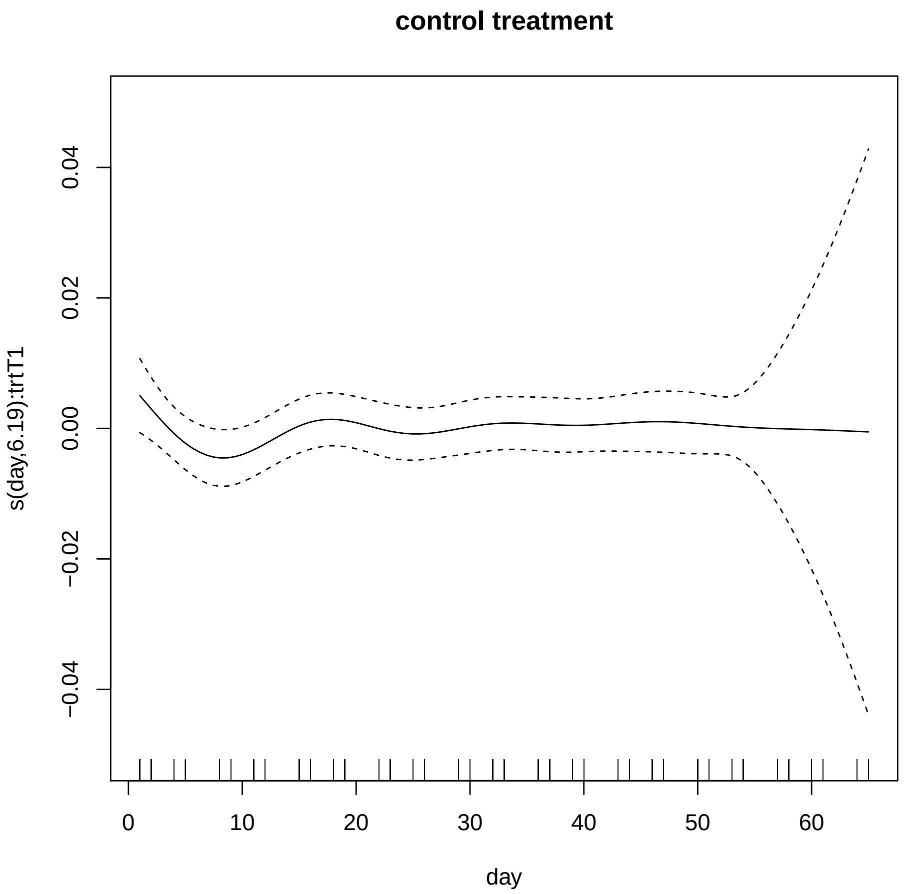
```
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=1, main="body size effect")
```



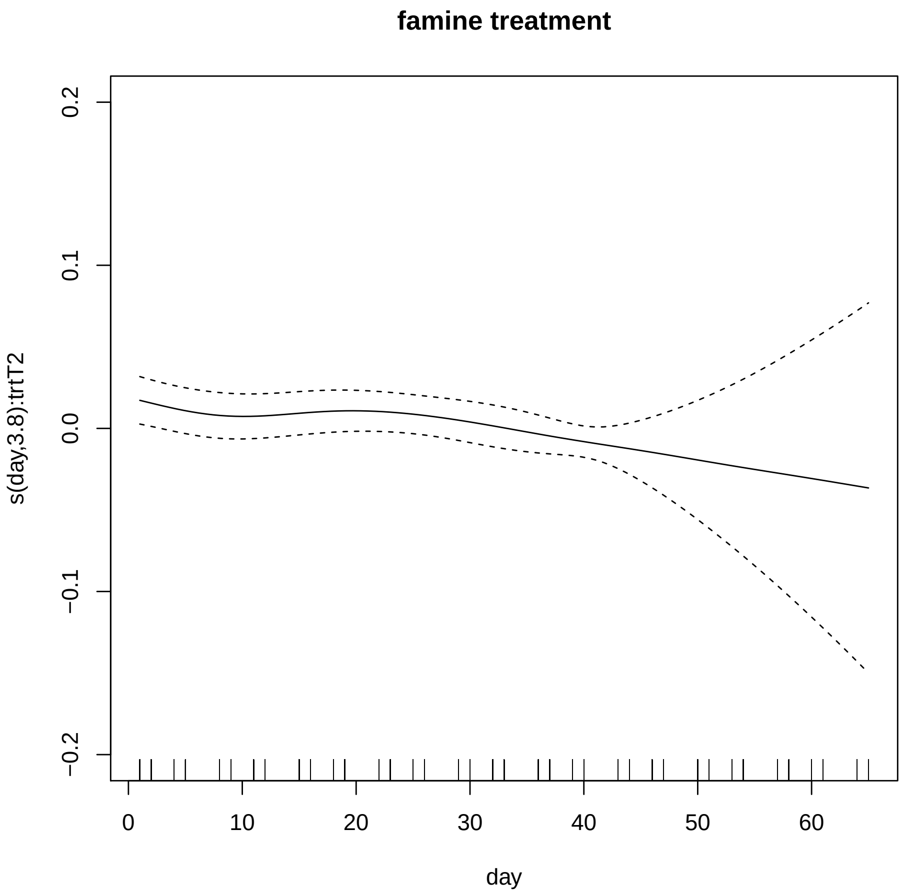
```
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=2, main="current environment effect")
```



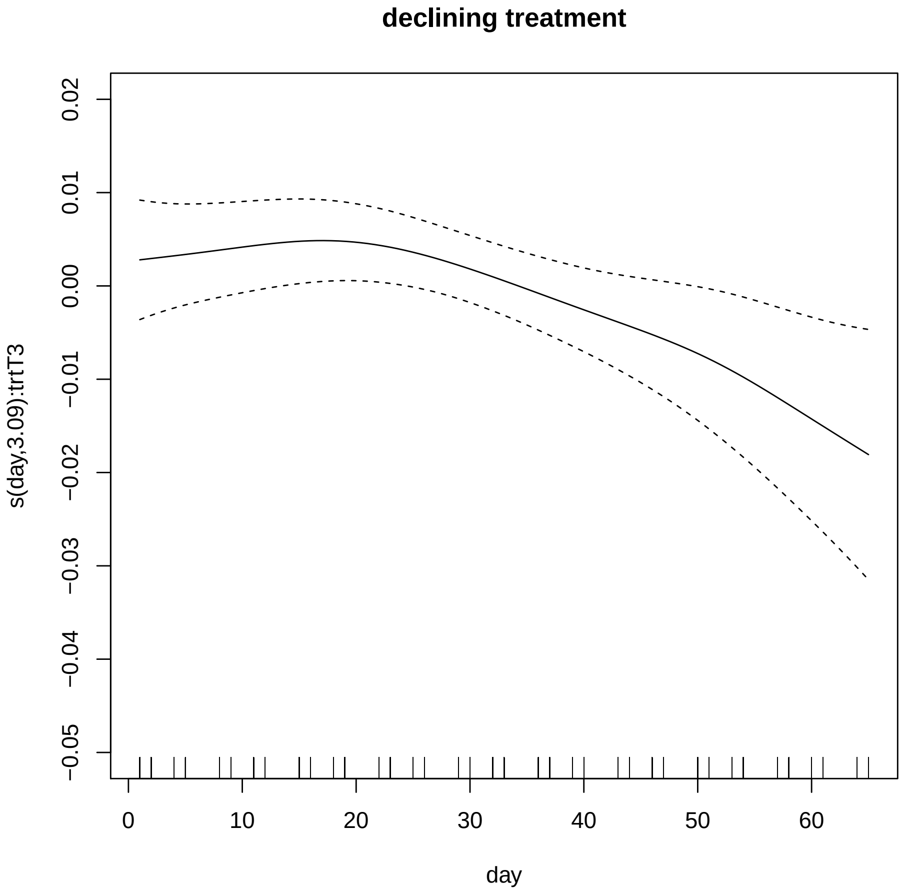
```
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=3, ylim=c(-0.05, 0.05), main="control treatment")
```



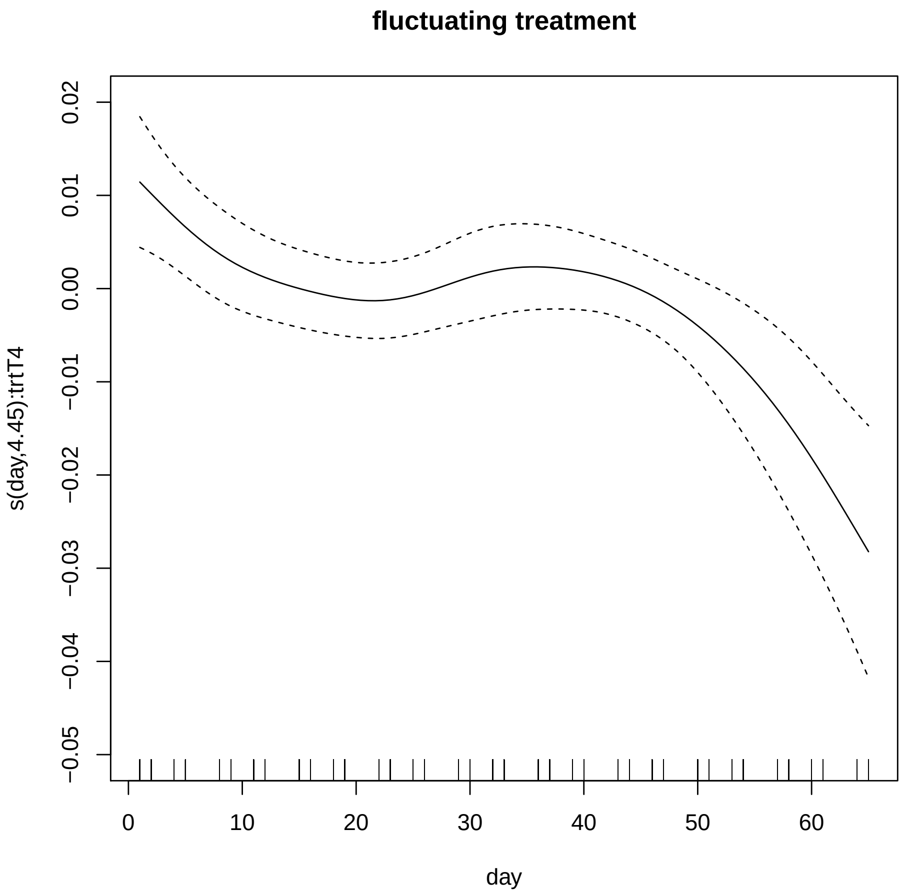
```
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=4, ylim=c(-0.2, 0.2), main="famine treatment")
```



```
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=5, ylim=c(-0.05, 0.02), main="declining treatment")
```



```
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=6, ylim=c(-0.05, 0.02), main="fluctuating treatment") #statistically significa
```



4 Transition

Subset data to only include the juvenile survivors.

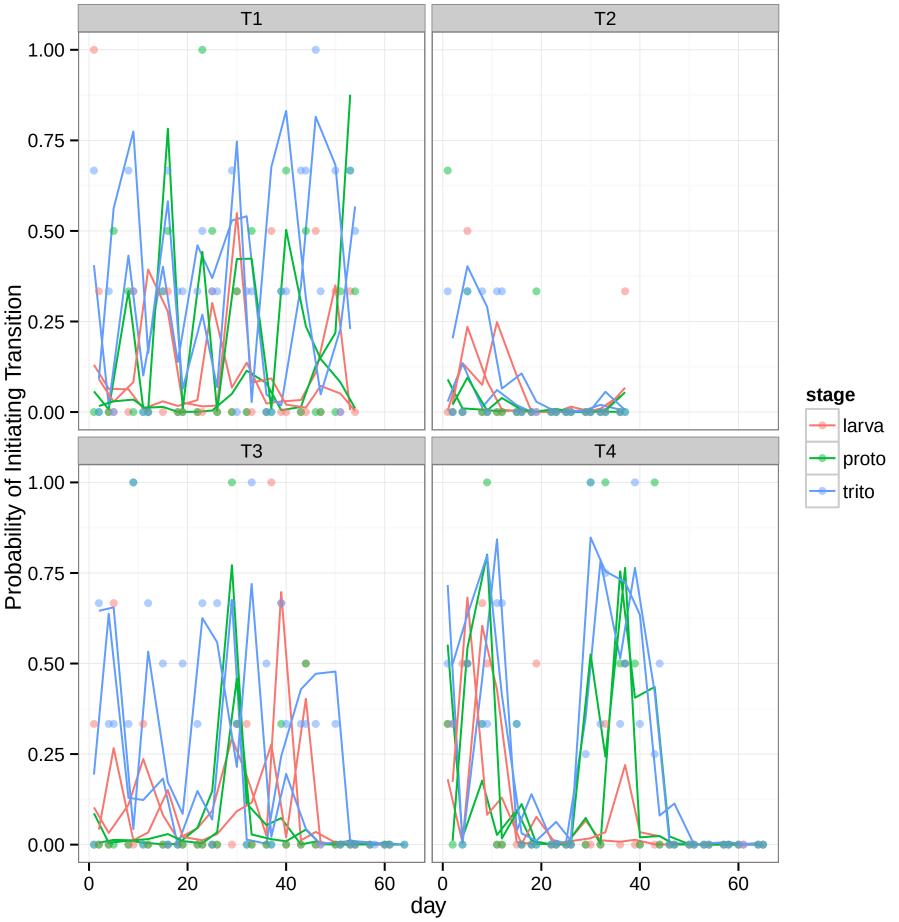
```
tempT=transform(subset(Indiv, (!stage %in% c("male","female") & (s24==1))),
        t.init.24=as.numeric(t24 %in% c("next stage", "quiescent")),
        t.done.24=as.numeric(t24 == "next stage"),
        stage=stage[, drop=TRUE]
        )
```

```
temp=na.omit(tempT[
        ,c("t.init.24","l0.s","trt","day","density.s", "supply.s", "stage", "pop.ID")
tempsum=ddply(temp, .(trt, day, stage, pop.ID), summarize, t.sum=mean(t.init.24))
```

```
t24m_full=gam(t.init.24~ stage +s(l0.s, k=kl)+
s(density.s, supply.s, k=ke)+trt+s(day, by=trt, k=kd), family=binomial, data=temp)
```

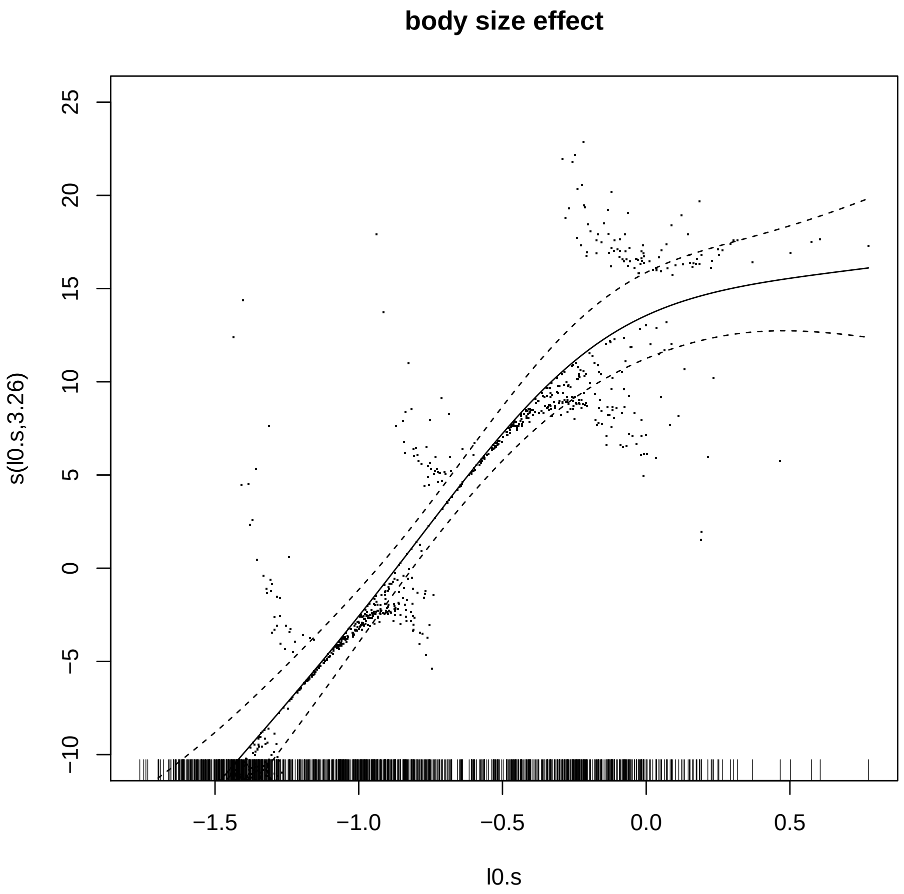
4.1 Predictions

```
tn=subset(newdata, ! stage %in% c("male", "female"))
tn$t.init.24=predict(t24m_full, tn, type="response")
p1=ggplot(tn, aes(x=day, y= t.init.24))+
        geom_line(aes(colour=stage, group=pop.ID:stage))+facet_wrap(~trt)
p1+ylab("Probability of Initiating Transition")+theme_bw()+
        geom_point(data=tempsum, aes(x=day, y=t.sum, colour=stage), alpha=.5)
```

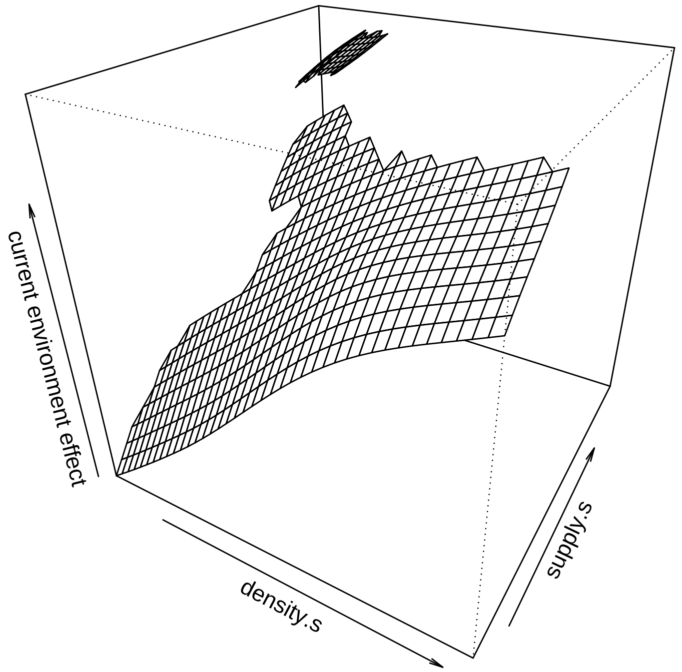


4.2 Explanatory Variable Effects

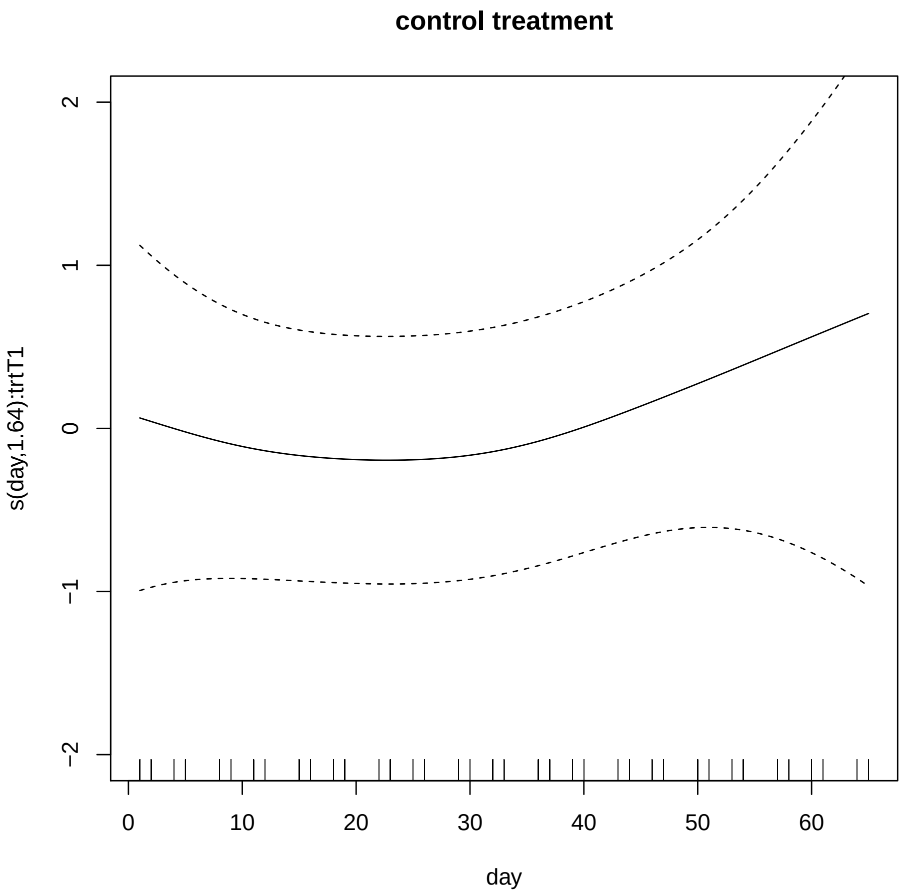
```
plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=1, ylim=c(-10, 25), main="body size effect")
```



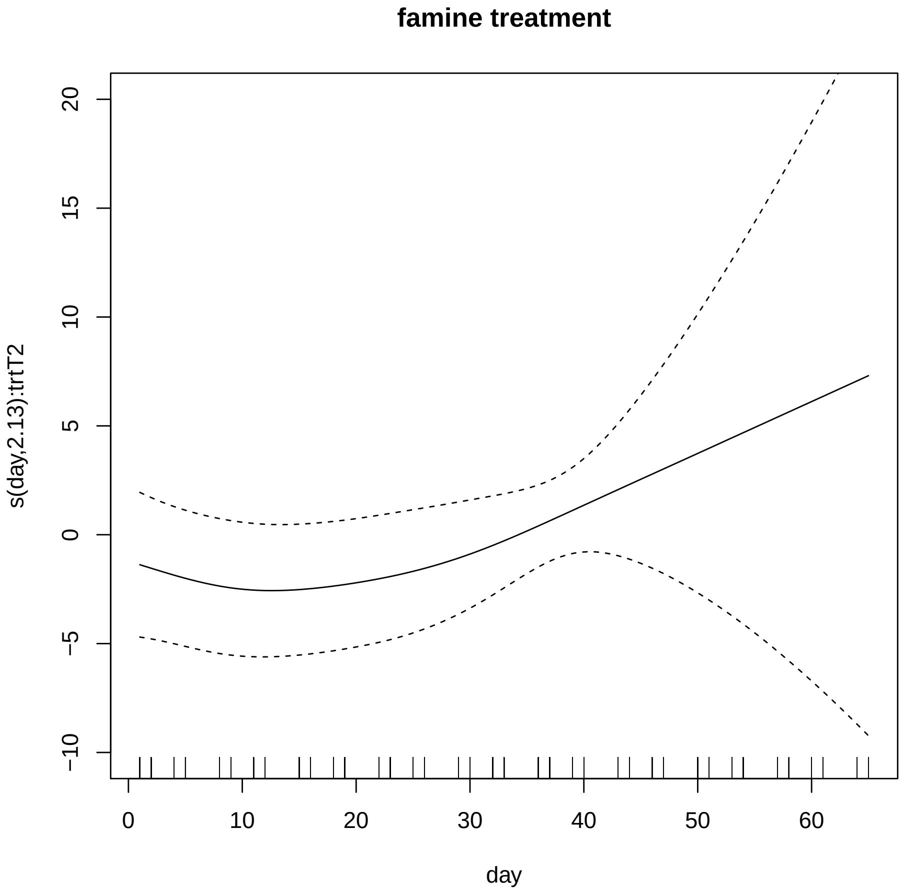
```
plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=2, main="current environment effect")
```



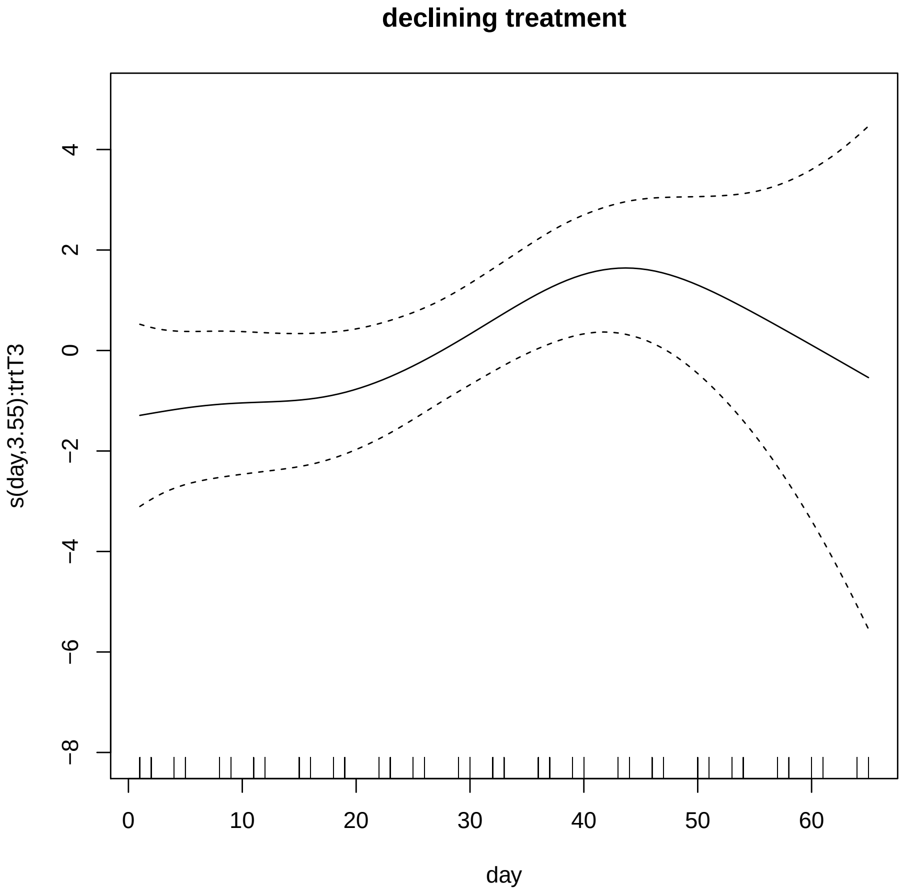
```
plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=3, ylim=c(-2, 2), main="control treatment")
```



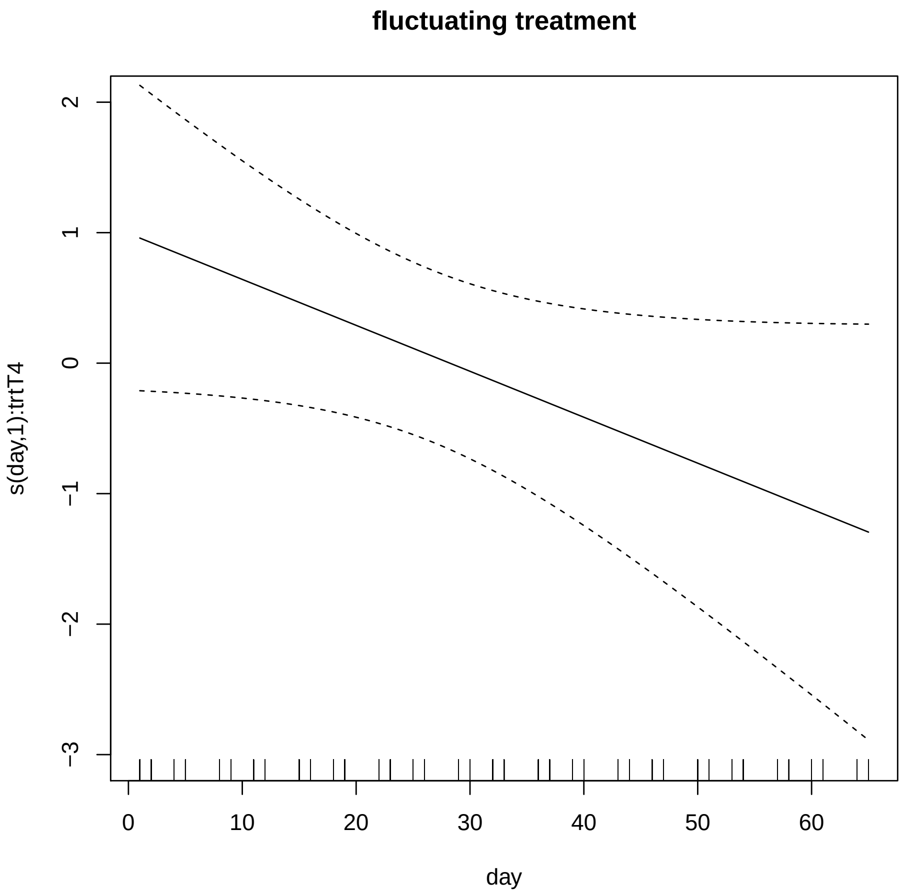
```r
plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=4, ylim=c(-10, 20), main="famine treatment")
```



```
plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=5, ylim=c(-8, 5), main="declining treatment")#marginally statistically signifi
```



```r
plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=6, ylim=c(-3, 2), main="fluctuating treatment")#marginally statistically signi
```



5 Probability of Reproducing

Remove ones that were dead at 24hrs. Use females only.

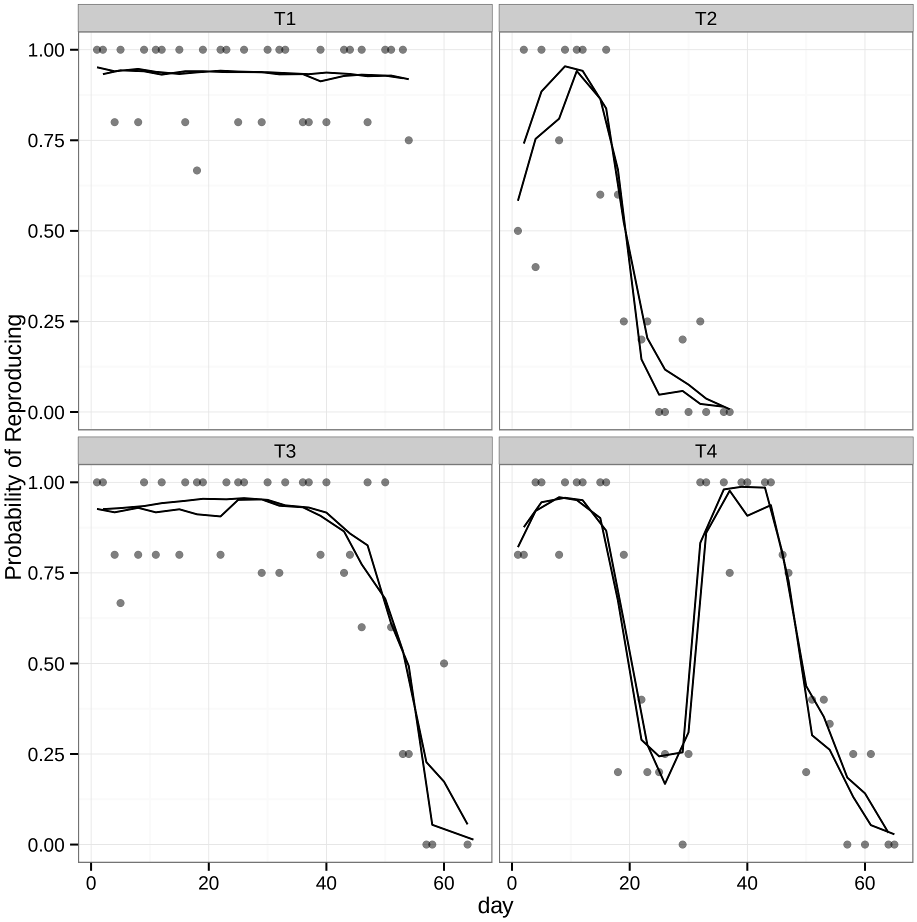
```
Indivtmp=subset(Indiv, stage=="female" & !is.na(s24))
```

```
temp=subset(Indivtmp, !is.na(l0.s*as.numeric(trt)*f24) & (s24==1))[
        ,c("f24","l0.s","trt","day","density.s", "supply.s","stage", "pop.ID")]
tempsum=ddply(temp, .(trt, day, pop.ID), summarize, f.sum=mean(f24>0))
```

```
fbm_full=gam(as.numeric(f24>0)~s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+trt+s(day,
```

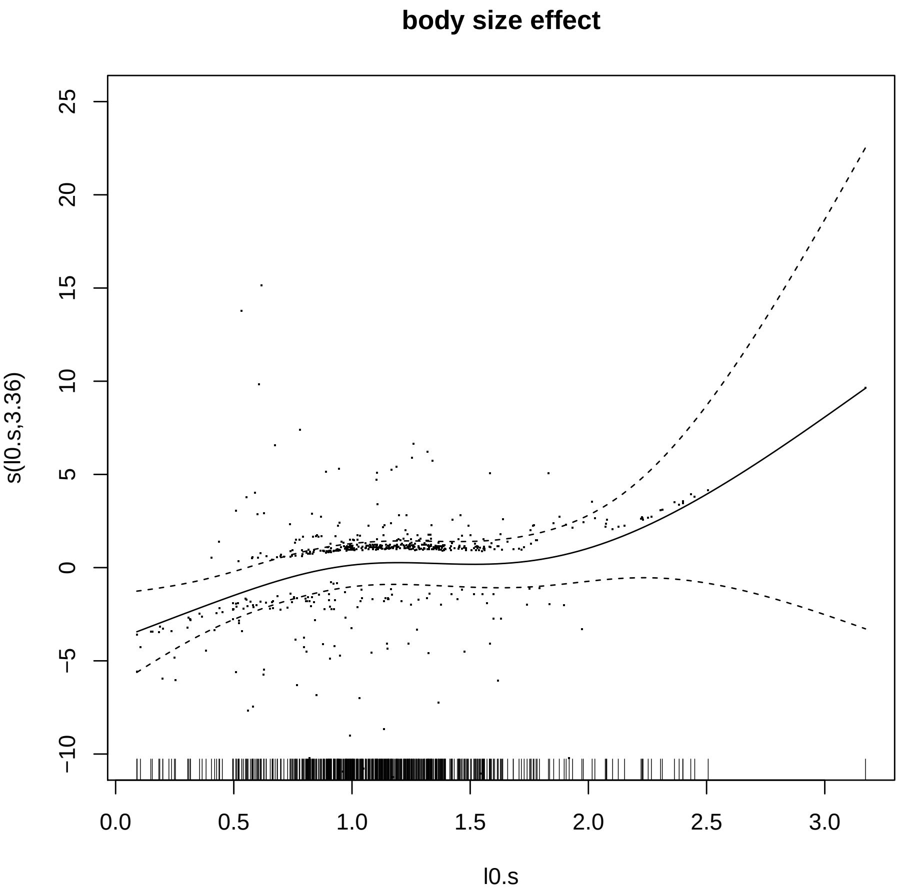
5.1 Predictions

```
fn=subset(newdata, stage == "female")
fn$f24pos=predict(fbm_full, fn, type="response")
p1=ggplot(fn, aes(x=day, y=f24pos))+
        geom_line(aes(group=pop.ID))+facet_wrap(~trt)+
        geom_point(data=tempsum, aes(x=day, y=f.sum), alpha=.5)
p1+ylab("Probability of Reproducing")+theme_bw()
```

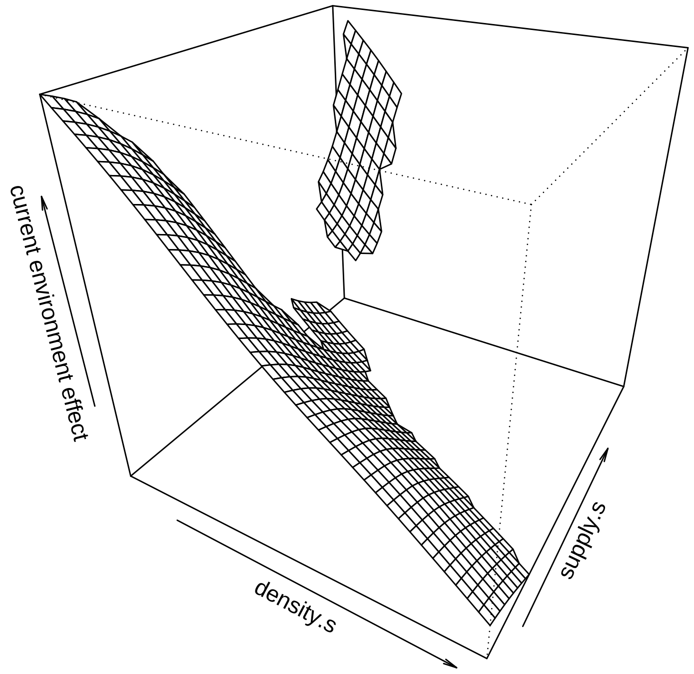


5.2 Explanatory Variable Effects

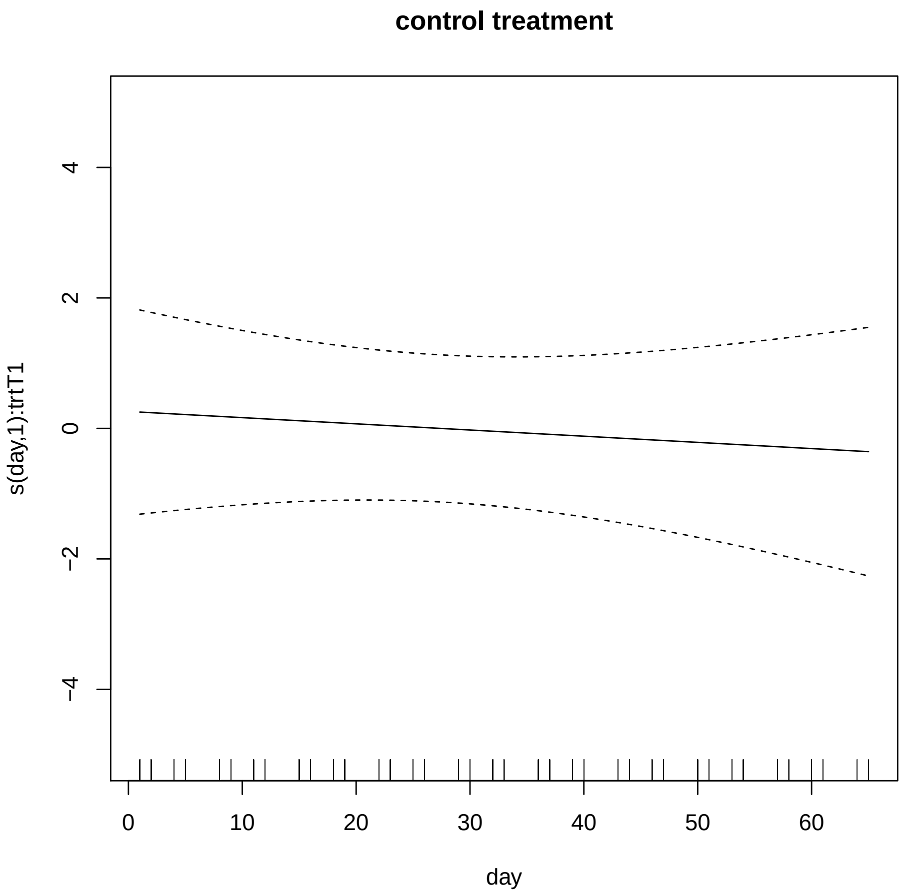
```
plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=1, ylim=c(-10, 25), main="body size effect")
```



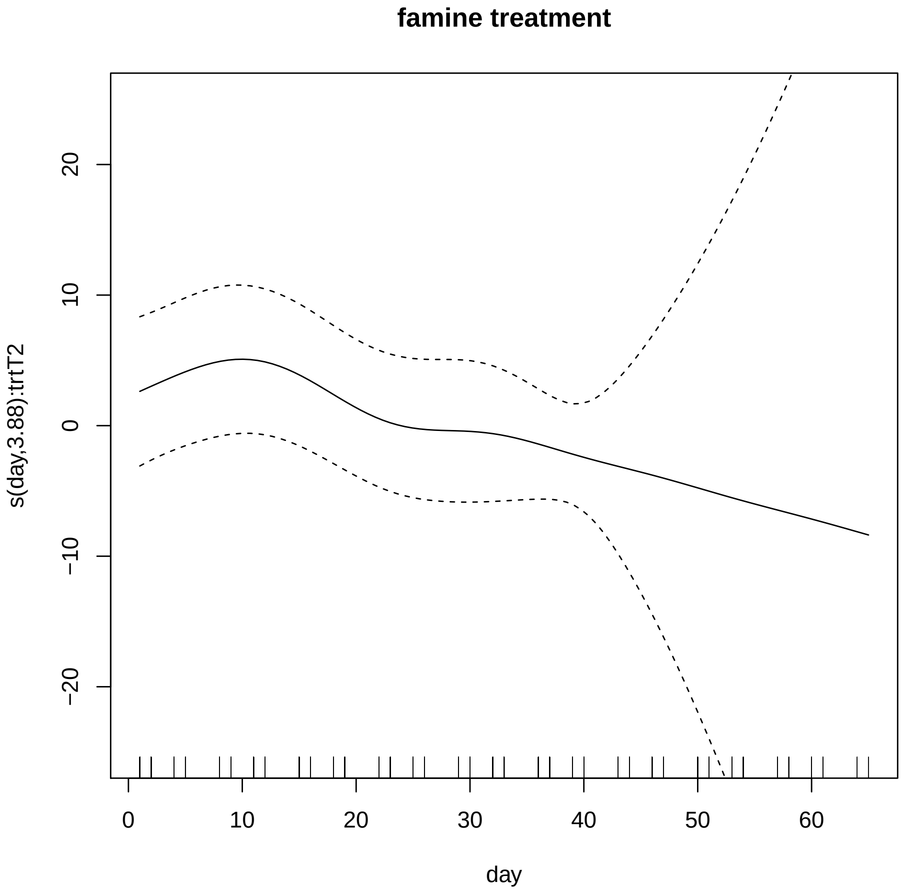
```
plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=2, main="current environment effect")
```



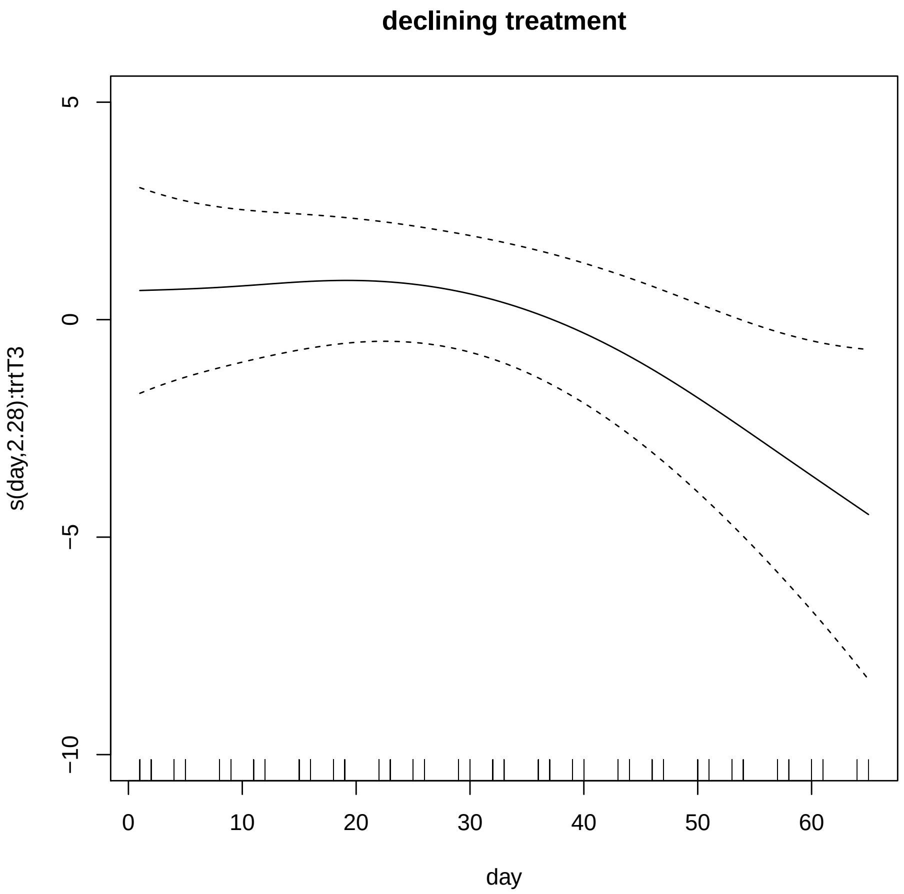
```
plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=3, ylim=c(-5, 5), main="control treatment")
```



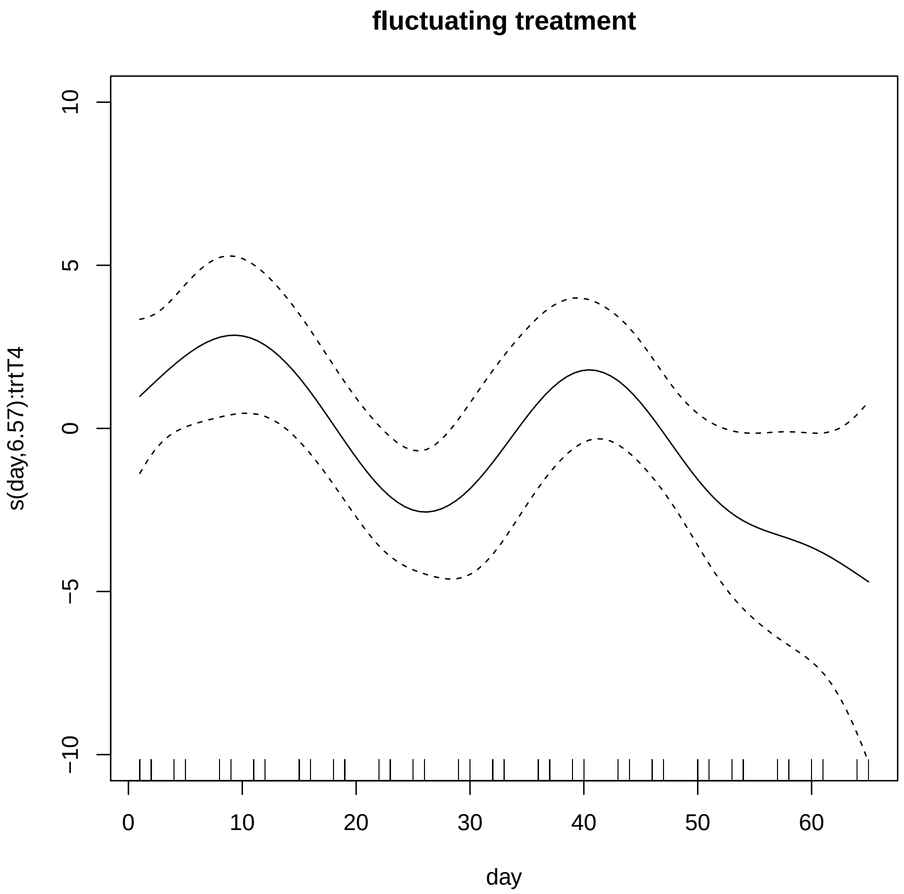
```
plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=4, ylim=c(-25, 25), main="famine treatment")
```



```
plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=5, ylim=c(-10, 5), main="declining treatment")#statistically significant
```



```
plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=6, ylim=c(-10, 10), main="fluctuating treatment")
```



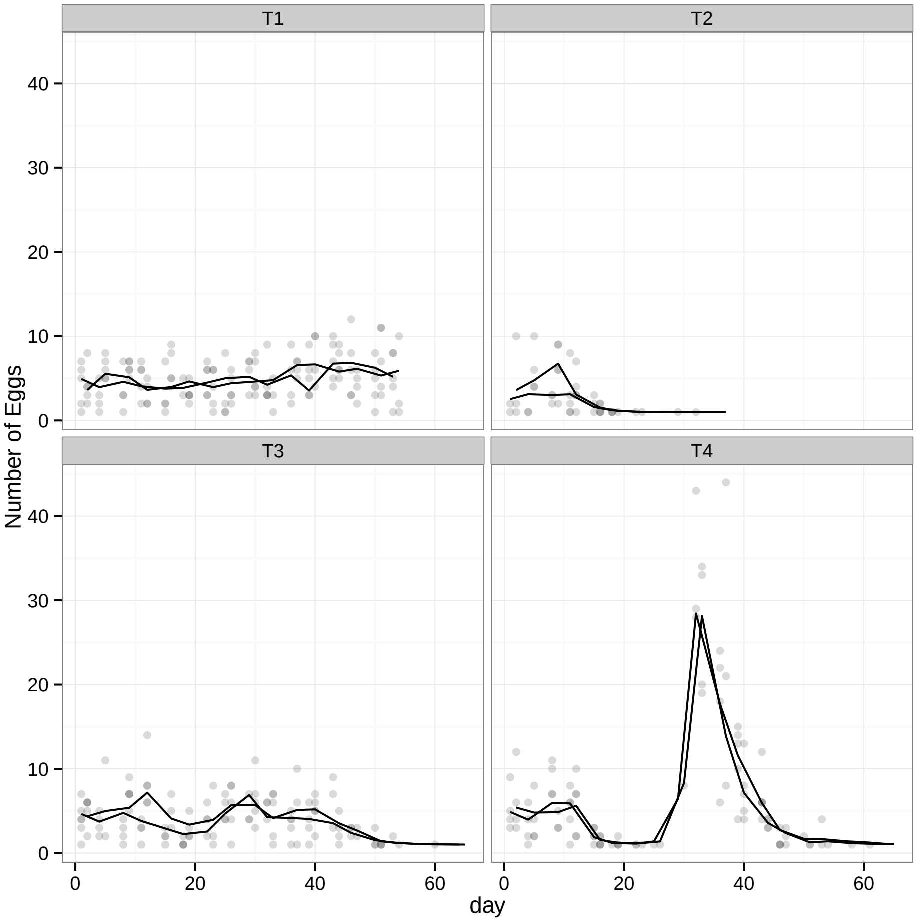
6 Egg Counts, Given Reproduction

```
temp=na.omit(subset(Indivtmp, (f24>0) & (s24==1))[
        ,c("f24","l0.s","trt","day","density.s", "supply.s","stage")])
```

```
fcm_full=gam(f24-1~s(l0.s, k=kl)+s(density.s, supply.s, k=ke)+
        trt+s(day, by=trt, k=kd),
        family=poisson, data=temp)
```

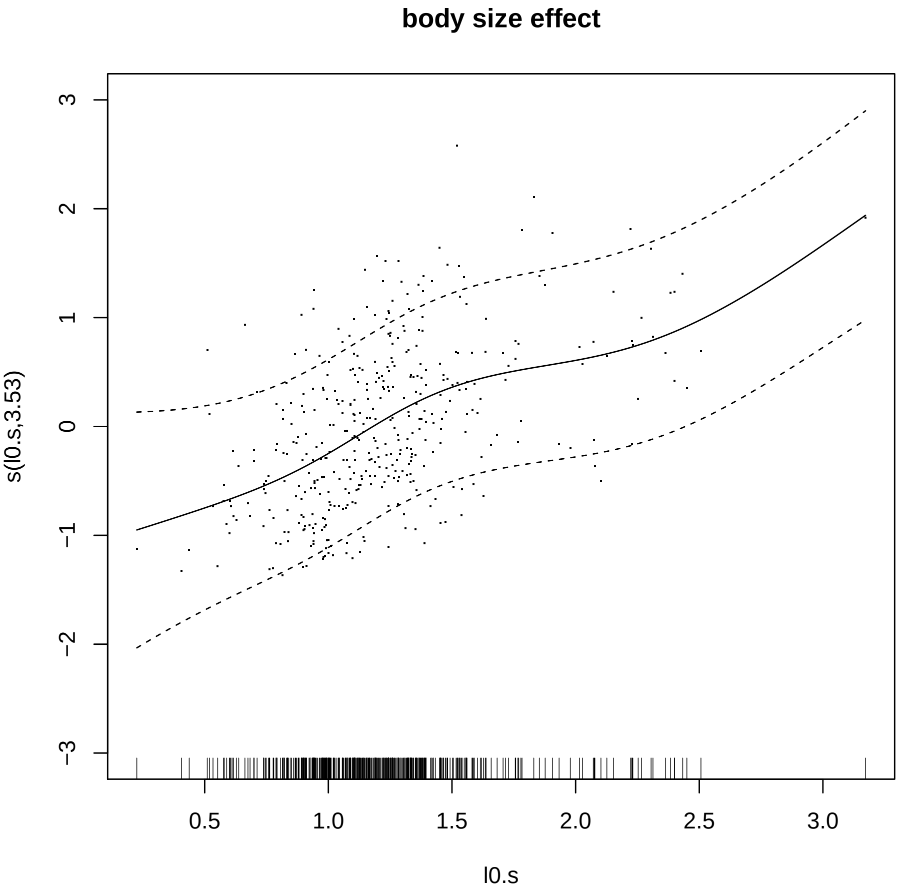
6.1 Predictions

```
fn$f24=predict(fcm_full, fn, type="response")+1
p1=ggplot(fn, aes(x=day, y=f24))+
        geom_line(aes(group=pop.ID))+facet_wrap(~trt)
p1+ylab("Number of Eggs")+geom_point(data=temp, alpha=.15)+theme_bw()
```

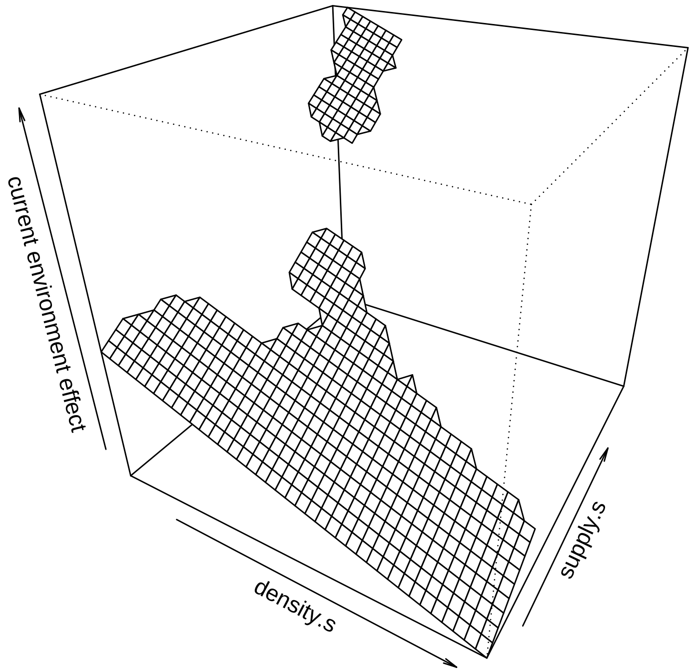


6.2 Explanatory Variable Effects

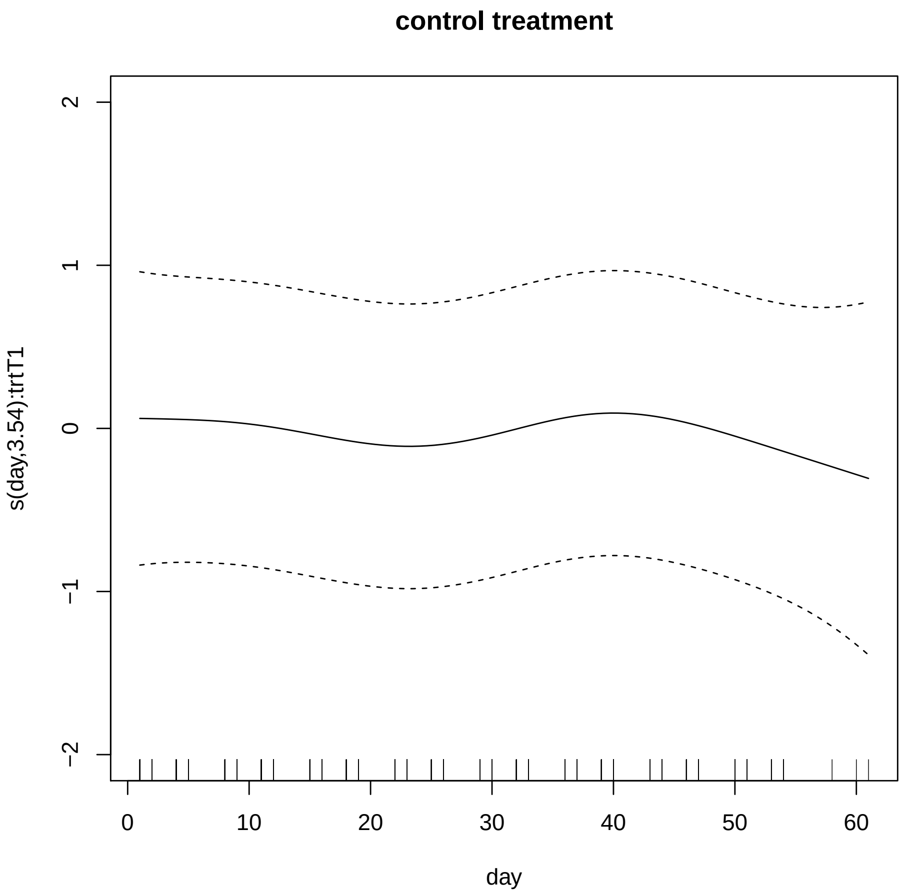
```
plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=1, ylim=c(-3, 3), main="body size effect")
```



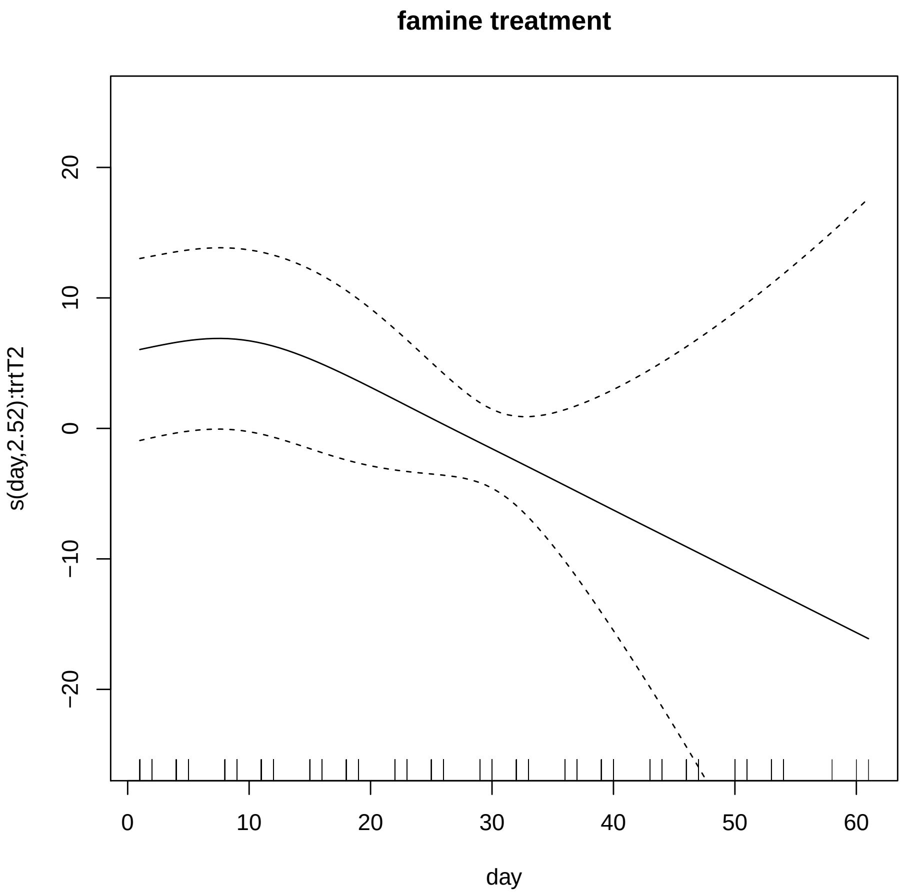
```
plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=2, main="current environment effect")
```



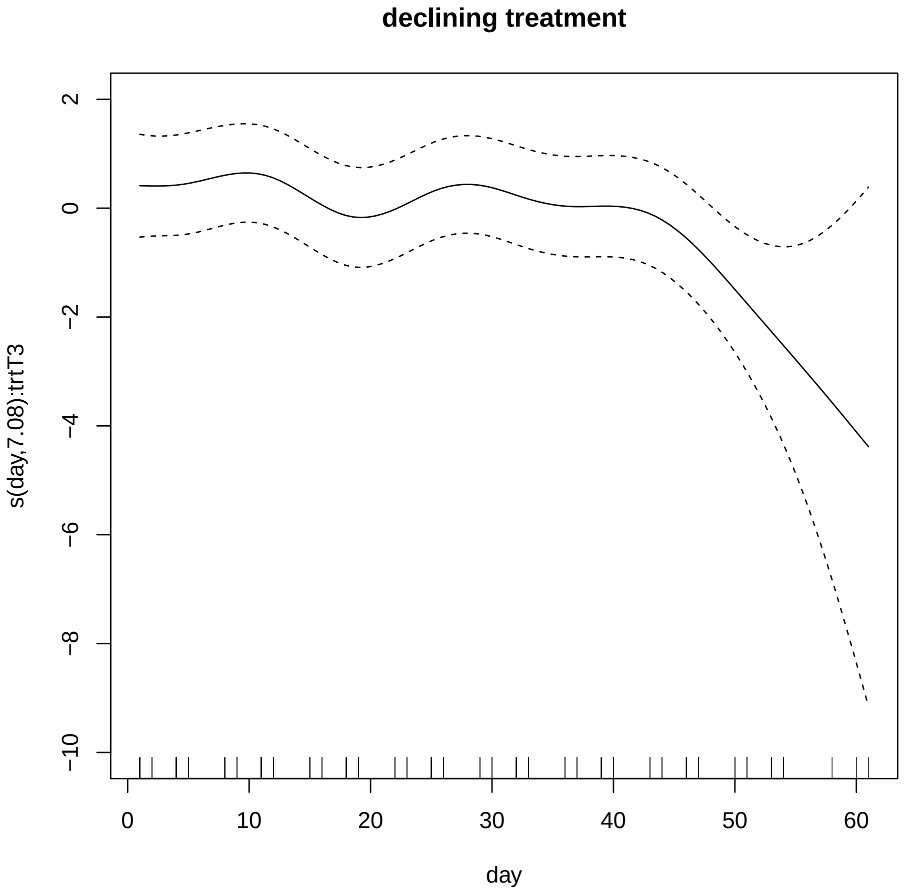
```
plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=3, ylim=c(-2, 2), main="control treatment")
```



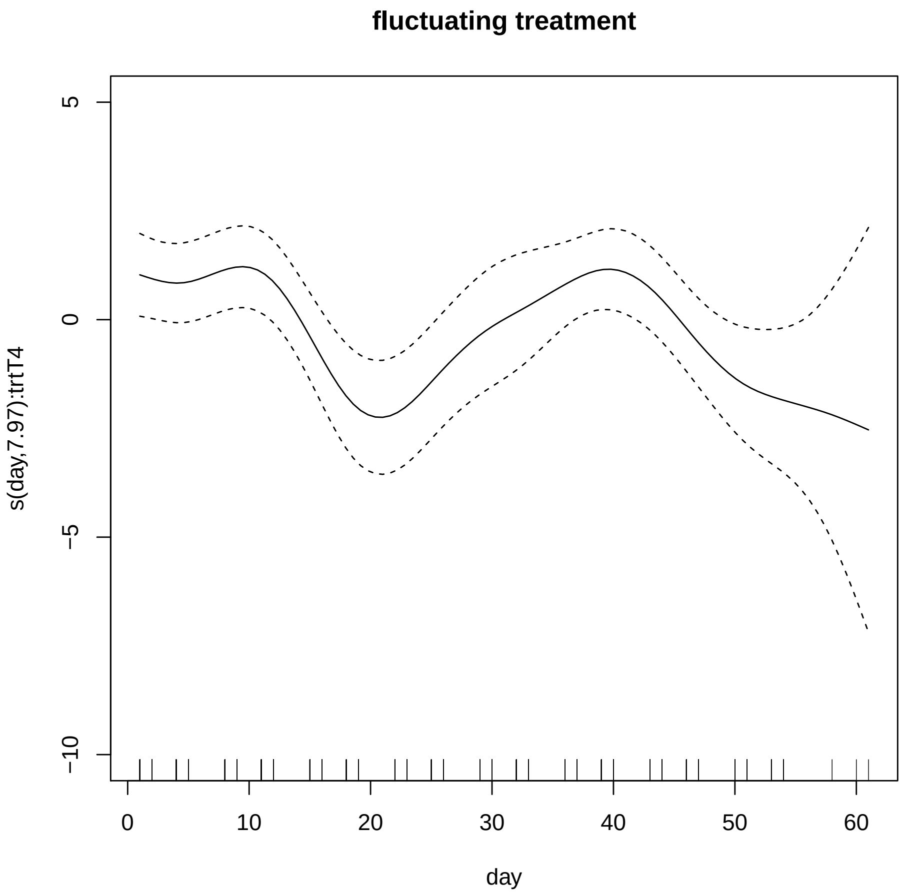
```r
plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=4, ylim=c(-25, 25), main="famine treatment")
```



```
plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=5, ylim=c(-10, 2), main="declining treatment")#statistically significant
```



```
plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=6, ylim=c(-10, 5), main="fluctuating treatment")#marginally statistically sign
```

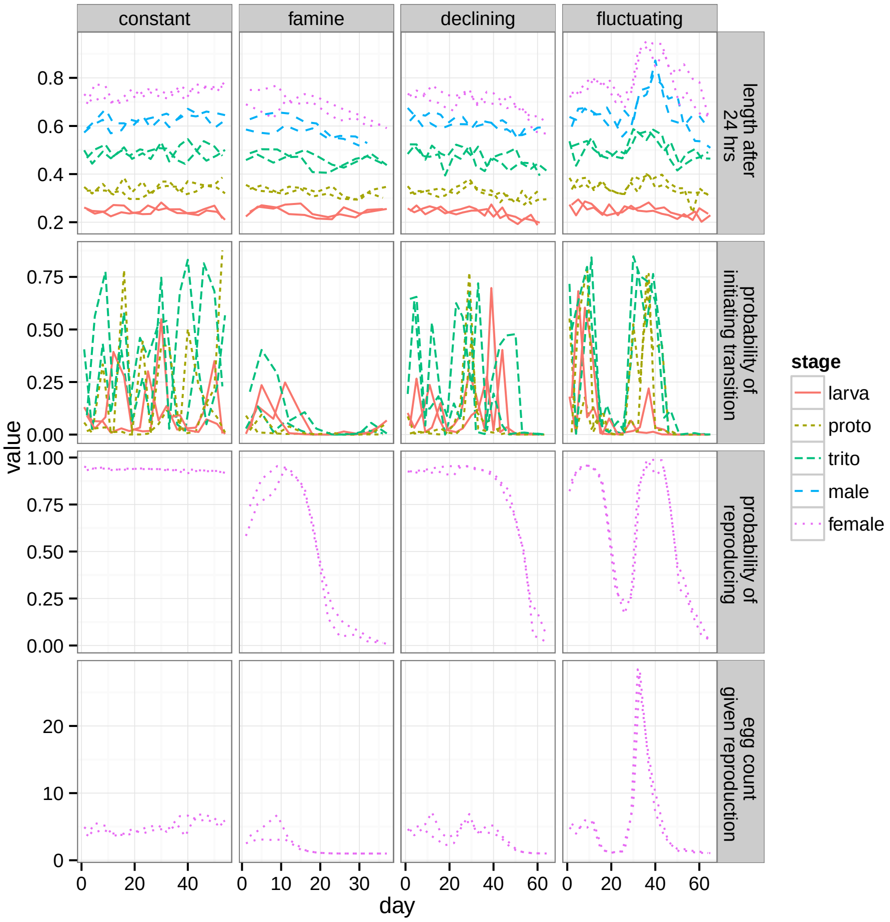


7 All Predictions Combined

```
dat0=merge(gn, tn, all=TRUE)
dat=merge(dat0, fn, all=TRUE)
dm=melt(dat, id.vars=1:8)
levels(dm$trt)=c("constant", "famine", "declining", "fluctuating")
tmplabel=function(variable, x)
{
        if (variable=="variable")
        {
                c("length after \n 24 hrs",
```

```
                "probability of \n initiating transition",
                "probability of \n reproducing",
                "egg count \n given reproduction")[x]
        }
        else
        {
                c("constant", "famine", "declining", "fluctuating")[x]
        }
}
p1=ggplot(dm, aes(x=day, y=value))+
                geom_line(aes(colour=stage,lty=stage, group=pop.ID:stage))+
                facet_grid(variable~trt, scale="free", labeller=tmplabel)+
                theme_bw()
p1

## Warning:  Removed 1 rows containing missing values (geom_path).
```



8 All past environment effects

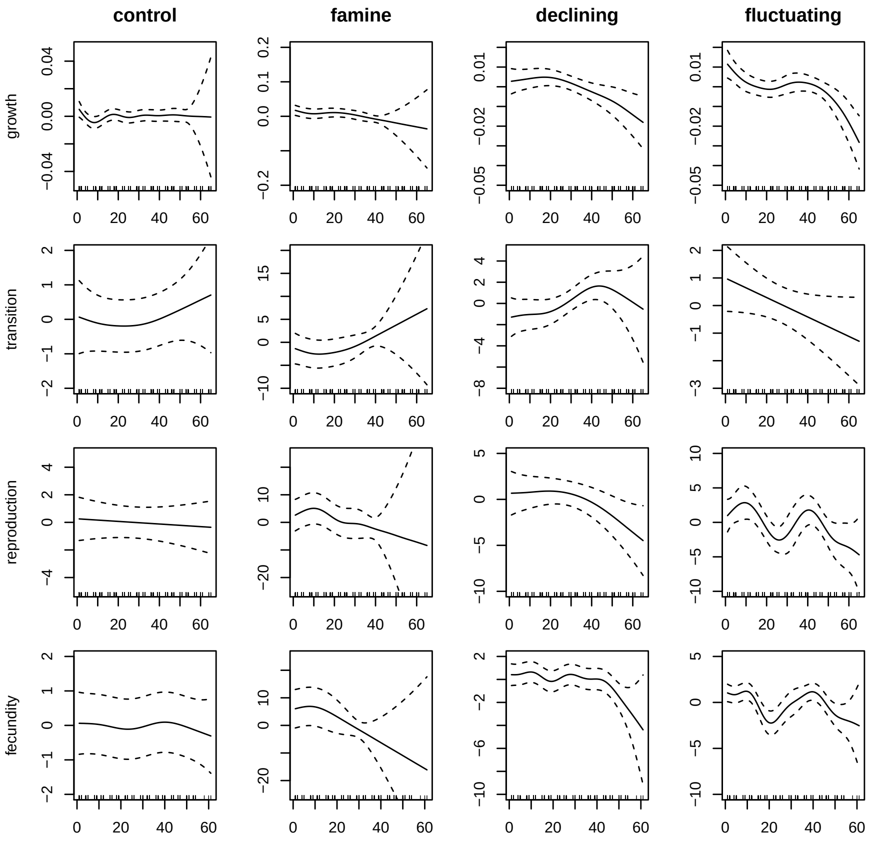
```
#pdf("Effects of past environments.pdf")
par(mfrow=c(4,4), mar=c(0,4,3,0.1), oma=c(4,5,4, 0.1) )
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=3, ylim=c(-0.05, 0.05), main="control", ylab="growth", xlab="")
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=4, ylim=c(-0.2, 0.2), main="famine", ylab="", xlab="")
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=5, ylim=c(-0.05, 0.02), main="declining", ylab="", xlab="")
plot(gm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
```

```
select=6, ylim=c(-0.05, 0.02), main="fluctuating", ylab="", xlab="") #statistically s

plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=3, ylim=c(-2, 2), ylab="transition", xlab="")
plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=4, ylim=c(-10, 20), ylab="", xlab="")
plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=5, ylim=c(-8, 5), ylab="", xlab="")#marginally statistically significant
plot(t24m_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=6, ylim=c(-3, 2), ylab="", xlab="")#marginally statistically significant

plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=3, ylim=c(-5, 5), ylab="reproduction", xlab="")
plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=4, ylim=c(-25, 25), ylab="", xlab="")
plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=5, ylim=c(-10, 5), ylab="", xlab="")#statistically significant
plot(fbm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=6, ylim=c(-10, 10), ylab="", xlab="")

plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=3, ylim=c(-2, 2), ylab="fecundity")
plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=4, ylim=c(-25, 25), ylab="")
plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=5, ylim=c(-10, 2), ylab="")#statistically significant
plot(fcm_full , pers=TRUE, residuals=TRUE, seWithMean=TRUE,
select=6, ylim=c(-10, 5), ylab="")#marginally statistically significant
```



```
#dev.off()
```

9 Version Info

```
sessionInfo()

## R version 3.2.1 (2015-06-18)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.10.4 (Yosemite)
##
```

```
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats4    stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
## [1] plyr_1.8.3    bbmle_1.0.17  mgcv_1.8-6    nlme_3.1-120  ggplot2_1.0.1
## [6] reshape_0.8.5 knitr_1.11
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.0       magrittr_1.5      MASS_7.3-40
##  [4] munsell_0.4.2     colorspace_1.2-6  lattice_0.20-31
##  [7] stringr_1.0.0     highr_0.5         tools_3.2.1
## [10] grid_3.2.1        gtable_0.1.2      digest_0.6.8
## [13] numDeriv_2014.2-1 Matrix_1.2-1      reshape2_1.4.1
## [16] formatR_1.2       evaluate_0.7.2    labeling_0.3
## [19] stringi_0.5-5     scales_0.2.5      proto_0.3-10
```